



262

STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 202292

TO: Jane Zara
Location: REM-2A59&2C18
Art Unit: 1635
Monday, October 02, 2006
Case Serial Number: 10/642946

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1a69
Phone: 571-272-2518

BOB
barbara.obryen@uspto.gov

Search Notes

Hi Jane,

For the score over length search, neither fragment had hits in the EST database, so no EST results are included with the S/L output.

Barb

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9-981

Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: JANE ZARA Examiner #: 77572 Date: 9/19/06
 Art Unit: 1635 Phone Number: 2-0765 Serial Number: 10/642,946
 Location (Bldg/Room#): 2A59 (Mailbox #): 2C18 Results Format Preferred (circle): PAPER DISK

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: ISOLATED Genomic polynuc's ... chrom 7
 Inventors (please provide full names): JW RYAN

Earliest Priority Date: 028800 9-24-01 CYRE

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

- ① Please Search ~~Seq~~ Seq ID No: 3
 Nucleic Acid DATA BASES only
~~no size limits~~
 NO size limits
- ② Please Search Seq ID No: 6
 Between nucleotides 1967-2208
 Between nucleotides 3002-3237
~~between 40-60~~
 Length Limit To 50 NTS.
 seq 3-11500A
 6-45980NA
 Score over Length For ② only
 70% Homology size 10-241 nt

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 30, 2006, 23:28:37 ; Search time 13965 Seconds

(without alignments)
7953.933 Million cell updates/sec

Title: US-10-642-946-3

Perfect score: 6272
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Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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Database :

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8: gb_sy:.*
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10: gb_vl:.*
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13: gb_in:.*
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15: gb_ba:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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6	6246	99.6	3913	5	CQ116956	CQ116956 Sequence
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10	5054	80.6	3728	2	E07353	E07353 cdna encodi
11	5054	80.6	3728	2	I15213	I15213 Sequence 1
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13	4771	76.1	153303	5	AC006454	AC006454 Homo sapi
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15	4003	63.8	2759	14	AF043942	AF043942 Bos tauru
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18	3621	57.7	22245	12	AC095141	AC095141 Rattus no
19	3598	57.4	2571	2	CQ850412	CQ850412 Sequence
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38	2053.5	32.7	2430	6	BC021444	BC021444 Mus muscu
39	2015	32.1	2392	2	AX254979	AX254979 Sequence
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41	1811.5	28.9	125384	12	AC135546	AC135546 Tetradon
42	1767.5	28.2	2379	2	CS208029	CS208029 Mus muscu
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ALIGNMENTS

RESULT 1
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LOCUS AR240603 3935 bp DNA
DEFINITION Sequence 1 from patent US 6468766.
ACCESSION AR240603
VERSION AR240603.1 GI:27285699
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3935)
AUTHORS Lee,M.-E., Layne,M.D. and Yet,S.-F.
TITLE Aortic carboxypeptidase-like polypeptide
JOURNAL Patent: US 6468766-A 1 22-OCT-2002;
President and Fellows of Harvard College; Cambridge, MA
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source location/Qualifiers
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Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0

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Db	260 TTCCTGTCAAGACTGAGACCTGAGCCCGGGAGAGACGATGAGAGCCCGCGCTCTCC	319	
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 DEFINITION Sequence 128 from Patent WO02081745.
 ACCESSION AX578006
 VERSION AX578006.1 GI:27647214
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 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE
 1 Garcia,T., Roman,R., Baron,R., Call,K., Theilhaber,J.,
 AUTHORS Connolly,T., Jackson,A., Bushnell,S.E. and Rawadi,G.
 TITLE Genes involved in osteogenesis, and methods of use
 JOURNAL Patent: WO 02081745-A 128 17-OCT-2002;
 Aventis Pharma S.A. (FR)
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 Best Local Similarity: 100.0% Mismatches: 0
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Db AAGGAGAGAGCCCAAGGCCACCAAGAAAGCCCAAGAGAGCCCACTTAAGGCCACCAAG 559
QY LysProLysGluLysProProLysAlaThrLysLysProLysGluLysProProLysAla 160
Db AAGCCCAAGAGAGAGAGCCCAAGGCCACCAAGAAAGCCCAAGAGAGAGCCCAAGGCC 619
QY ThrLysLysProProSerGlyLysArgProProIleLeuAlaProSerGluThrLeuGlu 180
Db ACCAAGAAAGCCCCGCTCAGAGGAAGAGGCCCCCATTTGCTCTCCCTCAGAAACCTTGAG 679
QY TrpProLeuProProProSerProGlyProGluLysLeuProGluGluGlyAla 200
Db TGGCCACTGTCCCAAGCCCCCAGCCCTGGGCCCGAGAGACTACCCCAAGAGAGAGGGCG 739
QY ProLeuSerAsnAsnTrpGluAsnProGlyGluThrIleValGluAlaGluGluHis 220
Db CCCCTCTCAATTAATCTGGCAAACTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 799
QY GlnProGluProGluGluGluThrGluGluGlnProThrLeuAspTyrAsnAspGluIleGlu 240
Db CAGCTCTGAGCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 859
QY ArgGluAspTyrGluAspPheGluTyrIleArgArgGluLysGluLysProArgProPro 260
Db AAGGAGAGACTATGAGAGACTTTGATGATCATTCGCGCCGAGAGAGAGAGAGAGAGAGAG 919
QY SerArgArgArgArgProGluLysArgValTrpProGluProProGluGluLysAlaProAla 280
Db AACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 979
QY ProAlaProGluLysArgIleGluProProValLysProLeuLeuProProLeuProPro 300
Db CCAAGCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1039
QY AspTyrGlyAspGlyTyrValIleProAsnTyrAspAspMetAspTyrTyrPheGlyPro 320
Db GACTATGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1099
QY ProProProGluLysProAsnAlaGluArgGluLysAspGluLysGluLysGluLysGlu 340
Db CTTCCGCCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1159
QY LysProLysLysGluAspSerSerProLysGluGluLysArgIleAspIleValGluLys 360
Db AAACCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1219
QY GlyLysAspHisLysGluProArgLysGlyGluLysGluLysGluLysGluLysGluLys 380
Db GGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1279
QY GlnLysValLysCysProProIleGlyMetGluSerHisArgIleGluAsnAsnGluIle 400
Db GAGAAAGTAAAGTGTCCCTCCCTTTGGAGTGAAGTCAACCGTATTGAGAGAGAGAGAG 1339
QY ArgAlaSerSerMetLeuArgHisGlyLeuGlyAlaGluArgIleArgLeuAsnMetGlu 420
Db CGAAGCTCTCCATGTGTGGCCACGGCTGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1399
QY ThrGlyValThrGluAspAspTyrTyrAspGlyAlaTrpCysAlaGluAsnAspAlaArg 440
Db ACCGGTGCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1459
QY ThrGlnTrpIleGluValAspThrArgArgThrThrArgPheThrGlyValIleThrGln 460
Db ACCCAAGTGAATGAGGTGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1519
QY GlyArgAspSerSerIleHisAspAspPheValThrThrPhePheValGlyPheSerAsn 480
1520 GGCAAGAGACTCCAGACTCATGACGATTTTGTGACCACTTTCTTGTTGGCTTCAGCAAT 1579
QY AspSerGlnThrTrpValMetTyrThrAsnGlyLysGluLysMetThrPheHisGlyAsn 500
Db GACAGCCAGAGATGGGTATATACCAACGGCTATGAGAAATGACCTTTCATATGGAGAC 1639
QY ValAspLysAspThrProValLeuSerGluLeuProGluProValAlaIleArgPheIle 520
Db GTGACAAAGAGACACCCGCTGAGTGAAGTCCCAAGAGCCGGTGTGGCTGTTTCAATC 1699
QY ArgIleTyrProLeuThrTrpAsnGlySerLeuCysMetArgLeuValLeuGluCys 540
Db CGCATCTACCACTACACTGGAATGGAGCTGTGTGACAGCCCTGAGAGGTGTGTGGGTGTC 1759
QY SerValAlaProValTyrSerTyrTyrValAlaGluAsnGluValAlaThrAspAspLeu 560
Db TCTGTGGCCCTGTCTTACAGCTACTACGACAGAAATGAGGTGGTGGCCAGATACCTG 1819
QY AspPheArgHisHisSerTyrLysAspMetArgGluLeuMetLysValIleAsnGluLys 580
Db GATTTCCGGACACACAGCTACAGAGACATGGCCAGCTCATGAAAGTGTGTGAAGAGAG 1879
QY CysProThrIleThrArgThrTyrSerLeuGlyLysSerSerArgGlyLeuLysIleTyr 600
Db TGCCCAACCATCACCCGCACTTACAGCTGGGCAAGAGCTGACAGAGGCTCTCAAGATCTAT 1939
QY AlaMetGluIleSerAspAsnProGlyGluHisGluLeuGlyGluProGluPheArgTyr 620
Db GCCATGAGATCTCAGACAAACCTGGGAGAGATGAACTGGGGAGAGCCGAGTTCCGCTAC 1999
QY ThrAlaGlyIleHisGlyAsnGluValLeuGlyArgGluLeuLeuLeuLeuMetGlu 640
Db ACTGTGGAGATCATGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2059
QY TyrLeuCysArgGluTyrArgAspGlyAsnProArgValArgSerLeuValGlnAspThr 660
Db TACCTGTCCGAGATCCGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2119
QY ArgIleHisLeuValProSerLeuAsnProAspGlyTyrGluValAlaAlaGluMetGly 680
Db CGCATTCACCTGTGTGCTCTCACTGAAACCTGATGGCTACAGAGTGGACGAGAGATGGCC 2179
QY SerGluPheGlyAsnTrpAlaLeuGlyLeuTrpThrGluGluGlyPheAspIlePheGlu 700
Db TCAAGTGTGGAGATGGAGCGCTGGGAGCTGGAGACTGAGAGAGAGAGAGAGAGAGAGAG 2239
QY AspPheProAspLeuAsnSerValLeuTrpGlyAlaGluGluArgLysTrpValProTyr 720
Db GATTTCCCGGATCTCAACTGTGTCTGTGGGAGCTGAGAGAGAGAGAGAGAGAGAGAGAG 2299
QY ArgValProAsnAsnAsnLeuProIleProGluArgTyrLeuSerProAspAlaThrVal 740
Db CGGGTCCCAACATTAATCTGTCCATCTCTGAAACCTTACCTTTCCGAGATCCACGGTAT 2359
QY AsnLeuAsnGlyGlyGluArgLeuValSerTyrProTyrAspMetAlaArgThrProThr 780
Db TCCAGAGAGAGTCCGGGCAATCATTCCTGAGATGAGAGAGAGAGAGAGAGAGAGAGAG 2419
QY SerThrGluValArgAlaIleIleAlaTrpMetGluLysAsnProPheValLeuGlyAla 760
Db AATCTGAACCGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2479
QY GlnGluGluLeuLeuAlaAlaIleAlaMetAlaAlaIleValGluAspGluAspGluVal 800
Db CAGGAGACAGCTGTGTGGCCAGCCATGGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2539
QY SerGluAlaGluGluThrProAspHisAlaIlePheArgTrpLeuAlaIleSerPheAla 820
Db TCCGAGGCCCAGAGAGATCCAGACAGAGCATCTCCGGTGGCTTGCCATCTCCTTCCGCC 2599
QY SerAlaHisLeuThrLeuThrGluProTyrArgGlyGlyCysGluAlaGlnAspTyrThr 840
Db TCCGACACATTCACCTTGAACGAGGCTTACCGGAGAGGCTGCCAAGGCCAGAGACTACCC 2659
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QY	841	GLYGLYMEGLYIILEVALASNGIYLAIVETRPANPROARGTGHLYTHRIILEASNP	860
DB	2660	GGCGGCATGGGCATGTCTCAACGGGGCCAGTGGAAACCCCGGACGGGACTACATGAC	2719
QY	861	PHESERTYLEUHIETHIASNCSYLEUGIULEUSERPHEITYLEUGLYCYSENPILYSPHE	880
DB	2720	TTCACTGTAACCTGCATACCAACCTGGCGTCTCTCTTACTACTGGGCTGTACAAGTTC	2779
QY	881	PROHISGLUSERGILEUPROARGIUTRPGLUANASNPYGLUALALEULEUTHRPH	900
DB	2780	CCTCATGAGAGTGAACCTGCCCCGACGTGGGAGAACACAGAGAGCGCTGCTCACTTC	2833
QY	901	METGUGIINVAIHIAARGGLYILEYSGIYVAIVATTPRPGIUNGIGLYILEPROILE	920
DB	2840	ATGGAGCCAGGTGACCCGGCGACTTAAAGGGGGTGGTGAAGAGACAGACAGACATCCCAAT	2899
QY	921	ALAAENALATHRIIESERVALSERGIYILEASNISGLIYVALYESTHRALASERGIYGLY	940
DB	2900	GCCAAAGCCCAACCATCTGTGTGATGGCATTAATCAAGGGGTGAACACAGCCAGTGTGTGT	2955
QY	941	ASPRTYTRPAIGIILELEUENPPOGIYGLUTYTRATGVALTHRALAHISGLIYTYR	960
DB	2960	GATTACTGGCGAATCTTGAAACCCGGGTGTGATCCCGACGACGCCACGGAGGGCTTAC	3019
QY	961	THRPROSERIALALYETHRCYASNPVALASPRTYAPPIISGLIYALATHGILCYSENPHE	980
DB	3020	ACCCGAGCGCCAAACCTGCATGTGACTATGACATGGGGCCACTCACTGACAACTTC	3079
QY	981	ILELEUALAARGSERASNPTRPYASARGIILEARGIUILEMEVALAMEASNPGLYASNPARG	1000
DB	3080	ATCTGGCTCGCTCCAACTGGAAAGGCATCCGGAGATCATGGCCATGAACGGAAACCGG	3139
QY	1001	PROILEPPOHISILEASPPROSERARGPONECTHRPROGLINGIARGYLEUGINGIN	1020
DB	3140	CCTATCCCAACATATGACCCCACTGGCGCTTATGACCCCCCAACAGCGACGCTGCAGCAG	3199
QY	1021	ARGARGLEUGINHIARGLLEUARYGLEUARYGLAIGIMETARGYLEUARYARGLEUASNPILA	1040
DB	3200	CGAGCCCTACACACACCCGCTCGGCTTGGGGACAGATGGCGCTCGGCGCTCAACGCC	3255
QY	1041	THRTHRTHRILEUGIYPROHIETHRVALEPROPTHRILEUPROPROIALAPROALATHRTHR	1060
DB	3260	ACCACCAACCTTAGGGCCCCCAACCTGTGCTCCACGCTGGCCCCCTGGCCACCAAC	3319
QY	1061	LEUSERTHRTHRIILEGIUPROTPRGLIYLEUILEPPOCTHRTHRALISGLIYTRPGIUGIU	1080
DB	3320	CTGAGCACTACCAATGAGCCCTCGGGGCTCTACATCCGCCAACACACCGCTGGCGGAGAG	3379
QY	1081	SERGIUTRGIUTHRITYRTHRGIVAIYVALITHRGIUPHEGIYTHGIUVAIGIUPROGIU	1100
DB	3380	TCCGAGACTGAGACCTTACACAGAGGTGTGACAGAGTTTGGGACCCGAGGTGAGCCCGAG	3439
QY	1101	PHEGIYTHRIYVAIGIUPROGIUPHEGIUTHRGINLEUGIUPROGIUPHEGIUTHRGIN	1120
DB	3440	TTTGGGACCAAGGTGAGCCCGAGTTTGAGACCAGTTGGAGCCGTGAAGTTCGAGCCAG	3499
QY	1121	LEUGIUPROGIUPHEGIUGIUGIUGIUGIUGIUGIUGIUGIUGIUGIUGIUGIUGIUGIUGI	1140
DB	3500	CTGGAAACCGGAGTTTGAAGAAAGAGAGGAGGAGAAAGAGAGAGATATGACCACTGGC	3559
QY	1141	GLINALAPHEPROPHETHRTHRVAGIUGIUTHRTYTRTHRVALASNPHEGLIYASPHE	1158
DB	3560	CAGGACTTCCCTTCAACAACAGTAGACACTTACACAGTGAACCTTTGGGGGACTTC	3613

[illegible]

Db 260 TTCCTGTACAGCTAGAACCTGAGCCCGGGAGAGACGAGCTGAGGCGCCGCGCTCCC 319
Qy 61 GIUProThrProArgValArgIysAlaGlnIleGlyLysProGlyLysArgProGly 80
Db 320 GAGCCACCCCGCGGTCGGAAAAAGCCAGCGGGGGGCAAGCCAGGAGGCGGCCAGG 379
Qy 81 ThrAlaIleGluValProProGlyLysThrLysAspGlyLysLysGlyLysLysAsp 100
Db 380 ACGCGCGGAGAGTGCCTCCGGAAAAAGCCAAAGACAAAGGAGAAAGGCAAGAAAGAC 439
Qy 101 LysGlyProLysValProLysGlySerLeuGlyLysSerProArgProProLysGly 120
Db 440 AAAGGCCCCAAGGTGCCCCAAGAGTCTTGAGGGGTCTCCCAAGCGCGCCAAAGAGGG 499
Qy 121 LysGlyLysProProLysAlaThrLysLysProLysGlyLysProProLysAlaThrLys 140
Db 500 AAGGAAAGACCAACCAAGGCCAACCAAGAGCCCAAGAGAGCACTTAAGGCCCAAG 559
Qy 141 LysProLysGlyLysProProLysAlaThrLysLysProLysGlyLysProProLysAla 160
Db 560 AAGCCCAAGAGAGGCCCAACCAAGGCCCAACCAAGAGGCCCAACCAAGGCC 619
Qy 161 ThrLysLysProProSerGlyLysArgProProIleLeuAlaProSerGlyThrLeuGln 180
Db 620 ACCAAGAGCCCCCTCAGGGAAGAGCCCCCACTTGCTGCTCCCTCAGAAACCTTGAG 679
Qy 181 ThrProLeuProProProProSerProGlyProGlyLysLeuProGlnGlyVal 200
Db 680 TGGCCACTGCCCCCAGCCCGAGCTGCGCCGAGAGCTACCCAGAGAGGAGGGGG 739
Qy 201 ProLeuSerAspAsnThrProGlnAsnProGlyLysGlyLysThrIleValGlnIleGln 220
Db 740 CCCCTCTCAATTAACCTGCGAGATCCAGAGAGAGAACCTATGAGGCCACAGAGCAC 799
Qy 221 GlnProGlyLysProGlyLysGlyLysGlyLysProThrLeuAspTyrAsnAspGlnIleGln 240
Db 800 CAGCTGAGCGCGAGAGAGAGACCGAGCAACCCAGCTGAGCTAATGACGATCGAG 859
Qy 241 ArgGlyLysAspTyrGlyLysAspPheGlyLysIleArgArgGlnLysGlnProArgProPro 260
Db 860 AAGGAGAGACTATAGACTTTGAGTACATTCGCGCAGAGCAACCCAGGCCACCCCA 919
Qy 261 SerArgArgArgArgProGlyLysValIleThrProGlyLysProGlyLysLysAlaProAla 280
Db 920 AGAGAAAGAGAGGCCCGAGCGGCTCTGCGCAGAGCCCCCTAGAGAGAGGCCCGGCC 979
Qy 281 ProAlaProGlyLysGlyLysGlyLysProProValLysProLeuLeuProProLeuProPro 300
Db 980 CCAAGCCCCGAGAGAGATGAGCTCTGCTGAGAGCTCTGCTGCCCCCGCTGCCCT 1039
Qy 301 AspTyrGlyLysAspGlyLysValIleProAsnTyrAspAspMetAspTyrTyrPheGlyPro 320
Db 1040 GACTATGAGTATGATGATACGTGATCCCACTACGATGACATGATCTTATCTTTGGGCT 1099
Qy 321 ProProProGlyLysProAspAlaGlyLysGlnThrAspGlyLysLysGlyLysLeuLys 340
Db 1100 CCTCCGCCCGAGAGCCGAGTGTGAGCGCCAGACGAGAGAGAGAGAGAGCTGAG 1159
Qy 341 LysProLysLysGlyLysAspSerSerProLysGlyLysGlyLysThrAspLysTrpAlaGlyLys 360
Db 1160 AAACCCAAAG 1219
Qy 361 GlyLysAspHisLysGlyLysProArgLysGlyLysGlyLysGlyLysGlyLysGlyLys 380
Db 1220 GGGAAAGACCAAAAGAGCCCGAAAGGGGAGAGAGTGGAGAGAGAGAGAGAGCTAG 1279
Qy 381 GlyLysValLysCysProProIleGlyMetGlySerHisArgIleGlyLysAspGlnIle 400
Db 1280 GAGAAAGTCAAGTCTCCCTCCCTGAGTGGATGAGTCAACCTGATTTAGAGACCAAGATC 1339
Qy 401 ArgAlaSerSerMetLeuArgHisGlyLysGlyLysGlyLysGlyLysGlyLysGlyLys 420
Db 1340 CGAGCTCTCTCATGTGTGCGCACGCGCTGAGGGGACAGCGCGGCGGCTCAACATGACAG 1399

Qy 421 ThrGlyAlaThrGlyLysAspAspTyrTyrAspGlyValaIleTrpCysAlaGlyLysAspAlaArg 440
Db 1400 ACCGGTGGCCACTGAGAGAGACTATGATGATGCTGTGTGTCGAGAGACATGCTCAG 1459
Qy 441 ThrGlnTrpIleGlyLysAlaAspThrArgArgThrThrArgPheThrGlyValIleThrGln 460
Db 1460 ACCGATGGATAGAGTGGAGACCAAGAGAGACTACCGGTTCAAGGGGTATTCACCCAG 1519
Qy 461 GlyArgAspSerSerIleHisAspAspPheValThrThrPhePheValGlyPheSerAsn 480
Db 1520 GGCAGAGACTCCAGATCATGACATTTTGTGACACCTTCTTGTGGCTTCAGCAT 1579
Qy 481 AspSerGlnThrTrpValMetCysThrThrAsnGlyTyrGlyLysMetThrPheHisGlyAsn 500
Db 1580 GACAGCCAGACATGGGTATGATGACCAAGGCTATGAGAAATACCTTTATGAGAAC 1639
Qy 501 ValaAspLysAspThrProValLeuSerGlyLysLeuProGlyLysProValValaIleArgPheIle 520
Db 1640 GTGACAAAGAGACACCGGTGCTGAGTGAAGTCCAGAGCGGTGTGCTGCTTATATC 1699
Qy 521 ArgIleTyrProLeuThrTrpAsnGlySerLeuCysMetArgLysGlyLysValLeuGlyCys 540
Db 1700 CCGATCTACCACTCACTGAGATGCGAGCTGTGCATGCGCTGAGGTGCTGAGGTGC 1759
Qy 541 SerValAlaProValTyrSerTyrTrpAlaGlnAsnGlyValaIleThrAspAspLeu 560
Db 1760 TTTGTGGCCCTGTCTTACAGTACTACGACAGATGAGTGTGTGCGACCATGACCTG 1819
Qy 561 AspPheArgHisHisSerTyrLysAspMetArgGlnLeuMetLysValaIleAsnGlyLys 580
Db 1820 GATTTCCGGACACACAGCTACAGAGCATGCGCCAGCTCATGAGTGTGTGAACGAGAG 1879
Qy 581 CysProThrIleThrArgThrTyrSerLeuGlyLysSerSerArgGlyLysLysIleTyr 600
Db 1880 TGCCCCACCATCACCCGACCTTACAGCTGTGGCAAGAGCTCAAGAGCTCATAT 1939
Qy 601 AlaMetGlyLysSerAspAsnProGlyLysGlyLysGlyLysGlyLysProGlyLysPheArgTyr 620
Db 1940 GCCATGAGATTTCAACAACCTTGGAGAGCTGAACTGAGGGAGACCGAGTTCCGCTAC 1999
Qy 621 ThrAlaGlyIleHisGlyLysAsnGlyValaIleGlyLysArgLysLeuLeuLeuLeuMetGln 640
Db 2000 ACTGCTGGGATCATGAGCAAGAGTGTGGGCCAGAGCTGTGCTGCTCATGACAG 2059
Qy 641 TyrLeuCysArgGlyLysTyrArgAspGlyLysAsnProArgValArgSerLeuValGlnAspThr 660
Db 2060 TACTGTGCGCGAGAGTACCGCATGAGAACCCAGCTGTGCGCAGCTGTGACAGACAC 2119
Qy 661 ArgIleHisLeuValProSerLeuAsnProAspGlyTyrGlyLysValaIleAlaGlnMetGly 680
Db 2120 CCGATCTCACTGTGCTCATCTGAACTTATGCTGAGTGTGAGTGTGAGTGTGAGTGTG 2179
Qy 681 SerGlyPheGlyLysTrpAlaLeuGlyLysLeuTrpThrGlyLysGlyLysPheAspIlePheGly 700
Db 2180 TCAGATTTGGGAACGTGGCGCTGGGACTGTGACTGAGAGAGGCTTTGACATCTTTGAA 2239
Qy 701 AspPheProAspLeuAsnSerValLeuTrpGlyValaGlyLysGlyLysGlyLysProTyr 720
Db 2240 GATTTCCCGATCTCAACTGTGCTGTGGGAGCTGAGAGAGAGAGAGAGAGAGAGAGAG 2299
Qy 721 ArgValProAsnAsnAsnLeuProIleProGlyLysTyrLeuSerProAspAlaThrVal 740
Db 2300 CCGGTCCCAACATTAACCTTGCCTTCAACCTTACCTTTCGCGAGATGCCAGGAT 2359
Qy 741 SerThrGlyValaArgAlaIleIleAlaTrpMetGlyLysAsnProPheValLeuGlyAla 760
Db 2360 TCACAGAGAGTCCGGGCGATCATGTGCTGTGAGAGAGAACCCCTTCTGCTGCGGAGCA 2419
Qy 761 AsnLeuAsnGlyGlyLysGlyLysValSerTyrProTyrAspMetAlaArgThrProThr 780
Db 2420 AATCTGAAGCGGGGAGAGGCTAGATTCCTACCTTATGATATGCGCCGACGCTTACC 2479

QY	781	GIINGIUGINLeuLeuAlaAlaAlaMetAlaAlaAlaArgGlyGlyAspGluAspArgVal	800
Db	2480	CAGAGACAGCTGTGGCCGACCCATGGAGACAGCCGGGGGAGAGATGAGACAGAGCTC	2533
QY	801	SerGluAlaGlnGluThrProAspHisAlaIlePheArgTyrLeuAlaIleSerPheAla	820
Db	2540	TCCGAGGCCAGAGAGCTCCAGACCAAGCCATCTTCGGGTGGCTTGCCATCTTCCTGGC	2592
QY	821	SerAlaHisLeuThrLeuThrGluProTyrArgGlyGlyCysGlnAlaGlnAspTyrThr	840
Db	2600	TCCGACACCTCACTTCACTCCAGGCCCTACCCGGAGGCTGGCAAGCCAGACCTACAC	2655
QY	841	GlyGlyMetGlyIleValAsnGlyAlaTyrTrpAsnProArgThrGlyThrIleAsnAsp	860
Db	2660	GCGCGGATGGGATGCTCAACGGGGCCAGATGGAAACCCCGGAGCGGAGCTATCAATGAC	2718
QY	861	PheSerTyrLeuHisLeuThrAsnCybLeuGluLeuSerPheTyrLeuGlyCysAspHisPhe	880
Db	2720	TTCAAGTACCTGCATACCAACAGCGCTGGAGAGCTCTCTTACTCTGGGCTGTACAAAGTTC	2779
QY	881	ProHisGluSerGluLeuProArgGluThrGluAsnAspLysGlnAlaLeuLeuThrPhe	900
Db	2780	CCTCATGAGAGTGAAGCTGGCCCGCAGTGGAGAAACAACAGAGAGCCCTGCTCACTTC	2839
QY	901	MetGluGlnValHisArgGlyIleLeuSerGlyValIleThrAspGlnGlnGlyIleProIle	920
Db	2840	ATGGAGACAGTGCACCGCGCGATTAAGGGGGTGGTACGAGACAGACCAAGGCATCCCAATT	2899
QY	921	AlaAsnAlaThrIleSerValSerGlyIleAsnHisGlyValIleThrAlaSerGlyGly	940
Db	2900	GCCAAAGCCACCATCTCTGTAGTGGCATTAATCAAGCGTGAACACAGCAAGTGGTGGT	2955
QY	941	AspTyrTyrArgIleLeuAsnProGlyGlyTyrArgValThrAlaHisAlaGlnGlyTyr	960
Db	2960	GATTACTGGCGAATCTTGAAACCGGGTGAATGACCGCGTACAGCCACGCGGAGGGCTAC	3019
QY	961	ThrProSerAlaLysThrCysAsnValAspTyrAspIleGlyAlaThrGlnCysAsnPhe	980
Db	3020	ACCCCGAGGCCAAGACCTGCATATGTGACTGTAGCATCGGGGCCACTCAGTCAAACTTC	3079
QY	981	IleLeuAlaArgSerAsnTyrLysArgIleArgGlyIleMetAlaMetAsnGlyValAsnArg	1000
Db	3080	ATCTCGGCTCGTCCAACTGGAAAGCGCATCCGGAGATCATGGCCATGAACGGAAACCGG	3139
QY	1001	ProIleProHisIleAspProSerArgProMetThrProGlnGlnArgIleGlnGln	1020
Db	3140	CCTATCCACACATAGACCCATCGGCGCTTAGACCCGCCAACAGACGAGCTGTGACGAG	3199
QY	1021	ArgArgLeuGlnHisArgLeuArgLeuArgAlaGlnMetArgLeuArgIleuAsnAla	1040
Db	3200	CGACGCCCTACAAACACCGGCTGGGCTGGGGCAGAGATGGCGGCTGGCGGCTCAACCC	3259
QY	1041	ThrThrThrLeuGluProHisThrValProProThrLeuProProAlaProAlaThrThr	1060
Db	3260	ACCACACACCTTAGGCCCCCACTGTGCTCCACAGCTGCCCCCTGGCCCTGGCACCAAC	3319
QY	1061	LeuSerThrThrIleGluProTyrGlyLeuIleProProThrThrAlaGlyTyrGluGlu	1080
Db	3320	CTGAGCACTACCATAGAGCGCTGGGGGCTCAATACGCCCAACACCGCTGGCTGGGAGAG	3379
QY	1081	SerGluThrArgLysValGluProGluPheGluThrGlnLeuGluProGluLysGluProGlu	1100
Db	3380	TCCGAGACTGAGACCTTACACAGAGGTGGTGCACAGGTTGGGAGCCAGAGTGAAGCCGAG	3439
QY	1101	PheGlyThrLysValGluProGluPheGluThrGlnLeuGluProGluLysGluLysGln	1120
Db	3440	TTTGGGACCAAGTGGAGCGCAGATTGAGACCCAGTTGAGAGCTCGAATTTGAGACCCAG	3499
QY	1121	LeuGluProGluPheGluGluGluGluGluGluGlyLysGluGluGluIleAlaThrArgIy	1140
Db	3500	CTGGAAACCGGAACTTTGAGGAAAGAGAGAGAGAGAAAGAGAGAGATAGACCACTGGC	3559
QY	1141	GlnAlaPheProPheThrThrValGluThrTyrThrValAsnPheGlyAspPhe	1158

DB	3560	CAGGCACTTCCCTTCACACAAGTAGAAGACTTACACAGTAACCTTTGGGGACCTTC	35613	
RESULT 4				
LOCUS	BC038588			
DEFINITION	Homo sapiens AE binding protein 1, mRNA (CDNA clone MGC:46180 IMAGE:576765), complete cds.			
ACCESSION	BC038588			
VERSION	BC038588.1	GI:24047246		
SOURCE	MGC.			
ORGANISM	Homo sapiens (human)			
REFERENCE	Bukacinski, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo. 1 (bases 1 to 4125) Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Bluetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, A.I., Wang, J., Haileh, F., Dietchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Speltz, M., Soares, M.B., Donaldson, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshitsuki, S., Carninci, P., Prange, C., Raja, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., Mckernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Woley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulik, S.W., Viall, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, J., Whiting, M., Madan, A., Young, A.C., Shvachenko, Y., Bonfield, W.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickinson, K.C., Rodriguez, A.C., Grimwood, J., Schwartz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalski, U., Smalls, D.E., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) 12477932 2 (bases 1 to 4125) Strausberg, R. Direct Submission Submitted (15-OCT-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: gcborg-remail.nih.gov CDS Library Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/ Contract: nisc_mgc@nhgri.nih.gov Akhter, N., Aytekin, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakeley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karilins, E., Khong, P., Laric, P., Legaasi, R., McDuff, Q.L., Mesillo, C., Moskeri, B., Masirian, S.D., McCloskey, J.C., McCormick, J., Pearson, R., Stancutis, S., Thomas, P.J., Touchman, J.W., Tsurgon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.			
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 ACCESSION AB209744

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Mammalia; Eutelesia; Euarctontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Totoki, Y., Toyoda, A., Takeda, T., Sakaki, Y., Tanaka, A., Yokoyama, S., Ohara, O., Nagase, T. and F.Kikuno, R.
TITLE None Title
JOURNAL Published Only in Database (2005)
REFERENCE 2 (bases 1 to 4038)
AUTHORS Totoki, Y., Toyoda, A., Takeda, T., Sakaki, Y., Tanaka, A., Yokoyama, S., Ohara, O., Nagase, T. and F.Kikuno, R.
TITLE Direct Submission
JOURNAL Submitted (22-MAR-2005) Osamu Ohara, Kazusa DNA Research Institute, Department of Human Gene Research; 2-6-7 Kazusa-kamatari, Kisarazu, Chiba, 292-0818, Japan (E-mail:cdnaif@kazusa.or.jp, URL:http://protein.gsc.riken.go.jp/, Tel:81-438-52-3930, Fax:81-438-52-3931)
COMMENT This work was supported in part by the National Project on Protein Structural and Functional Analysis, Ministry of Education, Culture, Sports, Science and Technology of Japan. Totoki Y, Toyoda A, Takeda T, Sakaki Y, Tanaka A, Yokoyama S, RIKEN Genomic Sciences Center, 1-7-22 Suehiro-cho, Tsurumi, Yokohama 230-0045, Japan.
E-mail: aktanaka@postman.riken.go.jp
URL: http://protein.gsc.riken.go.jp/.
FEATURES
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Qy 941 AspTyrTrpArgLysLeuAsnProGluGluTyrTrpArgValThrAlaHisAlaGluGlu 960
Db 3080 GATTTAGCGAATCTTGAACCCGGGTGATACCGGTGACAGCCGAGAGAGGCTAC 3139
Qy 961 ThrProSerAlaLysThrCysAsnValAspTyrAspLysGluValAlaThrGlnCysAsn 980
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Db	3380	ACCACCAACCCTAGGGCCCCACACGTGGCTCCACAGCTGCCCTGGCCCCCACCAC	3439
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Db	3440	CTGAGACATTACCAATAGACCCCTGGGGCTCAATACCGCCACACCGCTGGCTGGGGG	3499
Qy	1081	SerGluThrGluThrTrpThrGluValValThrGluPheGlyTrpThrGluValGluProGlu	1100
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Qy	1101	PheGlyThrTrpValGluProGluPheGluThrGluLeuGluProGluPheGluThrGln	1120
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Qy	1121	LeuGluProGluPheGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu	1140
Db	3620	CTGGAAACCGAGTTTGAGAGAAAGAGAGAGAGAGAGAGAGAGAGATGAGCTTGGC	3679
Qy	1141	GlnAlaPheProPheThrThrValGluThrTrpThrValaPheGlyAspPhe	1158
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DEFINITION	Sequence 2890 from Patent WO02068579.		
ACCESSION	CQ716956		
VERSION	CQ716956.1 GI:42277813		
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Homnidae; Homo.		
REFERENCE			
AUTHORS	1		
TITLE	Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.		
	Kites, such as nucleic acid arrays, comprising a majority of		
	humanecons or transcripts, for detecting expression and other uses		
	thereof		
JOURNAL	Patent: WO 02068579-A 2890 06-SEP-2002;		
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Alignment Scores:			
Pred. No.:	0	Length:	3913
Score:	6246.00	Matches:	1154
Percent Similarity:	99.8%	Conservative:	2
Best Local Similarity:	99.7%	Mismatches:	2
Query Match:	99.6%	Indels:	0
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Qy	41	PheLeuSerGluLeuGluProGluProArgGluAspAspValGluAlaProProProPro	60
Db	258	TTCCTGTGAGACTGAGACCTAGCGCCCGGAGAGACGATGAGGCCCCCGCGCTGCC	317
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Dd	1458	ACCCAGTGGATGAGAGTGGAGACACGAGAGACTACCCGGTTCAACGAGCGTCATCACCCAG	1517
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Dd	1578	GACAGCCAGACATGGGTATGTATGACCAACGGCTATGAGAAATGAACTTTTCAATGGGAAAC	1637
Oy	501	ValAspIlyAspThrProValIleuSerGluLeuProGluProValValAlaArgPheIle	520
Dd	1638	GTGGACAAAGACACACCCGCTGTGATGATGCTCCAGAGCCGGTGTGTGCTCGTTTCATC	1697
Oy	521	ArgIleTrpProLeuThrTrpAsnGlySerLeuCyMetArgLeuGluValIleuGlyCys	540
Dd	1698	CGCACTCTCCACTCACCTCGGAATGGCAGCTGTGCAAGCCCTGAGAGTCTCTGGGGTGC	1757
Oy	541	SerValAlaProValTrpSerTrpTrpArgIleAsnGluValAlaAlaThrAspAspLeu	560
Dd	1758	TCTGTGGCCCTGTGTACTACGCTACTACCAACGAATGAGTGGTGGCCAGCAAGACTGTG	1817
Oy	561	AspPheArgHisLeSerTrpIlyAspMetArgGluIleuMetIlyValValAsnGluGlu	580
Dd	1818	GATTTCCGGACACACAGCTTACAGAGCAATGGCCAGCTCATGAAAGTGTGTAACAGAGAG	1877
Oy	581	CysProThrIleThrArgThrTrpSerLeuGlyIlySerSerArgGlyLeuIlyIleTrp	600
Dd	1878	TGCCCCACATACACCCGCACTTACAGCTGTGGGCAAGACTCAGACAGGCGCTCAAGATCTAT	1937
Oy	601	AlaMetGluIleSerAspAsnProGlyGluHisGluLeuGlyGluProGluIlePheArgTrp	620
Dd	1938	GCCATGAGATCTCAGACAAACCCTGGGGAGATGAATCGGGGAGAGCCCAATTTCCGCTAC	1997
Oy	621	ThrAlaGlyIleHisGlyAsnGluValIleuGlyArgGluLeuLeuLeuLeuMetGln	640
Dd	1998	ACTGTGGGATTCATGGCAACGAGTGTGGGGCGAGAGCTGTGTCTGTCTCATGTGAG	2057
Oy	641	TyrLeuCyAspArgIlyTrpArgAspGlyAsnProArgValArgSerLeuValGlnAspThr	660
Dd	2058	TACCTGTCCGAGAGTACCGGATGGGAAACCAAGTGGCGCACTGTGTGCATGACAGACACA	2117
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QY	841	GlyGlyMetGlyIleValAsnGlyAlaLysTrpAsnProArgThrGlyTyrlleAsnAsp	860
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QY	1061	LeuSerThrThrIleGluProTrpGlyLeuIleProProThrThrAlaGlyTyPArgGlu	1080
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QY	1101	PheGlyThrLysValGluProGluPheGluThrGlnLeuGluProGluPheGluThrGln	1120
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AKI28980 Mus musculus AB binding protein 1 (Aebp1).
ACCESSION
AKI28980.1 GI:34536646
VERSION
oligo capping; file (full insert sequence).
KEYWORDS
Mus musculus (house mouse)
SOURCE
Mus musculus
ORGANISM
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REFERENCE
1 Kanehori, K., Ishibashi, T., Chiba, Y., Fujimori, K., Hirooka, S., Tanai, H., Watanabe, S., Ishida, S., Ono, Y., Hokuwa, T., Watanabe, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Oca, T., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Matsuo, K., Nakamura, Y., Sakine, M., Kikuchi, H., Kanda, K., Magatsuma, M., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahara, K., Masuno, Y., Nagai, K. and Isogai, T.
TITLE
NEDO cDNA sequencing project
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 3909)
AUTHORS
Isogai, T. and Yamamoto, J.
JOURNAL
Direct Submission
TITLE
Submitted (15-JUL-2003) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: f13-cdna@hifcy.com, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT
NEDO cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan. cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
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Query Match: 81.0% Indels: 36
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ACCESSION BC082577
VERSION BC082577.1 GI:52139026
SOURCE MGC
ORGANISM Mus musculus (house mouse)
MUS musculus
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REFERENCE
1 (bases 1 to 3869)
Straussberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altshul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Heide,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Rana,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S., Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakeley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butlerfield,Y.S., Krzywinski,M.I., Skalska,U., Smallus,D.E., Scherch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
2 (bases 1 to 3869)
Director MGC Project.
Direct Submission
Submitted (15-SEP-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr. Thomas L. Casavant.
Web site: <http://genome.uiowa.edu>
Contact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu
Bonaldo,M.F., Akabogu,I., Bair,T., Bair,J., Crouch,K., Davis,A., Fishler,K., Keppe,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K., Scheetz,T., Smith,C., Smlr,E., Tack,D., Trout,K., Walters,J., Casavant,T., Soares,M.B.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
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ORIGIN

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Gaps: 9

US-10-642-946-3 (1-1158) x BC082577 (1-3869)

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      VERSION    E07353.1 GI:2175493
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      SOURCE
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VERSION 115213.1 GI:1250121
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REFERENCE
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AUTHORS
Kawai, S., Takeshita, S., Okazaki, M. and Amann, E.
TITLE
Bone-related carboxypeptidase-like protein and process for its
production
JOURNAL
Patent: US 5460951-A 1 24-OCT-1995;
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OY	339	LeuLYsLYsProLYsLYsGIuAspSerSerProLYsGIuGIuThr---AspLYsTPrAla	357
Db	1053	ATGAAGAAAGCCCAAAAGAGGGTATGAGCCCCMAAGAGACACAGAGACAAAGTGAC	1112
OY	358	ValGIuLYsGIuLYsAspHisLYsGIuLProArGIuLYsGIuGIuLeuGIuGIuGIuTPr	377
Db	1113	GTGGAGAAACMAAGACCAACMAAGAGCCCGGAAAGGGTGAAGAGACTGAGAGAGACTGG	1172
OY	378	ThrProThrGIuLYsValLYsCyBProProIleGIuMetGIuSerHisArGIleGIuAsp	397
Db	1173	GCGCCAGTGGAGAAATCAAGTCCCACTATTGGATGGAGTCAACCCGCAATTGAGAC	1232
OY	398	AsnGIuIleArGIuAspSerMetLeuArGIuGIuLeuGIuAlaGIuArGIuArGIu	417
Db	1233	AACCGAGATCCGTCTCTCTCCATGTGGCCACCGGCTCGAGGCCACCGGGCGCGCTC	1282
OY	418	AsnMetGIuThrGIuAlaThrGIuAspAspTYrTYrAspGIYAlaTTrCyAlaGIuAsp	437
Db	1293	AACATGCAAGCTGGTGGCCATGAAATATCATATGACGGAGCTGTGTGTGCTGAGAC	1352
OY	438	AspAlaArGIuThrGIuTPrIleGIuValAspThrArGIuThrThArPheThrGIYAla	457
Db	1353	GAGTGGCAGACCCAGTGTATCGAGGTGACACCCGAGAGCAACTCGTTTACGGGCGTTC	1412
OY	458	IlleThrGIuGIuYArGIuAspSerSerIleHisAspAspPheValThrThrPhePheValGIY	477
Db	1413	ATCATCTAGGGCCCGTACTCCACGATCATGATACGATTCGTGGATCACTTTGTGTGGC	1472
OY	478	PheSerAsnAspSerGIuThrTYrValMetTYrThrAsnGIYTYrGIuGIuMetThrPhe	497
Db	1473	TTCAGCATGACAGCCACAGACTGGGTATGTATACCATGTGCTACGAGAAATGACTTTC	1532
OY	498	HisGIYAsnValAspLYsAspThrProValLeuSerGIuLeuProGIuProValYAla	517
Db	1533	TATGGAAATGTGGACAAGAGACACACTGTGTGAGCGAGCTCCCTGACAGCTAGTTGTGGCC	1592

QY	518	ArgPheIleArgIleTyrProLeuThrTrpPaenGlySerLeuCyMetArgLeuGluVal	537
Db	1593	CGTTTCATCCGATCTATCTCATCTCACTCCAGGAACGGTAGCTGTGCATYGGCCCTGGAGGGTG	165
QY	538	LeuGlyCySerSerValAlaProValTyrSerTyrTyrAlaGluAsnGluValAlaIleThr	557
Db	1653	CTAGGCTGCCCGTGAACCCCTGTCTTACAGCTTCTACGCACAGAAATGAGGTGGTACTACT	171
QY	558	AspAspLeuAspPheArgHisHisSerTyrLysAspMetArgGluMetLeuLysValAla	577
Db	1713	GACACGCTGGACTTCCGGCACACAGCTACAGAGCATCCGCGACGTGATGAAGCGCTGC	177
QY	578	AsnGluGluCyProThrIleThrArgThrTyrSerLeuGlyLysSerSerArgIleLeu	597
Db	1773	AATGAGAGTGGCCCAACATCACTCGACATACAGCTTGGGCAAGATTCAAGAGGGCTTC	183
QY	598	LysIleTyrAlaMetGluIleSerAspAsnProGlyGluHisGluGluGlyGluProGlu	617
Db	1893	AAGATCTACGCATAGAAATCTCAAGACAACCTGGGGAATCAATGAATCGGAGAGCCCGAG	189
QY	618	PheArgTyrThrAlaGlyIleHisGlyAsnGluValAlaGlyArgGluMetLeuLeu	637
Db	1893	TTCGCGCTACAGCGCGGATCCACGGCATGAGAGTGTCTTAGCCGAGAGCTCCTGCTCCTG	195
QY	638	LeuMetGluTyrLeuCyArgGluTyrArgAspGlyAsnProArgValArgSerLeuVal	657
Db	1953	CTCATGCAATACCTTATGCCAGAGATACCGCGATGGGAACCCGAGAGTGGCAACCTGGTG	201
QY	658	GlnAspThrArgIleHisLeuValProSerLeuAsnProAspGlyTyrGluValAlaIle	677
Db	2013	CAGGACACAGGATCCACTGGTGGCTTCGCTGAACCCGTAGGCTTATGAGGTGGCAGGG	207
QY	678	GlnMetGlySerGluPheGlyAsnTrpAlaLeuGlyLeuTrpThrGluGluGlyPheAsp	697
Db	2073	CAGATGGGCTCAGAGTTTGGGAACCTGGGCACTGGGGCTGTGACCTGAGAGAGGCTTTGAC	213
QY	698	IlePheGluAspPheProAspLeuAsnSerValLeuTrpGlyAlaGluGluArgLysTrp	717
Db	2133	ATCTTCAGAGACTTCCAGATCTCAACTGTGCTCTGGGGCAGCTGAGAGAAAGAAATGG	219
QY	718	ValProTyrArgValProAsnAsnAsnLeuProIleProGluArgTyrLeuSerProAsp	737
Db	2193	GTCCCCCTACAGGCTCCCAAAACAATTACTTGCCTGAACCTGTAACCTGTGCCAGAT	225
QY	738	AlaThrValSerThrGluValArgAlaIleIleAlaTrpMetGluLysAsnProPheVal	757
Db	2253	GCCACGGTCTCCACAGAGTCCGGGCCATTATTTCTTGATGAGAGAAACCCCTTTGTG	231
QY	758	LeuGlyAlaAsnLeuAsnGlyGlyGluArgLeuValSerTyrProTyrAspMetAlaArg	777
Db	2313	CTGGGTGCAATCTGACGGTGTGAGGGCTGTGTCTTATCCCTTATCATTGAGCCGG	237
QY	778	ThrProThrGlnGluGluLeuLeuAlaAlaMetValAlaAlaArgGlyGluAspGlu	797
Db	2373	ACACCTACCCAGAGACACTGTGGCCGAGGCACTGGCAGCGCCCGGAGAAAGATGAT	243
QY	798	AspGluValSerGluAlaGluGluThrProAspHisAlaIlePheArgTrpLeuAlaIle	817
Db	2433	GACGGGGGTCTGAGGGCCGAGGAGCTCCAGATCAACGCTATTTCCGCGGTGGCCATC	249
QY	818	SerPheAlaSerAlaHisIleLeuThrLeuThrGluProTyrArgGlyGlyCySerGluAlaGln	837
Db	2493	TCAATTGGCTCCGGCCATCTCAACCATGAGAGCCCTACCGGGAGGGGTGCCAGGCCAG	255
QY	838	AspTyrThrGlyGlyMetGlyTyrLeuValAsnGlyAlaLysTrpAsnProArgThrGlyThr	857
Db	2553	GACTACACACAGCGGATCGGAGATTGTCAACGGGGCCAAAGTGAAATCTCGCTCGAGACT	261
QY	858	IleAsnAspPheSerTyrLeuHisThrThrAsnCySerGluLeuSerPheTyrLeuGlyCys	877
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RESULT 12
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LOCUS AX473127 16161 bp DNA linear PAT 09-AUG-2002
DEFINITION Sequence 8 from Patent WO0224741.
ACCESSION AX473127
VERSION AX473127.1 GI:22207848
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 Ryan, J. W.

TITLE Isolated genomic polynucleotide fragments from chromosome 7
JOURNAL Patent: WO 0224741-A 8 28-MAR-2002;
AUTHOR Ryan, James W. (US)
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Score: 4791.00 Matches: 1149
Percent Similarity: 36.0% Conservative: 4
Best Local Similarity: 35.4% Mismatches: 5
Query Match: 76.4% Indels: 2051
DB: 2 Gaps: 20
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Db 10893 ATGGCGCCGTGCGCGCGCGCGCCCTGCTCAGCTGCTCTGCGCTGCTGCTGCTGCTG 10834
Qy 21 ProGlyIleArgProGluThrValLeuThrAspAspGluIleGluGluPheLeuGluGly 40
Db 10833 CTTGAGAGGCG 10774
Qy 41 PheLeuSerGluLeuGluProGluProArgGluAspAspValGluAlaProProProPro 60
Db 10773 TTCTGTGAGAGCTGAGACTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 10714
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Db 10713 GAGCCACCG 10654
Qy 81 ThrAlaAlaGlu----- 84
Db 10653 ACGCCCGAGAAAGTGAAGAGCCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 10594
Qy 84 ----- 84
Db 10593 TGGGAACAGGGGAGATTCGTAGAGTCTGCGCATCCAGTCTGTAGGGAGAGATGCG 10534
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OY	247	-----	247
Db	7834	CCTGGGTGGAACCCCTGGCTGGGGGATGTGCAATGGAGCCCATCCAGCCTTGGGGCCC	7775
OY	248	-----GluYrIleHArgArgGlnGlnProArgProp	259
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OY	259	roProSeArHArGArGArProGluAArgValITpProGluProProGluGluYsaIaP	279
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OY	279	roIaIaProIaIaProGluGluAArgIle-----	287
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OY	288	-----GluProProValIysProI	294
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OY	313	-----	313
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OY	313	-----	313
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QY	313	-----	313	-----	313
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QY	314	-----	MetAsp1YTYrPheGlyProProPro	322	
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Qy 383 ----- 383
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Qy 383 ----- 383
Db 5614 CTTGGTCTTGGGTTGGTGGAGGAAGATGAGCTAGTGAGCCACCATTTCTGGGGTAC 5555
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 SOURCE
 ORGANISM

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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 PUBMED

1 (bases 1 to 153203)
 Sulston, J.E. and Wilson, R.
 Toward a complete human genome sequence
 Genome Res. 8 (11), 1097-1108 (1998)
 9847074

REFERENCE
 AUTHORS
 TITLE
 JOURNAL

2 (bases 1 to 153203)
 Du, F.
 The sequence of Homo sapiens PAC clone RP5-852P6
 Unpublished (2001)
 3 (bases 1 to 153203)
 Waterston, R.H.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL

Submitted (28-JAN-1999) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 4 (bases 1 to 153203)
 Waterston, R.H.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL

Submitted (13-AUG-1999) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 5 (bases 1 to 153203)
 Waterston, R.H.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL

Submitted (30-SEP-2000) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 6 (bases 1 to 153203)
 Waterston, R.H.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL

Submitted (06-FEB-2003) Genome Sequencing Center, Washington
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,
 MO 63108, USA
 7 (bases 1 to 153203)
 Wilson, R.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL

Submitted (30-MAY-2003) Department of Genetics, Washington
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
 On Feb 6, 2003 this sequence version replaced gi:5732182.
 ----- Genome Center

Center: Washington University Genome Sequencing Center
 Center code: WUGSC
 Web site: <http://genome.wustl.edu/gsc>
 Contact: sapiens@wustl.wustl.edu
 ----- Summary Statistics
 Center project name: H_DJ0852P06

NOTICE: This sequence may not represent the entire insert of this
 clone. It may be shorter because we only sequence overlapping
 clone sections once, or longer because we provide a small overlap
 between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
 all regions were double stranded, sequenced with an alternate
 chemistry, or covered by high quality data (i.e., phred quality >=
 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by sequence
 from more than one subclone; and the assembly was confirmed by

restriction digest.

MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and
 sequencing collaboration between the NHGRI Chromosome 7 Mapping
 Project (Eric D. Green, Director), John D. McPherson in the
 Department of Genetics (Washington University), and the Washington
 University Genome Sequencing Center. For additional information
 about the map position of this sequence, see
<http://www.nhgri.nih.gov/DIR/GRB/CHR7>, send
<mailto:egreen@nhgri.nih.gov>, or see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

This clone was derived from human PAC library RPCT-5, prepared by
 Pieter de Jong and coworkers at <http://www.chori.org> using the
 method described by Ioannou et al., Nature Genetics 6:84-9 (1994).
 The library is from one male donor.
 The clone may be obtained either from Genome Systems, Inc.
 (<http://www.genomesystems.com>) or Research Genetics, Inc.
 (<http://www.researchgenetics.com>), or from Pieter de Jong.
 VECTOR: pCYPAC2

NEIGHBORING SEQUENCE INFORMATION:

This sequence is the entire insert of the clone. This clone is
 overlapped by AC017116 and AC093086.

FEATURES

source

1. 153203
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Homnidae; Homo.
1 (sites)
REFERENCE
AUTHORS Ohno,I., Hashimoto,U., Shimizu,K., Takaoka,K., Ochi,T.,
Matsumura,K. and Okubo,K.
TITLE A cDNA cloning of human AEBP1 from primary cultured osteoblasts and
its expression in a differentiating osteoblastic cell line
JOURNAL Biochem. Biophys. Res. Commun. 228 (2), 411-414 (1996)
PUBMED 8920928
REFERENCE 2 (bases 1 to 2839)

AUTHORS
JOURNAL

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FEATURES
source

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 REFERENCE
 1 (bases 1 to 2759)
 Flory, D.M., Kollar, J., Huynh, T.D. and Hering, T.M.
 Transcription factor AEBP1 expression during chondrocyte
 differentiation and phenotypic modulation
 JOURNAL
 Unpublished
 2 (bases 1 to 2759)
 Hering, T.M., Flory, D.M., Kollar, J. and Huynh, T.D.
 Direct Submision
 JOURNAL
 Submitted (20-JAN-1998) Medicine, Case Western Reserve University,
 10900 Euclid Avenue, Cleveland, OH 44106-4946, USA
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Qy 1017 gleuglnglaryarglueuglnhisargleuargleuarglalemeeargleuargar 1037
Db 2162 CATGCAAGCGCGCGCTCGATGATGGCTGGCGCAATGGCAACATGGCTCGAGC 2221
Qy 1037 gleuasnalathrthrthreuglylprohithrvalproprothrleuupropro 1055
Db 2222 CTTCAATGCAACACAGC-----CCAGCCAGACCCCACTCCCTCCCACTCC 2275
Qy 1056 -----Alaproalathrthrleuaserthrtthrlleglupr 1067
Db 2276 AACACTGCTCCCACTGCGGACCTTGCCTCCCAAGCCCAAGTTCTTACACTGGGGCC 2335
Qy 1067 otrpglyleuileproprothrtthralaglytrpgluluser----- 1081
Db 2336 CTGGAGGTTTTCACAGAGACCAAGTCAATTGGGAGATCGGAACGAGACGAGAC 2395

C	1	21.2	9.0	49	3	US-09-849-069-9	Sequence 9, April
C	2	20.8	8.8	43	2	US-08-334-001-19	Sequence 19, April
C	3	20.8	8.8	43	2	US-08-334-001-19	Sequence 20, April
C	4	19.6	8.3	50	3	US-10-131-827-584	Sequence 584, April
C	5	19.6	8.3	50	5	US-10-131-831-584	Sequence 584, April
C	6	19.4	8.2	45	3	US-08-480-540A-210	Sequence 210, April
C	7	19.4	8.2	45	3	US-08-686-968C-210	Sequence 210, April
C	8	19.4	8.2	45	3	US-08-488-237A-210	Sequence 210, April
C	9	19.4	8.2	45	3	US-08-375-992A-210	Sequence 210, April
C	10	19.4	8.2	45	3	US-08-472-679H-210	Sequence 210, April
C	11	19.4	8.2	50	3	US-10-131-827-4246	Sequence 4246, April
C	12	19.4	8.2	50	3	US-10-131-827-4412	Sequence 4412, April
C	13	19.4	8.2	50	5	US-10-131-831-4246	Sequence 4246, April
C	14	19.4	8.2	50	5	US-10-131-831-4412	Sequence 4412, April
C	15	19.2	8.1	50	3	US-10-131-827-1437	Sequence 1437, April
C	16	19.2	8.1	50	5	US-10-131-831-1437	Sequence 1437, April
C	17	19	8.1	36	3	US-08-805-813-7	Sequence 7, April
C	18	19	8.1	43	3	US-09-561-490S-49	Sequence 49, April
C	19	8.1	50	3	US-10-131-827-1800	Sequence 1800, April	
C	20	19	8.1	50	5	US-10-131-831-1800	Sequence 1800, April
C	21	18.6	7.9	50	3	US-10-131-827-2249	Sequence 2249, April
C	22	18.6	7.9	50	5	US-10-131-831-2249	Sequence 2249, April
C	23	18.4	7.8	47	3	US-09-422-878-765	Sequence 765, April

C 24	18.4	7.8	50	3	US-09-371-489-4	Sequence 4, Appl
C 25	18.4	7.8	50	3	US-10-131-821-2060	Sequence 2060, Ap
C 26	18.4	7.8	50	3	US-10-131-831-2060	Sequence 2060, Ap
C 27	18.2	7.7	44	2	US-08-471-791-39	Sequence 39, Appl
C 28	18.2	7.7	44	3	US-09-182-141-152	Sequence 152, Appl
C 29	18.2	7.7	44	7	PCT-US91-01746-39	Sequence 39, Appl
C 30	18.2	7.7	44	7	PCT-US91-01750-10	Sequence 10, Appl
C 31	18.2	7.7	47	3	US-09-422-978-2714	Sequence 2714, Ap
C 32	18.2	7.7	47	3	US-09-422-978-1100	Sequence 1100, Ap
C 33	18	7.6	47	3	US-09-422-978-2579	Sequence 2579, Ap
C 34	18	7.6	50	3	US-10-131-821-5658	Sequence 5658, Ap
C 35	18	7.6	50	5	US-10-131-831-5658	Sequence 5658, Ap
C 36	17.8	7.5	50	3	US-09-270-761-25514	Sequence 25514, A
C 37	17.8	7.5	50	3	US-10-131-821-2354	Sequence 2354, A
C 38	17.8	7.5	50	5	US-10-131-831-2354	Sequence 2354, Ap
C 39	17.6	7.5	40	3	US-09-721-543A-17	Sequence 17, Appl
C 40	17.6	7.5	42	3	US-09-551-731C-65	Sequence 65, Appl
C 41	17.6	7.5	42	3	US-09-551-731C-66	Sequence 66, Appl
C 42	17.6	7.5	43	3	US-08-331-625A-50	Sequence 50, Appl
C 43	17.6	7.5	43	3	US-09-494-151-50	Sequence 50, Appl
C 44	17.6	7.5	43	3	US-09-972-484-50	Sequence 50, Appl
C 45	17.6	7.5	43	7	PCT-US93-004384-21	Sequence 21, Appl

ALIGNMENTS

```

RESULT 1
US-09-849-069-9/C
? Sequence 9, Application US/09849069
? Patent No. 663036
? GENERAL INFORMATION:
? APPLICANT: Ronald R. Breaker
? TITLE OF INVENTION: Bioreactive Allosteric Polynucleotides
? FILE REFERENCE: OCR-794.CIP
? CURRENT APPLICATION NUMBER: US/09/849,069
? CURRENT FILING DATE: 2001-05-07
? PRIOR APPLICATION NUMBER: US 09/331,809
? PRIOR FILING DATE: 1999-06-18
? NUMBER OF SEQ ID NOS: 57
? SOFTWARE: MS-DOS
? SEQ ID NO 9
? LENGTH: 49
? TYPE: DNA
? ORGANISM: artificial sequence
? FEATURES:
? OTHER INFORMATION: G8 DNA
? US-09-849-069-9

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	9.0%;	Score 21.2;	DB 3;	Length 49;
Query Match Similarity	76.5%;	Pred. No. 2.5e+03;		
Best Local	Similarity			
Matches	26;	Conservative	0;	Mismatches 8;
				Indels 0;
				Gaps 0
Qy	100	CCCCCTCATTCCTCCGCTGCCACTCTTGATG	133	
Db	35	CCGGCTGTCAATCCTCCAGCTTCTACCCCTGGCTG	2	

RESULT 2
 US-08-324-001-19.
 ; Sequence 19, Application US/08324001
 ; Patent No. 5624803
 ; GENERAL INFORMATION:
 ; APPLICANT: NOONBERG, SARAH B.
 ; APPLICANT: HUNT, C. ANTHONY
 ; TITLE OF INVENTION: IN VIVO OLIGONUCLEOTIDE GENERATOR, AND
 ; TITLE OF INVENTION: METHODS OF TESTING THE BINDING AFFINITY OF TRIPLEX FORMING
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORRISON & FOERSTER
 ; STREET: 755 PAGE MILL ROAD
 ; CITY: PALO ALTO
 ;

STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/324,001
FILING DATE: 13-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MONROY, GLADYS H.
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 22000-20544.20
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141 MRSN FOERSSFO
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-324-001-19

Query Match 8.8%; Score 20.8; DB 2; Length 43;
Best Local Similarity 78.1%; Pred. No. 3.2e+03;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 137 CACCTGCTCCCTCTCTCTCTGCGCATGATT 168
DB 10 CTCCTCCTCACCCTCTCTCTCTCTGATT 41

RESULT 3

US-08-324-001-20/c
Sequence 20, Application US/08324001
Patent No. 5624803
GENERAL INFORMATION:
APPLICANT: NOONBERG, SARAH B.
TITLE OF INVENTION: IN VIVO OLIGONUCLEOTIDE GENERATOR AND
TITLE OF INVENTION: METHODS OF TESTING THE BINDING AFFINITY OF TRIPLEX FORMING
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/324,001
FILING DATE: 13-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MONROY, GLADYS H.
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 22000-20544.20
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141 MRSN FOERSSFO
INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-324-001-20

Query Match 8.8%; Score 20.8; DB 2; Length 43;
Best Local Similarity 78.1%; Pred. No. 3.2e+03;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 137 CACCTGCTCCCTCTCTCTCTGCGCATGATT 168
DB 34 CTCCTCCTCACCCTCTCTCTCTCTGATT 3

RESULT 4
US-10-131-827-584
Sequence 584, Application US/10131827
Patent No. 6905827
GENERAL INFORMATION:
APPLICANT: Wohlgenuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
FILE REFERENCE: 506612000120
CURRENT APPLICATION NUMBER: US/10/131,827
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9090
SOFTWARE: Patent in version 3.1
SEQ ID NO 584
LENGTH: 50
TYPE: DNA
ORGANISM: Homo sapiens
US-10-131-827-584

Query Match 8.3%; Score 19.6; DB 3; Length 50;
Best Local Similarity 66.7%; Pred. No. 8.1e+03;
Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 71 GTGAGCTGTTGTTGAAGAGCCGCCCCCTGATTC 112
DB 6 GTGACCTGTTGTTGAATATGTTCCCATGTCATC 47

RESULT 5
US-10-131-831-584
Sequence 584, Application US/10131831
Patent No. 7026121
GENERAL INFORMATION:
APPLICANT: Wohlgenuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
TITLE OF INVENTION: TRANSPLANT REJECTION
FILE REFERENCE: 506612000121
CURRENT APPLICATION NUMBER: US/10/131,831
CURRENT FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9190
SOFTWARE: Patent in version 3.1
SEQ ID NO 584
LENGTH: 50

TYPE: DNA
ORGANISM: Homo sapiens
US-10-131-831-584

Query Match
Best Local Similarity 66.7%; Score 19.6; DB 5; Length 50;
Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 71 GTGAGAGCTGCTTTGTTGAAAGCGCTGCGCCCTCTCATTC 112
DB 6 GTGAGACCTGTTGTTTAAATATTTCTGTCCTCATGCATC 47

RESULT 6
US-08-480-640A-210/c
Sequence 210, Application US/08480640A

PATENT No. 6033904
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D.
APPLICANT: Junker, David E.
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,640A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 210:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-480-640A-210

Query Match
Best Local Similarity 70.3%; Score 19.4; DB 3; Length 45;
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 199 ATGCTAACGCCAGCTTCTTGTCTGCTGCAAACT 235
DB 41 ATGATTACGCCAAGCTTCTAGTACAGTATTTCGACT 5

RESULT 7
US-08-686-968C-210/c
Sequence 210, Application US/08686968C
PATENT No. 6221361
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D.
APPLICANT: Junker, David E.
TITLE OF INVENTION: Recombinant Swinepox Virus
FILE REFERENCE: 39119-H/JML

CURRENT APPLICATION NUMBER: US/08/686,968C
CURRENT FILING DATE: 1996-07-25
NUMBER OF SEQ ID NOS: 231
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 210

LENGTH: 45
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Homology
US-08-686-968C-210

Query Match
Best Local Similarity 70.3%; Score 19.4; DB 3; Length 45;
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 199 ATGCTAACGCCAGCTTCTTGTCTGCTGCAAACT 235
DB 41 ATGATTACGCCAAGCTTCTAGTACAGTATTTCGACT 5

RESULT 8
US-08-488-237A-210/c
Sequence 210, Application US/08488237A
PATENT No. 6251403
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D.
APPLICANT: Junker, David E.
TITLE OF INVENTION: Recombinant Swinepox Virus
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,237A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 210:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-488-237A-210

Query Match
Best Local Similarity 70.3%; Score 19.4; DB 3; Length 45;
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 199 ATGCTAACGCCAGCTTCTTGTCTGCTGCAAACT 235
DB 41 ATGATTACGCCAAGCTTCTAGTACAGTATTTCGACT 5

RESULT 9
US-08-375-992A-210/C
; Sequence 210, Application US/08375992A
; Patent No. 6328975
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D.
; APPLICANT: Junker, David E.
; TITLE OF INVENTION: Recombinant Swinepox Virus
; NUMBER OF SEQUENCES: 220
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/375,992A
; FILING DATE: Herewith
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 210:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; US-08-375-992A-210

Query Match 8.2%; Score 19.4; DB 3; Length 45;
Best Local Similarity 70.3%; Pred. No. 9e+03;
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 199 ATGCTAACGCCATGCTTCTGTCGCAAACT 235
Db 41 ATGATTACGCCAAGCTTCTAGTACAGTATTACGACT 5

RESULT 10
US-08-472-679H-210/C
; Sequence 210, Application US/08472679H
; Patent No. 6497882
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D.
; APPLICANT: Junker, David E.
; TITLE OF INVENTION: Recombinant Swinepox Virus
; NUMBER OF SEQUENCES: 267
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pamela G. Salkeld
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/472,679H
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Salkeld, Pamela G.
REGISTRATION NUMBER: 38,607
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 298-2135
TELEFAX: (908) 298-5388
INFORMATION FOR SEQ ID NO: 210:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHEICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 210:
US-08-472-679H-210

Query Match 8.2%; Score 19.4; DB 3; Length 45;
Best Local Similarity 70.3%; Pred. No. 9e+03;
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 199 ATGCTAACGCCATGCTTCTGTCGCAAACT 235
Db 41 ATGATTACGCCAAGCTTCTAGTACAGTATTACGACT 5

RESULT 11
US-10-131-827-4246
; Sequence 4246, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4246
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-131-827-4246

Query Match 8.2%; Score 19.4; DB 3; Length 50;
Best Local Similarity 79.3%; Pred. No. 9.4e+03;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 104 CTCCTATCTCTGCTCCACTCTTGCACT 132
Db 22 CCTCATCTCTGCTCACTCTCTTCAT 50

RESULT 12
US-10-131-827-4412
; Sequence 4412, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert


```

; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4412
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-4412

Query Match      8.2% Score 19.4; DB 3; Length 50;
Best Local Similarity 79.3%; Pred. No. 9.4e+03;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      110 TTCTCTGCTCCCACTCTTGATGAGACA 138
DB      13 TTATCTGCTTCCACTATAGCATGATCA 41

RESULT 13
US-10-131-831-4246
; Sequence 4246, Application US/10131831
; Patent No. 7026121
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
; FILE OF INVENTION: TRANSPLANT REJECTION
; FILE REFERENCE: 506612000121
; CURRENT APPLICATION NUMBER: US/10/131,831
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9190
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4246
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-831-4246

Query Match      8.2% Score 19.4; DB 5; Length 50;
Best Local Similarity 79.3%; Pred. No. 9.4e+03;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      104 CTCTCATTCCTGCTCCCACTTTGCAT 132
DB      22 CCTCATCTTCTGCTCCTCATCTTCCAT 50

RESULT 14
US-10-131-831-4412
; Sequence 4412, Application US/10131831
; Patent No. 7026121
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
; FILE OF INVENTION: TRANSPLANT REJECTION
```

```

; FILE REFERENCE: 506612000121
; CURRENT APPLICATION NUMBER: US/10/131,831
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9190
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4412
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-831-4412

Query Match      8.2% Score 19.4; DB 5; Length 50;
Best Local Similarity 79.3%; Pred. No. 9.4e+03;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      110 TTCTCTGCTCCCACTCTTGATGAGACA 138
DB      13 TTATCTGCTTCCACTATAGCATGATCA 41

RESULT 15
US-10-131-827-1437/C
; Sequence 1437, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; FILE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1437
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-1437

Query Match      8.1% Score 19.2; DB 3; Length 50;
Best Local Similarity 67.5%; Pred. No. 1.1e+04;
Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY      66 TTCACGTGAGAGCTGTTGTAAGAGCCGCCCCCT 105
DB      46 TTCTCTCAGACACTGTGTGTAAGAAAGCCCTTGTCT 7

Search completed: October 1, 2006, 01:24:47
Job time : 112.569 secs
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 1, 2006, 00:30:21 ; Search time 115.431 Seconds
(without alignments)
3922.763 Million cell updates/sec

Title: US-10-642-946-6_COPY_1967_2208

Perfect score: 242
Sequence: 1 tctccagcagcagcactgga.....ccactcaactgattcac 242

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 1429044

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Maximum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents NA: *
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2: /EMC_Celerra_SIDS3/prodata/2/ina/5_COMB.seq: *
3: /EMC_Celerra_SIDS3/prodata/2/ina/6A_COMB.seq: *
4: /EMC_Celerra_SIDS3/prodata/2/ina/6B_COMB.seq: *
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9: /EMC_Celerra_SIDS3/prodata/2/ina/RE_COMB.seq: *
10: /EMC_Celerra_SIDS3/prodata/2/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20.8	8.6	50	US-10-131-827-7899	Sequence 7899, Ap
2	20.8	8.6	50	US-10-131-831-7899	Sequence 7899, Ap
3	19.6	8.1	42	PCT-US94-14106-20	Sequence 20, App1
4	19.6	8.1	50	US-08-503-730-37	Sequence 37, App1
5	19.6	8.1	50	US-10-131-827-1159	Sequence 1159, Ap
6	19.6	8.1	50	US-10-131-831-1159	Sequence 1159, Ap
7	19.2	7.9	39	US-08-644-664B-35	Sequence 35, App1
8	19.2	7.9	39	US-08-761-277A-35	Sequence 35, App1
9	19.2	7.9	42	US-08-391-000-25	Sequence 25, App1
10	19.2	7.9	42	US-08-741-931-25	Sequence 25, App1
11	19.2	7.9	39	US-09-475-947A-43	Sequence 43, App1
12	19.2	7.9	50	US-10-131-827-6394	Sequence 6394, Ap
13	19.2	7.9	50	US-10-131-827-6394	Sequence 6394, Ap
14	19.2	7.9	50	US-10-131-831-6394	Sequence 6394, Ap
15	19.2	7.9	50	US-10-131-831-6394	Sequence 6394, Ap
16	18.6	7.7	47	US-08-642-045B-20	Sequence 20, App1
17	18.6	7.7	47	US-08-852-268-20	Sequence 20, App1
18	18.6	7.7	50	US-08-325-243A-4	Sequence 4, App1
19	18.6	7.7	50	US-08-171-389-504	Sequence 504, App
20	18.6	7.7	50	US-08-123-536-504	Sequence 504, App
21	18.6	7.7	50	US-08-475-228A-504	Sequence 504, App
22	18.6	7.7	50	US-08-482-080A-504	Sequence 504, App
23	18.6	7.7	50	US-09-354-947-504	Sequence 504, App

C 24	18.6	7.7	50	US-09-993-346-504	Sequence 504, App
C 25	18.6	7.7	50	PCT-US93-12388-504	Sequence 504, App
26	18.4	7.6	45	US-09-794-368-12	Sequence 12, App1
27	18.2	7.5	25	US-09-396-196G-18892	Sequence 18892, A
28	18.2	7.5	47	US-09-641-638-1005	Sequence 1005, Ap
29	18.2	7.5	47	US-10-170-097-1005	Sequence 1005, Ap
C 30	18.2	7.4	45	US-08-975-699-26	Sequence 26, App1
C 31	18.2	7.4	45	US-08-972-089-26	Sequence 26, App1
C 32	18.2	7.4	45	US-09-307-794A-313	Sequence 313, App
C 33	18.2	7.4	45	US-09-505-125A-313	Sequence 313, App
C 34	18.2	7.4	45	US-09-302-775A-313	Sequence 313, App
C 35	18.2	7.4	45	US-09-906-700-313	Sequence 313, App
C 36	18.2	7.4	45	US-09-903-603A-313	Sequence 313, App
C 37	18.2	7.4	45	US-09-804-920A-313	Sequence 313, App
C 38	18.2	7.4	45	US-09-909-064-313	Sequence 313, App
C 39	18.2	7.4	45	US-09-905-381A-313	Sequence 313, App
C 40	18.2	7.4	45	US-09-906-618-313	Sequence 313, App
C 41	18.2	7.4	45	US-09-906-646-313	Sequence 313, App
C 42	18.2	7.4	45	US-09-904-462-313	Sequence 313, App
C 43	18.2	7.4	45	US-09-902-736A-313	Sequence 313, App
C 44	18.2	7.4	45	US-09-906-722A-313	Sequence 313, App
C 45	18.2	7.4	45	US-09-905-449-313	Sequence 313, App

ALIGNMENTS

```
RESULT 1
US-10-131-827-7899
; Sequence 7899, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wollgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUN
; FILE REFERENCES: 506612000120
; CURRENT APPLICATION NUMBER: US/10131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7899
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-7899

Query Match      8.6%; Score 20.8; DB 3; Length 50;
Best Local Similarity 70.0%; Pred. No. 1.7e+03;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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Db 54 AGCTGCTGCTTCTTCTTCAATCCCAACCTGTAA 93
1 AGCTGCTGCTTCTTCTTCAATCCCAACCTGTAA 40

RESULT 2
US-10-131-831-7899
; Sequence 7899, Application US/10131831
; Patent No. 7026121
; GENERAL INFORMATION:
; APPLICANT: Wollgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
; TITLE OF INVENTION: TRANSPLANT REJECTION

FILE REFERENCE: 506612000121
CURRENT APPLICATION NUMBER: US/10/131,831
CURRENT FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9190
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 7895
LENGTH: 50
TYPE: DNA
ORGANISM: Homo sapiens
US-10-131-831-7895

Query Match
Best Local Similarity 8.6%; Score 20.8; DB 5; Length 50;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Db 54 AGCTGCTGCCTCACCTGCTTTTCCAAACCCCACTGTAA 93
1 AGCTGCTGCTTCTTCTTCAATGCATACTGTAA 40

RESULT 3
PCT-US94-14106-20/c
Sequence 20, Application PC/TUS9414106
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Process for Generating Specific Antibodies
NUMBER OF SEQUENCES: 61
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14106
FILING DATE:
CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
PCT-US94-14106-20

Query Match
Best Local Similarity 8.1%; Score 19.6; DB 7; Length 42;
Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Db 177 TTAAGCCACCGTGTGTGTAGGGTGTCTAGGCTGTATCAG 218
42 TTGAGCCACGCGGCGCCACTAGATATCTGGGCGCAACAG 1

RESULT 4
US-08-503-730-37
Sequence 37, Application US/08503730
Patent No. 5780269
GENERAL INFORMATION:
APPLICANT: Inouye, Sumiko
APPLICANT: Inouye, Masayori
TITLE OF INVENTION: NEW HYBRID MOLECULES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSER: Weiser & Associates
STREET: 230 South Fifteenth Street Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA

ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/503,730
FILING DATE: 18-JUL-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/817,430
FILING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 377(913).6277P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8394
TELEFAX: 215-875-8383
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-503-730-37

Query Match
Best Local Similarity 8.1%; Score 19.6; DB 2; Length 50;
Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Db 41 GCTCACCTCCCGACCTGCTGCTCACCTGCTTTCCAAAC 82
2 GGTAACCTCCACCTGCTGCTCACCTGCTTGGCACAC 43

RESULT 5
US-10-131-827-1159/c
Sequence 1159, Application US/10131827
Patent No. 6905827
GENERAL INFORMATION:
APPLICANT: Wohlgenuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
FILE REFERENCE: 506612000120
CURRENT APPLICATION NUMBER: US/10/131,827
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9090
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 1159
LENGTH: 50
TYPE: DNA
ORGANISM: Homo sapiens
US-10-131-827-1159

Query Match
Best Local Similarity 8.1%; Score 19.6; DB 3; Length 50;
Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Db 35 CTGAGAGCTCACCTCCAGCTGCTGCTCACTGCTTTTC 76
50 CTGTGCTGCTCCCTTTCAGTTACAGCCCAAGCCTTTTC 9

RESULT 6

NT, 1967 = 1

US-10-131-831-1159/c
; Sequence 1159, Application US/10131831
; Patent No. 7026121
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
; TITLE OF INVENTION: TRANSPLANT REJECTION
; FILE REFERENCE: 506612000121
; CURRENT APPLICATION NUMBER: US/10/131,831
; CURRENT FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9190
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1159
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-831-1159

Query Match 8.1%; Score 19.6; DB 5; Length 50;
Best Local Similarity 66.7%; Pred. No. 4.5e+03;
Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 35 CTGGAGCTCCACCTCCAGCTGCTCCTCCTCCTTTTC 76
Db 50 CTGGCGCTTCCCTTCCAGTTACAGCCCGAGCTTCTC 9

RESULT 7
US-08-644-664B-35/c
; Sequence 35, Application US/08644664B
; Patent No. 5776746
; GENERAL INFORMATION:
; APPLICANT: Denney Jr., Dan W.
; TITLE OF INVENTION: Gene Amplification Methods
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medien & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/644,664B
; FILING DATE: 01-MAY-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET INFORMATION:
; TELECOMMUNICATION INFORMATION: GENTOPE-00912
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-644-664B-35

Query Match 7.9%; Score 19.2; DB 2; Length 39;
Best Local Similarity 75.0%; Pred. No. 5.6e+03;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 211 TGTATCAGTACCCCACTAAACTGATTCAC 242
Db 37 TGAACAGTACGAACTTAACCTGATTCAC 6

RESULT 8
US-08-761-277A-35/c
; Sequence 35, Application US/08761277A
; Patent No. 5972334
; GENERAL INFORMATION:
; APPLICANT: Denney Jr., Dan W.
; TITLE OF INVENTION: Vaccines For Treatment Of Lymphoma And
; TITLE OF INVENTION: Leukemia
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medien & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/761,277A
; FILING DATE: 06-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/644,664
; FILING DATE: 01-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: GENTOPE-02406
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-761-277A-35

Query Match 7.9%; Score 19.2; DB 2; Length 39;
Best Local Similarity 75.0%; Pred. No. 5.6e+03;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 211 TGTATCAGTACCCCACTAAACTGATTCAC 242
Db 37 TGAACAGTACGAACTTAACCTGATTCAC 6

RESULT 9
US-08-391-000-25
; Sequence 25, Application US/08391000
; Patent No. 5723752
; GENERAL INFORMATION:
; APPLICANT: Houtz, Robert L.
; TITLE OF INVENTION: CLONING AND DEVELOPMENTAL EXPRESSION OF
; TITLE OF INVENTION: PEA RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE
; TITLE OF INVENTION: SUBUNIT N-METHYLTRANSFERASE
; NUMBER OF SEQUENCES: 41

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Burns, Doane, Swecker & Mathis
;; STREET: P.O. Box 1404
;; CITY: Alexandria
;; STATE: Virginia
;; COUNTRY: United States
;; ZIP: 22313-1404
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/391,000
;; FILING DATE: 21-FEB-1995
;; CLASSIFICATION: 800
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Meuth, Donna M.
;; REGISTRATION NUMBER: 36,607
;; REFERENCE/DOCKET NUMBER: 028750-123
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 836-6620
;; TELEFAX: (703) 836-2021
;; INFORMATION FOR SEQ ID NO: 25:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 42 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; US-08-391-000-25

Query Match 7.9%; Score 19.2; DB 2; Length 42;
Best Local Similarity 75.0%; Pred. No. 5.8e+03;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 39 GAGCTCCACCTCCCGAGCTGCTGCTCACCTG 70
Db 8 GAACCTGCTGCTGCTGCTGCTGCTTACCTG 39

RESULT 10
US-08-741-931-25
; Sequence 25, Application US/08741931
; Patent No. 5866394
; GENERAL INFORMATION:
; APPLICANT: HOUTZ, Robert L.
; TITLE OF INVENTION: CLONING AND DEVELOPMENTAL EXPRESSION OF
; TITLE OF INVENTION: PEA RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE
; TITLE OF INVENTION: SUBUNIT N-METHYLTRANSFERASE
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/741,931
; FILING DATE: 31-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/391,000
; FILING DATE: 21-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M.
; REGISTRATION NUMBER: 36,607

;; REFERENCE/DOCKET NUMBER: 028750-123
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 836-6620
;; TELEFAX: (703) 836-2021
;; INFORMATION FOR SEQ ID NO: 25:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 42 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; US-08-741-931-25

Query Match 7.9%; Score 19.2; DB 2; Length 42;
Best Local Similarity 75.0%; Pred. No. 5.8e+03;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 39 GAGCTCCACCTCCCGAGCTGCTGCTCACCTG 70
Db 8 GAACCTGCTGCTGCTGCTGCTGCTTACCTG 39

RESULT 11
US-09-475-947A-43
; Sequence 43, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTS0667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 43
; LENGTH: 39
; TYPE: DNA
; ORGANISM: human
; US-09-475-947A-43

Query Match 7.9%; Score 19; DB 3; Length 39;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 44 CCACCTCCCGAGCTGCTGC 62
Db 13 CCACCTCCCGAGCTGCTGC 31

RESULT 12
US-10-131-827-6394/C
; Sequence 6394, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6394
; LENGTH: 50

TYPE: DNA
ORGANISM: Homo sapiens
US-10-131-827-6394

Query Match
Best Local Similarity 71.4%; Score 19; DB 3; Length 50;
Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 20 ATTTGTGACCTGGCTGGAGCTCCACCTCCCA 54
DB 46 ATTCTGTCTCCAGCCAGGTGCTGCACCTCCCA 12

RESULT 13

US-10-131-827-6784
Sequence 6784, Application US/10131827
Patent No. 6905827
GENERAL INFORMATION:
APPLICANT: Wohlgenuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
FILE REFERENCE: 506612000120
CURRENT APPLICATION NUMBER: US/10/131,827
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9090
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6784
LENGTH: 50
TYPE: DNA
ORGANISM: Homo sapiens
US-10-131-827-6784

Query Match
Best Local Similarity 71.4%; Score 19; DB 3; Length 50;
Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 20 ATTTGTGACCTGGCTGGAGCTCCACCTCCCA 54
DB 5 ATTCTGTCTCCAGCCAGGTGCTGCACCTCCCA 39

RESULT 14

US-10-131-831-6394/C
Sequence 6394, Application US/10131831
Patent No. 7026121
GENERAL INFORMATION:
APPLICANT: Wohlgenuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
FILE REFERENCE: 506612000121
CURRENT APPLICATION NUMBER: US/10/131,831
CURRENT FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9190
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6394
LENGTH: 50
TYPE: DNA
ORGANISM: Homo sapiens
US-10-131-831-6394

Query Match
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Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 20 ATTTGTGACCTGGCTGGAGCTCCACCTCCCA 54
DB 46 ATTCTGTCTCCAGCCAGGTGCTGCACCTCCCA 12

RESULT 15

US-10-131-831-6784
Sequence 6784, Application US/10131831
Patent No. 7026121
GENERAL INFORMATION:
APPLICANT: Wohlgenuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING
FILE REFERENCE: 506612000121
CURRENT APPLICATION NUMBER: US/10/131,831
CURRENT FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: US 10/006,290
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/296,764
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 9190
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6784
LENGTH: 50
TYPE: DNA
ORGANISM: Homo sapiens
US-10-131-831-6784

Query Match
Best Local Similarity 71.4%; Score 19; DB 5; Length 50;
Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 20 ATTTGTGACCTGGCTGGAGCTCCACCTCCCA 54
DB 5 ATTCTGTCTCCAGCCAGGTGCTGCACCTCCCA 39

Search completed: October 1, 2006, 01:24:47
Job time: 116.431 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: September 30, 2006, 23:53:03 ; Search time 488 Seconds

(Without alignments)
6660.074 Million cell updates/sec

Title: US-10-642-946-3

Perfect score: 6272
Sequence: 1 MAVRGAPLISCLALLALC.....TGAFFTYVTYVNFGR 1158

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Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Database : Issued Patents NA.*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	5054	80.6	3728	US-08-111-839-1	Sequence 1, App1
4	4787	76.3	14205	US-09-949-016-14464	Sequence 14464, A
5	2171.5	34.6	3772	US-09-991-181-61	Sequence 61, App1
6	2171.5	34.6	3772	US-09-990-444-61	Sequence 61, App1
7	2171.5	34.6	3772	US-09-997-333-61	Sequence 61, App1
8	2171.5	34.6	3772	US-09-992-598-61	Sequence 61, App1

9	2171.5	34.6	3772	US-09-989-735-61	Sequence 61, App1
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14	2171.5	34.6	3772	US-09-997-653-61	Sequence 61, App1
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16	2106.5	33.6	3470	US-09-976-594-345	Sequence 345, App
17	1748.5	27.9	2382	US-09-641-741-1	Sequence 1, App1
18	1748.5	27.9	2719	US-08-706-216-1	Sequence 1, App1
19	1748.5	27.9	2719	US-09-650-284B-1	Sequence 1, App1
20	1733.5	27.6	2585	US-09-774-828-270	Sequence 270, App
21	1733.5	27.6	2585	US-10-120-988-270	Sequence 270, App
22	1653	26.4	2624	US-09-370-838-19	Sequence 19, App1
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ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/09060482
; Patent No. 6468766
; GENERAL INFORMATION:
; APPLICANT: Lee, Mu-En
; APPLICANT: Layne, Matthew D.
; TITLE OF INVENTION: AORTIC CARDIOPROTECTANT-LIKE POLYPEPTIDE
; FILE REFERENCE: 05433/036001
; CURRENT APPLICATION NUMBER: US/09/060,482
; EARLIER FILING DATE: 1998-04-15
; EARLIER APPLICATION NUMBER: US 08/818,009
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: US 60/103,439
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3935
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (140)...(3613)
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Score: 6272.00
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Best Local Similarity: 100.0%
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Conservative: 0
Mismatch: 0

Query Match: 100.0% Indels: 0
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Qy 1101 PheGlyThrThrValGluProGluPheGluThrGlnLeuGluProGluPheGluThrGln 1120
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RESULT 2

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; Sequence 2722, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTNER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2722
; LENGTH: 4082
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2722
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Best Local Similarity: 99.8% Mismatches: 0
Query Match: 99.9% Indels: 0
DB: 3 Gaps: 0
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US-10-642-946-3 (1-1158) x US-09-949-016-2722 (1-4082)

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Db 367 CCGGAGGCGGCGGCGGAGAGCGGTGCTGACGAGACGAGATGAGAGATTCCTCGAGGGG 426
Qy 41 PheLeuSerGluLeuGluProGluProArgGluAaPASPAGluAaIaProProProPro 60
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Db 487 GAGCCACCCCGGCGGCTCCGAAAGCCAGGCGGCGGCGGAGAGAGAGAGAGAGAGAGAGAG 546
Qy 81 ThrAaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 100
Db 547 ACGGCGGAGAAAGTGTCTCCGGAAGAGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 606
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QY 101 LysGlyProLeuValProlyseGluSerLeuGluGlySerProArgProProlyValGly 120
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QY 121 LysGlyLysProProlyValThrLysLysProLysGlyLysProProlyValThrLys 140
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QY 161 ThrLysLysProProseGlyLysArgProProLysLeuAlaProseGlyThrLeuGlu 180
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RESULT 3
US-08-111-939-1
; Sequence 1, Application US/08111939
; Patent No. 5460951
; GENERAL INFORMATION:
; APPLICANT: Kawai, Shinji
; APPLICANT: Takehita, Sunao

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; APPLICANT: Okazaki, Makoto
; APPLICANT: Amann, Egon
; TITLE OF INVENTION: Bone-Related Carboxypeptidase-Like
; TITLE OF INVENTION: Protein and Process for its Production
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/111,939
; FILING DATE: 26-AUG-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 324033/92
; FILING DATE: 03-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 230029/92
; FILING DATE: 28-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Foreman, David S.
; REGISTRATION NUMBER: 33,694
; REFERENCE/DOCKET NUMBER: 02481.1321-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4000
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3728 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; STRAIN: osteoblastic cell line MC3T3E1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 69..3452
; US-08-111-939-1
;
; Alignment Scores:
; Pred. No.: 0 Length: 3728
; Score: 5054.00 Matches: 956
; Percent Similarity: 87.1% Conservative: 56
; Best Local Similarity: 82.3% Mismatches: 112
; Query Match: 80.6% Indels: 38
; DB: 2 Gaps: 9
;
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      129  CCTGAGGGGAGACCAACAGACGGTCTGACGAGACGAGATCGAGAGTCTCTGAGAGGC 188
Qy      41  PheLeuSerGluLeuGluProGlu-----ProArgGluAspAspValGluAlaProPro 58
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Db 3033 GGGAACTGCTCCATTTCCGAGAGTGAACCTTCACGACCCATGACCCCGCAGCGCGC 3092
QY 1018 LeuGlnGlnArgIleGlnHisArgLysLeuArgLeuArgIleGlnMetArgLysArg 1037
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Db 3093 ATGCACAGCGCGCTACAGTACCGGCTCCGATGAGGAGAACAGATGCACTGCGTGC 3152
QY 1038 LeuAsnAlaThrThrLeuGlyProHisThrValPro--ProThrLeuProProAla 1056
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QY 1077 GlyTyrGluGluSerGluThrGluThrTyrThrGluValAlaThrGluPheGlyThrGlu 1096
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QY 1117 PheGluThrGlnLeuGluProGluPheGluGluGluGluGluGluGluGluGluGlu 1136
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Db 3447 GACTTC 3452

RESULT 4
US-09-949-016-14464
; Sequence 14464, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 14464
; LENGTH: 14205
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14464

Alignment Scores:
Pred. No.: 6,15e-309 Length: 14205
Score: 4787.00 Matches: 1148
Percent Similarity: 36.0% Conservative: 6
Best Local Similarity: 35.8% Mismatches: 4
Query Match: 76.3% Indels: 2051
DB: Gaps: 20

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QY 199 ----- G1yAlaProLeuSerAsnAsnTrpGlnAsnProGlyGlnGlnThrH1 214
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QY 495 ----- 495
Db 8486 CATTGTGGGCGAGGGGTGGGCTCTCAGAGGGGCTGCAGTACTCTGAGGCTGCC 8545
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QY 677 AGIuMet ----- 679
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72	PRIOR FILING DATE: 1998-07-02
73	PRIOR APPLICATION NUMBER: 60/091978

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RESULT 6
US-09-990-444-61
Sequence 61, Application US/09990444
Patent No. 6930170
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Boctstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottlieb, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kjaevik, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C19
CURRENT APPLICATION NUMBER: US/09/990,444
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
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 US-09-997-333-61
 ; Sequence 61, Application US/09997333
 ; Patent No. 6953836
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
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 ; APPLICANT: Debnayere, Luc
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P27301C27
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CURRENT FILING DATE: 2001-11-15
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PRIOR FILING DATE: 1998-06-24

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RESULT 8

US-09-992-596-61

Sequence 61, Application US/09992598

Patent No. 6956108

GENERAL INFORMATION:

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APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.

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APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

Acids Encoding the Same

FILE REFERENCE: P2730PIC20

CURRENT APPLICATION NUMBER: US/09/992,598

CURRENT FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

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      :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
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      :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Db      2152 CTACGCGGCTGTGATTAATACCCACATGAGAGCCAGCTGCCGAGAGAGAGATTA 2211
      :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
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      :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
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      :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Qy      913 rAePgluGlnGlylAlProIlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAl 933
      :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
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      :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
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APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunes, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C60
CURRENT APPLICATION NUMBER: US/09/989,726
PRIOR APPLICATION NUMBER: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1997-11-12
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PRIOR APPLICATION NUMBER:	60/092182
PRIOR FILING DATE:	1998-07-09

Alignment Scores:

Pred. No.:	3 02-135
Score:	2171.50
Percent Similarity:	58.3%
Best local Similarity:	45.7%
Query Match:	34.6%
DB:	5
	Gaps:
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US-10-642-946-3 (1-1158) x US-09-989-726-61 (1-3772)

[illegible]

[illegible]

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QY	516	lAlaYArpheHleArglleTyRProLeuThrTP-----AsnGlySerLeuCYwMetAr	534
Db	1126	GGCCCGCTACATCCGACATAAACCTCCAGTCCGTGGTTGATTAATGGAGCATCTGCATCAG	1185
QY	534	gLeuGluValIleuGlyCySerSerValAProValTySerTyTyR---AlaGlnAsnG	553
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QY	553	vUalValAlaThrAspAAspLeuAspPheArGHisHisSerTyRlYsaAspMetArGlnLe	573
Db	1246	GATGACCAACCATGATACCTGGAATTTTAAGACACCAATATTAAGAAATGGCCAGTT	1305
QY	573	uMetLysValValAsnGluGluCyRProThrIleThrArGThrTyRSerLeuGlyLysE	593
Db	1306	GATGAAAGTGTGTAATGAATAATGTGTCCCAATATCACACGAATTTACAACTGGAAAAAG	1365
QY	593	rSerArGlyLeuIuYsIleTyRlAmetGluIleSerAspAsnProGluGlnHieglIuLe	613
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QY	613	uGlyGluProGluPheArGlyTyRThrIaGlyIleHieglYAasnGluValIleuGlyArG	633
Db	1426	CGGTGAGCCGCAATTCACATCACTGGGGGGCCCAAGGCATGAGGTGCTGGGCCGGGA	1485
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Db	1546	CGTCCACCTGTGTGAGGAGAGCGGAGTTCACGTCTCTCCCTCAACCCCGATGGCTA	1605
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Db	1726	GGATTCGACAGATTCGCCAGGAAAGTCCCAATCACTATATTCATTCACCTCGAGTGT	1785
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QY	813	gTrpLeuAlaIleSerPheAlaSerAlaHisLeuThrIleuThrGluProTyRArgGlyG	833
Db	1972	CTGGCTGGCCCACTCTATATGCTTCACACACACGGCTCATGACAGACGCGGAGGAGGCT	2031
QY	833	YCyGlnAlaGlnAspTyRThrGlyGlyMetGlyTleValAsnGlyAlaLysTrpAsnPr	853

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Qy 873 eTYrleuGlCYeAhpYrPheProHlsgluserGluenProahrglulrpglUAAna 893
Db 2152 CTAGTGGGCTGTGATTAATCCCATGAGAGCCAGCTGGCCGAGAGATGGAGATTA 2211
Qy 893 nlysglUAlaleuLeuThrPheMetGluInvalHlAargGlYlIelYsglYVal1th 913
Db 2212 CCGGGAATCTCTGATCTGTTCATGAGAGGTTTCATCGTGGCATTAAGCTTGGTGA 2271
Qy 913 rAeRglUglnglYlIeProHleAlaAna1athlIleSerValserGlYlIeAnHlsgl 933
Db 2272 AGATTCAATGAAAGAAAGAAATCCCAAGCCATTAATCTCGTGAAGAGCATTAACATGA 2331
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RESULT 11
US-09-97-514-61
Sequence 61, Application US/0997514
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottlieb, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730P1C46
CURRENT APPLICATION NUMBER: US/09/97,514
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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40	PRIOR FILING DATE: 1998-06-24
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45	PRIOR APPLICATION NUMBER: 60/090445
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64	PRIOR FILING DATE: 1998-06-25
65	PRIOR APPLICATION NUMBER: 60/090655

[illegible]

[illegible]

Db	1306	GATGAAAGCTTGTAATGAATATGTGTCCTCAATATATCAACGAATTTACCAATTTGAGAAAAAG	1365
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Db	1366	CCACCAGGGCCCTGAAGCTGTATGCTGTGTGAATCTTCAGATACACCTGGGAGCATGAAGT	1425
Qy	613	uglygluproglupheargtyrthralaglyllesglyanquilvalleuglyargyl	633
Db	1426	CGGTGAGCCCGAGTTCCACTACATGCGGGGGGCCACGGCAATAGAGGTGCGGCCGGGA	1485
Qy	633	uileuleuleuleuleumetiintyrlleucyargylutyrrargyapgluayanproargva	653
Db	1486	GCTGTGCTGCTGCTGCTGTCAGATTCCGTGTGTGACAGAGTACTTGGCCCGGAATGCGCGCAT	1545
Qy	653	largserleuvalginapthrargilehsileuvalproserleuanproaparglyty	673
Db	1546	CGTCAACCTTGGTGGAGAGACGGGATTCACGTCTCTCCCTCCCTCAACCCCGATGGCTTA	1605
Qy	673	rgluvalalaaglnmetgysergluphegilyasntrpalaaleuglyleutrprrgl	693
Db	1606	CGAAGAGGCTCATCAAGAAAGGGGCTCGAGACTGGAGGCTGTCCTCGGAGCCTGACCA	1665
Qy	693	uglulglypheaprllephegluapheproapleuanservalleutrpgllyagl	713
Db	1666	CGATGAATTGATCAATCAACAACTTCTCGAATTTAAACCGTGTCTGTGGAGGCAGA	1725
Qy	713	ugluargystrpvalprotyrargvalproasnashanleuproileoprogluargty	733
Db	1726	GGATGACAGAAATGTCCTCCAGAAAGTTCCAAATCATATATGCAATCCTTGAGTGCTT	1785
Qy	733	rleuserproapalathralvalserthrngluvalarglalellealatrpmetgily	753
Db	1786	TCTGTGGAATAATGCAAGCGTGGCTGGCAGACACAGCAAGCACTATAGCTGTGATGAAAA	1845
Qy	753	apasnrophevalleuglyalasnleuannglyglygluargleuvalsertyrproty	773
Db	1846	AATCCCTTTTGTGCTGGCGGCAACCTGTCAAGGGGGGAGCTGTGTGGTGTATCCCTTA	1905
Qy	773	raspmerlalargthrprothrnglungluileuleualalalameclalalalar	793
Db	1906	CGACCTGTGGCGGTCCCTCTGAAAGCCGAC-----	1936
Qy	793	gglglynapgluapgluvalsergyluaglnluthrproapnhalalephear	813
Db	1937	-----GAAACACCCCAACCCCGATGACACAGTTCGG	1971
Qy	813	gtrpleualalieserphealaseralahnleuthrleuthrgluupotyralarglygl	833
Db	1972	CTGGTGTGCTCTATGCTCTACACACCGGCTCATGTACACAGCCCGAGAGAGGCT	2031
Qy	833	ycysglnalaglnaptyrthrnglylmeaglylvalasnnglylalystrpanpr	853
Db	2032	GTGCCACCGAGAGCTTCCAGAAAGAGAGGAGCTGTCAATGGGGCTCTTGACACAC	2091
Qy	853	oargthrglythrleasnashpnesertyrleuhslethrasncysleugluuuserph	873
Db	2092	CGTGCTGGAGAGTGTGAACGATTTCAAGTACCTTCATACAAACGCTTCAACAGTGCAT	2151
Qy	873	etyrleuglycysaplyspheprohlesgusergluueuproarglulutrpgluaans	893
Db	2152	CTACGTGGGCTGTGATTAATATCCACATGTAGAGCACTGCCCGAGAGATGTGGGAATTA	2211
Qy	893	nlysglnalaleuueuthrphmetglnvalhlsargglyllelysglyvalvalth	913
Db	2212	CGGGAAATCTGTAGTCGTTCATGAGCAAGGTTCATGTGGCATTAAGGCTTGATGAG	2271
Qy	913	raspglunclnlytleuproilealaasnalarthrlleservalserglylleasnhsgl	933
Db	2272	AGATTTCACATGAAAAGAAATCCAAAGCGCATATATCTCGTGAAGAGCATTAACATGA	2331
Qy	933	yvallystrhalaserglylasybtyrtrparglleleuanbproglylutyralargva	953
Db	2332	CATCGAAGACCAACATGGGAGATTAATGCGCGCTCTGAACCTCTGAGAGATATGTGGT	2391

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Score:	2171.50	Matches:	466
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QY	100	AspIysGLYProLySValProLySGIuSerIeuGIuGIySerProaIyProLyS	110
DB	86	-----GAAAGGGCGGGCGGGCCCCCTG-----	100
QY	120	GIYLySGILySProProLySaIaThrlYsYProLySGILySProProLyS---Ala	133
DB	109	-----CGCGCGCGCGCGCTCTGGCGCCCC-----TGTCCCGCGCGCGCGC	153
QY	139	ThrlYsApyrProLySGILuProProLySaIaThrlYsYProLySGILySProPro	150
DB	154	CGAGCCAGCGCGCGCGCGCGGTCAACGCGCGAGCGAGCGCGCG-----	190
QY	159	LySaIaThrlYsYProProSerGIyLySaIaIaProProIleuAlaProSerGIuThr	178
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QY	179	LeuGIuTrProIeuPro-----ProProSerProGIY	190
DB	238	-----CCCTTGGCGCGCGCGAGCTTCTGCGCGCGAGCGCGCGCGCGCGCGGT	288
QY	191	ProGIuGIuIeuPro---GIuGIuGIYLaIaProIeuSerAmaIaIaProGIuIaIa	205
DB	289	GACCGTGAACCTGCTCTGGAGCGCGAGCGAGCGAGCATGTCC-----CGCCC	336
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Db 617 -----CCGCTCCACCA-----GCTAA 633
Qy 336 gGluGluLeuLeuYlyPProLYsPProLYsGluAspSerPProLYsGluGluThrAspLYsTr 356
Db 634 ACACAGCAACAAAAAGTTATGAGAACCAAGAGCTCTGAGAAAGGCTGCCAAGAT----- 688
Qy 356 pAlaValGluYlybGlyLYsAspHiLYsGluPProLYsGluYlybGluGluGluGlu 376
Db 689 -----GATCACAAGTCCCTGCTGGCCCGTGAAGATGTCAGAGAG-- 727
Qy 376 uTrpThrProThrGluYlyValLYsCyPProPProLYsGluMetGluSerHiLYsGlu 396
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Qy 396 uAspAsnGluLYsLeuGlaSerSerMetLeuLYsGluYlybGluYlybGluYlybGluYlyb 416
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Qy 436 uAspAspAlaArgThrGlnTrpLYsGluValAspThrArgArgThrThrArgPheThrGlu 456
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Qy 516 LAlaArgPheLYsGluYlybTrpLeuThnTrp-----AsnGlySerLeuCYsMetLYs 534
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Db 1246 GATGACCAACCATGATGATCTGATTTTAAGCACCAATTAATTAAGAAATGGCCAGAT 1305
Qy 573 uMetLYsValAlaAsnGluYlybCyPProThrLYsTrArgThrLYsSerLeuGluYlybSe 593
Db 1306 GATGAAAGTTGTAAGAAATGTCTCCAAATACACAGAAATTTAAACAATGGAAAGA 1365
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Db 1426 CGGTGAGCCGAGTTCCACTACATCCGGGGGCCCAAGCAATGAGTGTGGCGCGGGA 1485
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Db 1486 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1545
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Db 1606 CGAAGAGGCTTACGAAGGGGCTCGAGAGCTGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 1665

Qy 693 uGluGlyPheAspLYsPheGluAspPhePProAspLeuAsnSerValLeuTrpGluYlybAla 713
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Qy 713 uGluArgLYsTrValPProLYsArgValPProAsnAsnAsnLeuPProLYsTrArgLYsTr 733
Db 1726 GGATGAGAGAAATGCTCCAGAGAAATGCTCCCAATCTCAATATGGAATCCCTGATGGT 1785
Qy 733 rLeuSerPProAspAlaThrValSerThnGluValArgAlaLeuAlaLeuAlaTrpMetGluYly 753
Db 1786 TCTGTCCGAAATATGCACAGGTGGCTGCCAGACCCAGACAGACATGATGCTGATGAAA 1845
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Db 1846 AATCCCTTTTGTGGCGGCGACCTTCAGAGGCGGCGAGCTGGTGGTGGCTATCCCTGA 1905
Qy 773 rAspMetAlaArgThrPProThrGlnGluGluLYsLeuLeuAlaAlaMetAlaAlaAla 793
Db 1906 CGACTGTGGGTCTCCCTGGAAGCCAG----- 1936
Qy 793 gGlyGluAspGluAspGluValSerGluAlaGluGluThnTrpAspHiLYsAlaLeuPheArg 813
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Qy 813 gTrpLeuAlaLeuSerPheAlaSerAlaHiLYsLeuThnTrpGluPProLYsArgGluYly 833
Db 1972 CTGGCTGGCTATCTCTATGCTTCACACACCGCTCTACAGACGCCCGGAGAGGCT 2031
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Db 2212 CCGGAAATCTGATCGGTTCATGAGACAGGTTATGATGATGATTAAGCTTGATGAG 2271
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RESULT 13
US-09-997-349-61
Sequence 61, Application US/09997349
Patent No. 7034106
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavyn, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C37
CURRENT APPLICATION NUMBER: US/09/997,349
CURRENT FILING DATE: 2001-11-15
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

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Score: 2171.50 Matches: 466
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Best Local Similarity: 45.7% Mismatches: 227
Query Match: 34.6% Indels: 199
DB: 5 Gaps: 24

US-10-642-946-3 (1-1158) x US-09-997-349-61 (1-3772)

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DB 86 -----GAAGGCGGGGCGGCGCCCTG--- 108
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DB 154 CCAGCCAGCCCGCGCGCGCTGACACGCGCAGCAGCCGCGC----- 198
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DB 199 -----CTCCCGCGCCAGAGCGCGCGCTGCTGCGCTCG----- 237
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DB 689 -----GATCACAGTGTCCGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 727
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DB 728 -----AGTTGCCACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 765
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/ Sequence 61, Application US/0997653
/ Patent No. 7034122
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi J.
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Bosteys, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan J.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerritsen, Mary B.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Kljavin, Ivar J.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James

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APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ACIDS
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PLC38
CURRENT FILING DATE: 2001-11-15
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Db	1246	GATGACCAACCACTGATGACTGGATTTTAAGACCAACATTAATAGAAGAAATGGCCAGTT		1305
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Db	1366	CCACGAGGCGCTGAAGCTGTAATGCTGTGGAGATCTCAATATCACTGGGGAGCATGAAGT		1425
Oy	613	uGlyGluProGluPheArgTyrThrAlaGlyIleHisGlyAsnGluValLeuGlyIaArgI		633
Db	1426	CGGTAGCCCGAGTTCCACTATCGCGGGGGCCACGCGCATAGAGTGGCTGGGGCCGGGA		1485
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Db	1937	-----GAACACACCCCCACCCCCGATGACCAACGATGTCG		1971
Oy	813	gTrpLeuAlaIleSerPheAlaSerAlaHisIleuThrIleuThrGluuProTYrArgGlyG1		833
Db	1972	CTGGCTGGCTACTCTTATGCTTCCACACACGCGCTCATGAAGAGCGCCCGAGGAGGCT		2031
Oy	833	yCyAsGlnAlaGlnAspTyrThrGlyGlyMetGlyIleValaAnGlyAlaIyAsTrpAsnPr		853
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Db	2092	CGTGCCTGGAAGTCTGAAGATTTTCAAGCTTATCAAACTCTTCAACCTGTCAT		2151
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Db	2152	CTACGTGGGCTGTGATTAATACCCACATAGAGCCACGCTGCCGAGAGTGGGAGAAATA		2211
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RESULT 15
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/ Sequence 61, Application US/09989293A
/ Patent No. 7034136
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi J.
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Botstein, David
/ APPLICANT: Deenoyers, Luc
/ APPLICANT: Eaton, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Kijavlin, Ivar J.
/ APPLICANT: Knapier, Mary A.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zenith
/ TITLE OF INVENTION: Seceted and Transmembrane Polypeptides and Nucleic
/ FILE OF INVENTION: Acids Encoding the Same
/ FILE REFERENCE: P27301C66
/ CURRENT APPLICATION NUMBER: US/09/989, 293A
/ PRIOR FILING DATE: 2001-11-20
/ PRIOR APPLICATION NUMBER: 60/049787
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/ PRIOR APPLICATION NUMBER: 60/062250
/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/065186
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/

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17	PRIOR FILING DATE: 1998-06-18
18	PRIOR APPLICATION NUMBER: 60/089944
19	PRIOR FILING DATE: 1998-06-19
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28	PRIOR APPLICATION NUMBER: 60/090252
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33	PRIOR FILING DATE: 1998-06-22
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35	PRIOR FILING DATE: 1998-06-23
36	PRIOR APPLICATION NUMBER: 60/090355
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38	PRIOR APPLICATION NUMBER: 60/090429
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40	PRIOR APPLICATION NUMBER: 60/090431
41	PRIOR FILING DATE: 1998-06-24
42	PRIOR APPLICATION NUMBER: 60/090435
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44	PRIOR APPLICATION NUMBER: 60/090444
45	PRIOR FILING DATE: 1998-06-24
46	PRIOR APPLICATION NUMBER: 60/090445
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Score: 2171.50 Matches: 466
Percent Similarity: 58.3% Conservative: 129
Best Local Similarity: 45.7% Mismatches: 227
Query Match: 34.6% Indels: 199
DB: Gaps: 24

US-10-642-946-3 (1-1158) x US-09-989-293A-61 (1-3772)

QY 80 GYThrAlAlAGluValProProGluYulYrThrLysAspLysGlyLysLysLys 99
DB |||||:|||||
DB 44 GACCGCGCTCGAGGGGTCGCGCGG-----GGAAGGAGGAGGAAG 85
QY 100 AspLysGlyProLysValProLysGluSerLeuGluGlySerProArgProLysLys 119
DB 86 -----GAGGGCGGGGCGCGCCCTCG----- 108
QY 120 GlyLysGluYrProLysAlaThrLysLysProLysGluLysProLys---Ala 138
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 109 -----CGCCCGCGCGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 153
QY 139 ThrLysLysProLysGluGluProLysAlaThrLysLysProLysGluLysProPro 158
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 154 CCAAGCCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 198
QY 159 LysAlaThrLysLysProLysGlyLysArgProLysLysLysLysLysLysLys 178
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 199 -----CCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 237
QY 179 LeuGluTrpProLysPro-----ProProProProProProProProProPro 190
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 238 -----CCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 288
QY 191 ProGluGlu-LysPro---GlnGluGlyAlaProLysSerAspAsnTrpGlnAsnPr 209
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 289 GACCGTGAACCTGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 336
QY 209 ogLysGluThrHisVal----- 215
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 337 GGGGACCGGTACCCAGCGCGTGGCGCTGCGCGAGTGACCTGTGCGCGGGTGG 396
QY 216 -----G1 216
DB 397 AGCCAGGCGCGAGCCCTCGAGAGCCTGATTATACGGGAGAGAGATCTGAGCGGGA 456
QY 216 uAlaGlnGluHisGlnProGluProGluGluGluGluGluGluGluGluGluGlu 236
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 457 GCGCTTCTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 516
QY 236 nAspGlnIleGluArgLysAspTyrgLysAspPheGluTyrlLeuArgGlnLysGlnPr 256
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 517 G-----CCGGGAGAGAGTGGGAG-----CGGCGCGCGCGAGAGGCC 552
QY 256 oArgProProProSerArgArgArgArgProGluLysValTrpProGluProProGlu 276
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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QY 276 uLysAlaProAlaProAlaProGluGluArgIleGluProProValLysProLeuLeuPr 296
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DB 601 GAGTCG-----GCTCCGAGC----- 616
QY 296 oProLeuProProAspTyrgLysAspGlyTyrlValIleProAsnTyrlAspAspMetAspTy 316
DB ----- 616
QY 316 rTyrlPheGlyProProProProGluLysProAspAlaGluArgGlnThrAspGluGlu 336
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 617 -----CGGCTCCAGCA-----GCTGA 633
QY 336 sGluGluLeuLysLysProLysLysGluAspSerSerProLysGluGluThrAspLysTr 356
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 634 ACACAGCAACAAAAGTTATGAGAACAGAGCTCTGAGAAAGCTGCCAACGAT----- 688
QY 356 pAlaValGluLysGlyLysAspHisLysGluProArgLysGlyGluLeuGluGluGlu 376
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 689 -----GATCACAGTGTCCGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 727
QY 376 uTrpThrProThrGluLysValLysCysProProIleGlyMetGluSerHisArgIleG 396
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 728 -----AGTTGCCACCTTGTGTGTGTAAGAACTTAAATATC 765
QY 396 uAspAsnGlnIleArgAlaSerSerMetLeuArgHisGlyLeuGlyAlaGlnArgLysAr 416
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 766 AGACTTCACAGCTCCATGCTCCACGCGTAAGCGCATGCGCTGGGGGCACTCGAGGGAG 825
QY 416 gLeuAsnMetGlnThrGlyAlaThrGluAspAspTyrlTyrlAspGlyAlaTrpCysAlaG 436
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 826 ACTCAACATCCAGCGCGCGCATTAATGAATAATTTATATGACGAGCGTGTGCGCGG 885
QY 436 uAspAspAlaArgThrGlnTrpIleGluValAspThrArgArgThrArgPheThrG 456
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 886 AAGAAATACCTCCACAGTGAATGATGATGATCTGGCGCGCGCGCGCGCGCGCGCGCG 945
QY 456 yValIleThrGlnArgLysArgSerSerIleHisAspAspPheValThrThrPhePheVa 476
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 946 TGTCACTACTAAGGAGGAGATCTCCCTGGCTGAGTATCGGTGACATCTTAATAGGT 1005
QY 476 lGlyPheSerAspAspSerGlnThrTrpValMetTyrlThrAsnGlyTyrgLluMetTh 496
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1006 CATGTGTGACATGACAGCCACACCTGGGTCACTTTAAGATGATCTGAGACATGAT 1065
QY 496 rPheHisGlnValAspLysAspTrpProValLysSerGluLysProGluProValYa 516
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1066 ATTTAGAGGAACAGTGAAGAGAGATCCCTGTTCTCAATGAGCTAACCCCTCCATG 1125
QY 516 lAlaArgPheIleArgIleTyrlProLeuThrTrp-----AsnGlySerLeuCyMetAr 534
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1126 GGGCGGCTACATCCGCAATTAACCTCACTGCTGTTGATATGAGAGCATCTGATGAG 1185
QY 534 gLeuGluValLeuGlyCysSerValAlaLysSerTyrlTyrl---AlaGlnAsnG 553
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1186 AATGAGATCTCGGCTGCGCACTGCAAGATCTTAATATTTATACCGCGGAACA 1245
QY 553 uValValAlaThrAspAspLeuAspPheArgHisSerTyrlLysAspMetArgGlnLe 573
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1246 GATGACCACTGATGACCTGATTTTAAGACACCAATTTAAGAAATCGCCAGATT 1305
QY 573 uMetLysValValaGlnGluCysProThrTrpIleThrArgThrTyrlSerLeuGlyLysSe 593
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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QY 593 rSerArgGlyLeuLysIleTyrlAlaMetGluLysSerAspAsnProGluGluHisGluLe 613
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1366 CCACAGGCGCTGAAGCTGTATGCTGTGAGATCTCAGATCTCCCTGGGAGCACTGAAGT 1425
QY 613 uGlyGluProGluPheArgTyrlThrAlaGlyIleHisGlyAsnGluValLeuGlyYArgG 633
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1426 CGGTGAGCCCGAGTTCTCACTACATCGCGGGGCGCACGCAATGAGAGTCTGGCGCGGA 1485
QY 633 uLeuLeuLeuLeuMetGlnTyrlLeuCyArgGlyTyrlArgAspGlyAsnProArgVa 653

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Db      1486 GCTGCTCTGCTGCTGTCGAGTTCGTGTGTCAGAGATCTTGACCCCGGAATGCGCCCAT 1545
Qy      653 1AsgSerLeuValGlnAapThrArg11Eh1LeuValProSerLeuAapProAapGly 673
Db      1546 CTTCCACCTGCTGTGAGAGAGACGCGGATTCACGCTCCCTCCCTCAACCCCGATGCTA 1605
Qy      673 rGluValAlaAlaGlnMetGlySerGlnPheGlyAapThrAlaLeuGlyLeuThrPheGly 693
Db      1606 CGAAGAGGCTTACCAAGGAGGCTGAGAGCTGGAGGCTGGTCCCTGGAGACCTGGACCA 1665
Qy      693 uGluGlyPheAapThrPheGlnAapPheProAapLeuAapSerValLeuThrPheGlyAlaGly 713
Db      1666 CGATGGAATGACATCAACAACACTTCTCGATTAAACCGCTGCTGGAGGCGAGA 1725
Qy      713 uGluArgLeuThrValProThrArgValProAapAapAapLeuProIleProGluArgTy 733
Db      1726 GGATCGACAGAAATGTCCCGAAGAAAGTTCCCAATCATATGTCAATCCCTGAGTGT 1785
Qy      733 rLeuSerProAapAlaThrValSerThrGluValArgAlaIleLeuAlaThrMetGly 753
Db      1786 TCTGTGGAATAATGCCAGGCTGCTGCCAGAACCCAGACAGCATAGCTGGAATGAAA 1845
Qy      753 AaapProPheValLeuGlyAlaAapLeuAapGlyGlyAargLeuValSerTyProTy 773
Db      1846 AATCCCTTTGTGCTGCGCGCAACTGCAAGGCGCGAGCTGTGTGCGTATCCCTA 1905
Qy      773 rAapMetAlaArgThrProThrGlnGlnLeuLeuAlaAlaMetAlaAlaAar 793
Db      1906 CGACCTGTGCTGCGGCTCCCTGGAAGACGAG----- 1936
Qy      793 gGlyGluAapGluAapGluValSerGluAlaGlnGluThrProAapHisAlaIlePheAr 813
Db      1937 -----GAACAACCCCGCCGATGACCAAGTGTCCG 1971
Qy      813 gTrPLeuAlaIleSerPheAlaSerAlaHisLeuThrLeuThrGluProTyArgGly 833
Db      1972 CTGGCTGCGCTACTCTCATGCTCCACACCGGCTCATAGACCGCCGAGAGAGGT 2031
Qy      833 yCyGlnAlaGlnAapTyThrGlyGlyMetGlyIleValAapGlyAlaAlaTyTrPAsnPr 853
Db      2032 GTGCCACACGAGGACTTCAGAAAGAGAGAGGACTGTCAATGGGGCTTCCTGGACAC 2091
Qy      853 oArgThrGlyThrIleAapAapPheSerTyTrLeuHisThrAapCyLeuGluLeuSerPh 873
Db      2092 CGTGGCTGGAAGTCTGAACGATTCACATTCATCAACAACCTTCGAACTGTCCAT 2151
Qy      873 eTyTrLeuGlyCyAapPhePheProHisGlnSerGluLeuProArgGluTrPgluAapA 893
Db      2152 CTACGTGGGCTGTGATTAATACCACTGAGACCACTGCCGAGAGTGGAGATTA 2211
Qy      893 nLyGluAlaLeuLeuThrPheMetGlnGluValHisArgGlyIleLyGlyValValTh 913
Db      2212 CCGGGAATCTCTGATGTTTATGAGCAGGTTTCATCGTGCAATTAAGCTTGGTAG 2271
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Db      2272 AGATTTCACATGAAGAAAGAAATCCCAACGCCATTATCTCGTAGAAGGCATTAAACATGA 2331
Qy      933 yValLyThrAlaSerGlyValAapTyTrPArgIleLeuAapProGlyValTyTrArgVa 953
Db      2332 CATCCGAACGCAACACATGGGATTACTGGCGCTCTTAACCTGGAGAGATGTGGT 2391
Qy      953 lThrAlaHisAlaGlnGlyTyTrThrProSerAlaAlaTyThrCyAapAapAapTyTrAapI 973
Db      2392 CACAGCAAAAGCGCAAGGTTTCACTGCATCCACCAAGAACTGTATGGTGTATGACAT 2451
Qy      973 eGlyAlaThrGlnCyAapAapPheIleLeuAlaArgSerAapTrPlyAargIleArgGluI 993
Db      2452 GGGGGGCAACAAGGTGATCTTCACTTAGCAAAACCAACATGCCCGCATCCGAGAGAT 2511
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Db      2512 CATGAGAACTTTGGAGACGCCCGTC----- 2539
Qy      1013 oGlnGlnAargLeuGlnGlnAlaArgLeuGlnHisAargLeuAargLeuAlaGlnMe 1033
Db      2540 -----AGCCTGCCAGCCAGCGGGCTGAAGCTGGGGGCGGAAAGAGACGACGCG 2589
Qy      1033 tAargLeuAargAargLeuAapAlaThrThrTrLeuGlyProHisThrValProProThr 1052
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Job time : 696 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: September 30, 2006, 23:57:50 ; Search time 2631 Seconds
(without alignments)
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Title: US-10-642-946-3

Perfect score: 6272

Sequence: 1 MAVRGAPLISCLALALC.....TGGAFFTYVETVNFGR 1158

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	6272	100.0	3935	US-10-238-876-1 Sequence 1, Appl1

2	6272	100.0	3935	7	US-10-177-293-1	Sequence 1, Appl1
3	6272	100.0	3935	7 <td>US-10-159-563-288</td> <td>Sequence 288, App</td>	US-10-159-563-288	Sequence 288, App
4	6272	100.0	3935	9 <td>US-10-775-820-194</td> <td>Sequence 194, App</td>	US-10-775-820-194	Sequence 194, App
5	6272	100.0	3935	9 <td>US-10-775-820-195</td> <td>Sequence 195, App</td>	US-10-775-820-195	Sequence 195, App
6	6272	100.0	3935	9 <td>US-10-473-974-128</td> <td>Sequence 128, App</td>	US-10-473-974-128	Sequence 128, App
7	6272	100.0	3935	10 <td>US-10-956-157-561</td> <td>Sequence 561, App</td>	US-10-956-157-561	Sequence 561, App
8	6272	100.0	3935	10 <td>US-10-947-249-162</td> <td>Sequence 162, App</td>	US-10-947-249-162	Sequence 162, App
9	6272	100.0	3935	16 <td>US-11-245-147-128</td> <td>Sequence 128, App</td>	US-11-245-147-128	Sequence 128, App
10	6264	99.9	3914	10 <td>US-10-956-157-5213</td> <td>Sequence 5213, App</td>	US-10-956-157-5213	Sequence 5213, App
11	6264	99.9	4125	9 <td>US-10-775-820-133</td> <td>Sequence 133, App</td>	US-10-775-820-133	Sequence 133, App
12	6256	99.7	3922	6 <td>US-10-116-802-133</td> <td>Sequence 490, App</td>	US-10-116-802-133	Sequence 490, App
13	5725	91.3	3523	7 <td>US-10-264-049-490</td> <td>Sequence 345, App</td>	US-10-264-049-490	Sequence 345, App
14	4925.5	78.5	3170	7 <td>US-10-101-510-345</td> <td>Sequence 8, Appl1</td>	US-10-101-510-345	Sequence 8, Appl1
15	4791	76.4	16151	3 <td>US-09-957-956-8</td> <td>Sequence 8, Appl1</td>	US-09-957-956-8	Sequence 8, Appl1
16	4791	76.4	16151	10 <td>US-10-642-946-8</td> <td>Sequence 196, App</td>	US-10-642-946-8	Sequence 196, App
17	4551	72.6	2839	9 <td>US-10-775-820-196</td> <td>Sequence 53, Appl</td>	US-10-775-820-196	Sequence 53, Appl
18	3488.5	55.6	2168	9 <td>US-10-473-974-53</td> <td>Sequence 53, Appl</td>	US-10-473-974-53	Sequence 53, Appl
19	3488.5	55.6	2168	16 <td>US-11-245-147-53</td> <td>Sequence 6085, App</td>	US-11-245-147-53	Sequence 6085, App
20	2974	47.4	2172	9 <td>US-10-775-820-197</td> <td>Sequence 20, Appl</td>	US-10-775-820-197	Sequence 20, Appl
21	2904	46.3	2555	9 <td>US-10-723-860-6085</td> <td>Sequence 197, App</td>	US-10-723-860-6085	Sequence 197, App
22	2508	40.0	1853	3 <td>US-09-925-302-20</td> <td>Sequence 61, Appl</td>	US-09-925-302-20	Sequence 61, Appl
23	2508	40.0	1853	3 <td>US-09-925-302-20</td> <td>Sequence 61, Appl</td>	US-09-925-302-20	Sequence 61, Appl
24	2171.5	34.6	3772	3 <td>US-09-989-723-61</td> <td>Sequence 61, Appl</td>	US-09-989-723-61	Sequence 61, Appl
25	2171.5	34.6	3772	3 <td>US-09-989-723-61</td> <td>Sequence 61, Appl</td>	US-09-989-723-61	Sequence 61, Appl
26	2171.5	34.6	3772	3 <td>US-09-989-723-61</td> <td>Sequence 61, Appl</td>	US-09-989-723-61	Sequence 61, Appl
27	2171.5	34.6	3772	3 <td>US-09-989-723-61</td> <td>Sequence 61, Appl</td>	US-09-989-723-61	Sequence 61, Appl
28	2171.5	34.6	3772	3 <td>US-09-989-723-61</td> <td>Sequence 61, Appl</td>	US-09-989-723-61	Sequence 61, Appl
29	2171.5	34.6	3772	3 <td>US-09-989-723-61</td> <td>Sequence 61, Appl</td>	US-09-989-723-61	Sequence 61, Appl
30	2171.5	34.6	3772	3 <td>US-09-991-073-61</td> <td>Sequence 61, Appl</td>	US-09-991-073-61	Sequence 61, Appl
31	2171.5	34.6	3772	3 <td>US-09-990-442-61</td> <td>Sequence 61, Appl</td>	US-09-990-442-61	Sequence 61, Appl
32	2171.5	34.6	3772	3 <td>US-09-991-163-61</td> <td>Sequence 61, Appl</td>	US-09-991-163-61	Sequence 61, Appl
33	2171.5	34.6	3772	3 <td>US-09-993-604-61</td> <td>Sequence 61, Appl</td>	US-09-993-604-61	Sequence 61, Appl
34	2171.5	34.6	3772	3 <td>US-09-990-456-61</td> <td>Sequence 61, Appl</td>	US-09-990-456-61	Sequence 61, Appl
35	2171.5	34.6	3772	3 <td>US-09-991-181-61</td> <td>Sequence 61, Appl</td>	US-09-991-181-61	Sequence 61, Appl
36	2171.5	34.6	3772	3 <td>US-09-989-730-61</td> <td>Sequence 61, Appl</td>	US-09-989-730-61	Sequence 61, Appl
37	2171.5	34.6	3772	3 <td>US-09-992-598-61</td> <td>Sequence 61, Appl</td>	US-09-992-598-61	Sequence 61, Appl
38	2171.5	34.6	3772	3 <td>US-09-989-293-61</td> <td>Sequence 61, Appl</td>	US-09-989-293-61	Sequence 61, Appl
39	2171.5	34.6	3772	3 <td>US-09-989-735-61</td> <td>Sequence 61, Appl</td>	US-09-989-735-61	Sequence 61, Appl
40	2171.5	34.6	3772	3 <td>US-09-990-444-61</td> <td>Sequence 61, Appl</td>	US-09-990-444-61	Sequence 61, Appl
41	2171.5	34.6	3772	3 <td>US-09-991-181-61</td> <td>Sequence 61, Appl</td>	US-09-991-181-61	Sequence 61, Appl
42	2171.5	34.6	3772	3 <td>US-09-989-730-61</td> <td>Sequence 61, Appl</td>	US-09-989-730-61	Sequence 61, Appl
43	2171.5	34.6	3772	3 <td>US-09-990-436-61</td> <td>Sequence 61, Appl</td>	US-09-990-436-61	Sequence 61, Appl
44	2171.5	34.6	3772	3 <td>US-09-993-687-61</td> <td>Sequence 61, Appl</td>	US-09-993-687-61	Sequence 61, Appl
45	2171.5	34.6	3772	3 <td>US-09-989-734-61</td> <td>Sequence 61, Appl</td>	US-09-989-734-61	Sequence 61, Appl

ALIGNMENTS

RESULT 1
US-10-238-876-1
Sequence 1, Application US/10238876
Publication No. US2003008464A1
GENERAL INFORMATION:
APPLICANT: Lee, Mu-En
APPLICANT: Layne, Matthew D.
TITLE OF INVENTION: AORTIC CARDIOPEPTIDASE-LIKE POLYPEPTIDE
FILE REFERENCE: 21509-036CIPCON
CURRENT APPLICATION NUMBER: US/10/238,876
CURRENT FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: US 09/060,482
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: US 08/818,009
PRIOR FILING DATE: 1997-03-14
PRIOR APPLICATION NUMBER: US 60/013,439
PRIOR FILING DATE: 1996-03-15
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 3935
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:

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; NAME/KEY: CDS
; LOCATION: (140) ... (3613)
US-10-238-876-1

Alignment Scores:
Pred. No.: 0 Length: 3935
Score: 6272.00 Matches: 1158
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-10-642-946-3 (1-1158) x US-10-238-876-1 (1-3935)

QY 1 MetAlaAlaValaArgGlyValaProLeuLeuSerCysLeuLeuAlaLeuLeuAlaLeuCys 20
Db ATGGCGGCGCGTGGCGGGGGCGCCCTGCTCAGCTGCTCTGGCGCTGCTGGCGCTGCTGCTG 199
QY 21 ProGlyValArgProGlnThrValaLeuThrAspAspGluIleGluGluPheLeuGluGly 40
Db CCTGGAGGGCGCGCCGAGAGGGTGTGACCGAGACGAGATCGAGAGATTCTTCAGAGGCG 259
QY 41 PheLeuSerGluLeuGluProGluProArgGluAspAspValGluAlaProProProPro 60
Db TTCCTGTCAAGAGCTAAGACCTGAGCCCGGAGAGACGAGCTGGAGGCGCCGCGCTCC 319
QY 61 GluProThrProArgValaArgGlyAlaGlnIleGlyValaProGlyValaArgProGly 80
Db GAGCCGACCCCGGGGTCCGAAAAGCCAGCGGGGGGCAAGCCAGGAGAAAGCGGCCAGGG 379
QY 81 ThrAlaAlaGluValaProProGluValaThrValaAspValaGlyValaProGlyValaAsp 100
Db ACGGCGCGAGAAATGCTCTCCGAAAGAACCAAGAACAAAGGAGAAAGCAAGAAAGAC 439
QY 101 LysGlyProLysValaProLysGluSerLeuGluGlySerProArgProProLysGly 120
Db AAAAGGCCCCAAGGTGCCCCAAGAGTCTTGGAGGGGTCCCGCCAGCGCCCAAGAGGGG 499
QY 121 LysGluLysProProLysAlaThrLysLysProLysGluLysProProLysAlaThrLys 140
Db AAGGAGAAAGCAACCCAGAGCCACCAAGAGCCCAAGAGAACCCAAAGAGAACCCAGAGG 559
QY 141 LysProLysGluGluProProLysAlaThrLysLysProLysGluLysProProLysAla 160
Db AAGCCCAAGAGAGAGCAACCCAGAGCCACCAAGAGAACCCAAAGAGAACCCAGAGGCG 619
QY 161 ThrLysLysProProSerGlyLysArgProProIleLeuAlaProSerGluThrLeuGlu 180
Db ACCAAGAAAGCCCCGTCAAGGAGAGAGGCCCCCATCTGGCTCCCTCAGAAACCCCTGGAG 679
QY 181 ThrProLeuProProProProSerProGlyProGluGluLeuProGluGluGlyAla 200
Db TGGCCACTGCCCCCAGCCCAAGCCCTGGCCCGAGAGAGCTACCCAGAGGAGGAGGCG 739
QY 201 ProLeuSerAspAsnThrGlnAsnProGlyGluGluThrIleValaGluAlaGlnGluHis 220
Db CCCCTCTCAAAATACCTGGCAGATTCAGAGAGAGAACCATGTGAGGACAGAGAGCAC 799
QY 221 GlnProGluProGluGluGluThrGluGlnProThrLeuAspTyrAsnAspGlnIleGlu 240
Db CAGCCTGAGGCGGAGAGAGAGACCGAGCAACCCACACTGGAATAACATGACAGATCGAG 859
QY 241 ArgGluAspTyrGluAspPheGluTyrIleArgArgGlnLysGlnProArgProProPro 260
Db AGGAGAGACTATAGAGCTTGTGATCAATTCGGCGCCAGAAAGCAACCCAGAGCAACCCCA 919
QY 261 SerArgArgArgArgProGluArgValaTyrProGluLysProGluGluLysAlaProAla 280
Db AGGAGAGAGAGAGGCGCCGAGCGGCTGTGACAGAGCCCTTGAAGAGAGAGGCGCCGCG 979
QY 281 ProAlaProGluGluArgIleGluProProValaLysProLeuLeuProProLeuProPro 300
Db CAGGCCCGGAGAGAGAGATGAGCTCTGTGAAGCTCTGTGCGCCCGCGCTGCCCT 1039
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QY 301 AspTyrGlyAspGlyTyrValIleProAsnTyrAspAspMetAspTyrTyrPheGlyPro 320
Db GACTATGGTGAATGATGATGATGATATCCCACTACGATGACATGAGACTATATCTTGGGCT 1099
QY 321 ProProProGluLysProAspAlaGluArgGluThrAspGluGluLysGluGluLeuLys 340
Db CCTCGGCCCCAGAAAGCCGATGTGAGGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1159
QY 341 LysProLysLysGluAspSerSerProLysGluGluThrAspLysTyrAlaValGluLys 360
Db AAACCCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1219
QY 361 GlyLysAspPheLysGluProArgLysGluGluGluGluGluGluGluGluGluGluThrProThr 380
Db GGCAAGAGACCAAGAAAGAGCCCGAAAGGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 1279
QY 381 GlyLysValaLysCysProProIleGlyMetGluSerHisArgIleGluAspAsnGlnIle 400
Db GAGAAAGTCAAGTGTCCCGCATTTGGAGTGAAGTCAACCCGTATTGAGAGCAACAGATC 1339
QY 401 ArgAlaSerSerMetLeuArgHisGlyLeuGlyAlaGlnArgGlyArgLeuAsnMetGln 420
Db CGAGCCTCCTCCATGCTGCGCCAGCGCTGGGGGACAGCGCGCGCGCTCAACATGACAG 1399
QY 421 ThrGluValaThrGluAspAspTyrTyrAspGlyAlaTyrCysAlaGluAspAspAlaArg 440
Db ACCGGTGCACCTGAGAGAGACTACTATATGATGATGATGATGATGATGATGATGATGAT 1459
QY 441 ThrGlnTyrIleGluValaAspThrArgArgThrArgThrArgPheThrGlyValIleThrGln 460
Db ACCGATGGATATGAGTGGAGACCAAGAGAGATCACCGGTTCAAGGCGTCAACCCAG 1519
QY 461 GlyArgAspSerSerIleHisAspAspPheValaThrThrPhePheValaGlyPheSerAsn 480
Db GGCAAGAGCTCCAGAGATCATGACATTTTGGACACACCTTCTTGCGGCTTCAGCAAT 1579
QY 481 AspSerGlnThrTyrValaMetTyrThrAsnGlyTyrGluGluMetThrPheHisGlyAsn 500
Db GACAGCCAGACATGGGTGATGATACCAAGGCTATGAGAAATGACCTTTATGGAGAC 1639
QY 501 ValaAspLysAspThrProValaLeuSerGluLeuProGluProValaValaAspPheIle 520
Db GTGACAAAGAGACACCGGTGTGATGAGTCCCAAGAGCCGATGGTGGCTGATTCAATC 1699
QY 521 ArgIleTyrProLeuThrTyrAsnGlySerLeuCysMetArgLeuGluValaLeuGlyCys 540
Db CCGATCTACCACTCACTGAGATGGAGCCGTGTCAATGCGCTGAGGGTGTGGGGTGC 1759
QY 541 SerValaIaProValaTyrSerTyrTyrAlaGlnAsnGluValaAlaThrAspAspLeu 560
Db TCTGTGGCCCTGTGTTACAGTACTACCAAGATGAGTGTGGTGGCCACCATGACTCG 1819
QY 561 AspPheArgHisIleSerTyrLysAspPheCysGlnLeuMetLysValaValaAsnGluGlu 580
Db GATTTCCGGCACACAGCTTACAGAGACATGCCAGCTCATAGAGTGTGAACGAGAG 1879
QY 581 CysProThrIleThrArgThrTyrSerLeuGlyLysSerSerArgGlyLeuLysIleTyr 600
Db TGCCCACCATCACCCGCACTTACAGCCCTGGGCAAGAGCTCACAGAGGCTTCAAGATCTAT 1939
QY 601 AlaMetGluIleSerAspAsnProGlyGluHisGluLeuGlyGluProGluPheArgTyr 620
Db GCCATGAGATCTTACAGACACCTTGGAGAGCTATGAATGGGGAGGCCGAGTTCCGCTAC 1999
QY 621 ThrAlaGlyIleHisGlyAsnGluValaLeuGlyArgGluLeuLeuLeuLeuMetGln 640
Db ACTGCTGGGATCATGAGCAACGAGGTGCTGGCCAGAGACTGTGTGCTGCTCAATGACAG 2059
QY 641 TyrLeuCysArgGluTyrArgAspGlyAsnProArgValaArgSerLeuValaGlnAspThr 660
Db TACCTGTGCGAGAGATGACCGATGGAGAACCAAGCTGTGCGAGCTGTGTGACAGACACA 2119
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QY	661	ArgILeHsleVuaIProSeSerLeuAnPProAaPgLYrYrGluVaIAlaIGImecIY	680
Db	2120	CGCArTCCACtGTGTCCCTCACTGAACCTGATGCTACGAAGTGGACCGCAATGGAGC	2179
QY	661	SerGIuPheGIyAsnTrPaIaleuGIyLeuTrPThrGIuGIuGIyPheAspIIePheGIu	700
Db	2180	TCAGAGTTTGGGACTGGAGCGCTGGGACTGTGACTGAAGAGGGCTTTGACATCTTTGA	2239
QY	701	AaPhePProAaPLeuAnSerValLeuTrPGLyAlaGIuGIuYrTrPaIProYrY	720
Db	2240	GATTTCCCGGACTCAACTGTGTCTCTGGGGAGCTGAGAGAAATGGGTCCCTTAC	2299
QY	721	ArgValProAsnAnAsnLeuProIIeProGuaYrYrLeuSePProAspAlaThrPaI	740
Db	2300	CGGGrCCCCACAArMArCTTGTCCCTCCCTGAACCTTACTTTGCCAGATGCCAGGTA	2358
QY	741	SeTrHrGIuVaIarGaIaIeIIeAlaTrPMeGtGlyyAsnProPheValLeuGIyAla	760
Db	2360	TCCAAGAGGTCCGGGCCATCTTGTCCGTGAGTGAAGAAACCCCTTGCTGTGGAGCA	2419
QY	761	AsnLeuAnGIyGLyGIuYrGLeuVaISeTrYrProYrAaPMeArIaYrThrProThr	780
Db	2420	AATCGAAGCGGGGGAGGGGTACTTACTTACCCCTACGATATGGCCCGCACGCTTACC	2479
QY	781	GIuGIuGIuLeuLeuAlaIaIaIaMeArIaIaIaIaYrGIyGLyAsnGIuAnGIyVaI	800
Db	2480	CAGGAGCAAGCTGTGGCGCGACCCATGGAGAGCGCGGGGGAGAAATGAGACCAAGTTC	2539
QY	801	SerGIuAlaGIuGIuThrProAaPriaIaIaIePheArGTTrPLeuAlaIeSerPheAla	820
Db	2540	TCCGAGGCCACGAGAACTCCAGAACCAACCCACTTCCGCTGGCTTGCCATCTCTTGCC	2599
QY	821	SerAlaHsleuThrLeuThrGIuProYrYrArGIyGLyYrGlnAlaGlnAaPTrYrThr	840
Db	2600	TCCGACACCTCACTTACCGAGCGCCCTACCGCGGAGGCTCGAACCCACAGACTACACC	2659
QY	841	GLyGLyMeTGIyIIeVaIAsnGIyAlaYrTrPaAnProArGTThrGIyThrIIeAsnAaP	860
Db	2660	GGCGGCATGGGAGCTGTCTACAGCGGGCCAArGTGAACCCCGGACCGGAGACTATCArTAC	2719
QY	861	PheSeTrYrLeuHsleThrAsnCYLeuGIuLeuSePheTrYrLeuGIyCyAsPLeYrPhe	880
Db	2720	TTCACTTACCTGCATrACCACTGCTGAAGCTCTCTTCTTACTTGAGCTGTGACAACTTC	2779
QY	881	ProHsGIuSeGIuLeuProArGIuTrPGLuAnAnGIyGLyAlaLeuLeuThrPhe	900
Db	2780	CCTCATGAGATGAGCTGCCCGCGAGGGAGAACAArAGAGGCGCTGCTCACCTTC	2839
QY	901	MeTGIuGIuVaIaHsArGIyIIeYrSeGLyAlaValThrAaPGLuGIuGIyIIeProIIe	920
Db	2840	ATGGAGCAGGTGCACCGCGGCArTMArGGGGGTGTGAGAGCArGACAArGGCATCCCArT	2899
QY	921	AlaAsnAlaTrPriaIeSerValSeGIyIIeAsnHsGIyVaIIyTrThrAlaSeSeGIyGLy	940
Db	2900	GCCAArGCGCACCATCTCTGTGAGTGGCArTTArTACGGCGGTGAACAGCCAGTGTGTGT	2959
QY	941	AaPTrYrTrPaGIleLeuAnProGIyGLyTrYrArGIaIThrAlaHsAlaGIuGIyYr	960
Db	2960	GATTACTGGCArTGTGAACCGGGGTAGrTACCGCGTGAACGCCACGGAGGGGTAC	3019
QY	961	ThrProSeArAlaYrThrCyAsnVaIaAaPTrYrAaPIIeGLyAlaThrGlnCyAsnPhe	980
Db	3020	ACCCGCArGCGCArGACCTGTCArTGTGACTATGCArTACrGCGGGCCACrTCArGTGCArTTC	3079
QY	981	IIeLeuAlaArGSeArAsnTrPriaYrGIyIIeArGIuIIeMeArIaMeArAsnGIyAsnArG	1000
Db	3080	ATCTTGCTCGCTCCACTGAGAGGCArTCCGGAGATCArGGCCArTGAAGAGGAACGG	3139
QY	1001	ProIIeProHsIleAaPProSeArYrGProMeTrThrProGIuGIuArGIyGLuGIuGIu	1020
Db	3140	CCTATCCCArCACArTGAACCArTCCGGCTATGAACCCCCCArCAGCArCGCTGAGAGG	3199
QY	1021	ArGaYrGLeuGIuHsIaYrGLeuYrGLeuYrAlaGlnMeArTrGLeuYrGIyLeuAnAla	1040

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Db      3200 CGAGCCCTACACACACCGCTGGGCTTCGGGGACAGATGGCGCTGGCGCCCTACAGCC 3259
Qy      1041 ThrThrThrLeuGlyProHisThrValProProThrLeuProAlaProAlaThrThr 1060
Db      3260 ACCACCACTGAGGCCCCACACTGTGCTCCACCGCTGCCCTGGCCCTGGACCAACC 3319
Qy      1061 LeuSerThrThrTlIleGluProTrpGlyLeuIleProProThrThrAlaGlyTrpGlu 1080
Db      3320 CTGACACACTACCATGAGAGCCCTGGGGCTCATACCGCAACACCGCTGAGTGGAGAGAG 3379
Qy      1081 SerGluThrGluThrTyThrGluValValThrGluPheGlyThrGluValGluProGlu 1100
Db      3380 TCGAGAGACTGAGACCTACACAGAGTGTGACAGAGTTTGGACCGAGGTGGAGCCCGAG 3439
Qy      1101 PheGlyThrLysValGluProGluPheGluThrGlnLeuGluProGluPheGluThrGln 1120
Db      3440 TTTGGAGCAACAGGTGGAGCCCGAGGTTGAGACCCAGTTGAGGCTGAGTTCGAGACCCAG 3499
Qy      1121 LeuGluProGluPheGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 1140
Db      3500 CTGGAACCCAGATTGAGAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3559
Qy      1141 GlnAlaPheProPheThrThrValGluThrTyThrValAsnPheGlyAspPhe 1158
Db      3560 CAGGCAATTCCTTCACACAGTAGACCTACACAGTGAATTTGGGGACTTC 3613

RESULT 2
US-10-177-293-1
; Sequence 1, Application US//10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Gannavarpu, Manjula
; APPLICANT: Kamatekar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Bast Jr., Robert C.
; APPLICANT: Horobagyi, Gabriel N.
; APPLICANT: Puzstai, Lajos
; APPLICANT: Meric, Punda
; APPLICANT: Sahin, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; FILE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3935
; TYPE: DNA
; ORGANISM: Homo sapiens

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Db 2120 CGATCCACCTGGTCCCTCACTGACCTTGTGCTACGAGTGGGAGCGGAGATGGGC 2179
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Db 2180 TCAGAGTTGGGAACTGGGCGCTGGGACTGTGAGCTGAGGAGGCGCTTTCATCTTTGAA 2239
Qy 701 AspPheProAspLeuAenSerValLeuTPhrGIyAlaGIuGIyAgluYlTPPvalProDyr 720
Db 2240 GATTTCCTGGAGTCTCACTGTGTCTCTGGGAGCTGAGGAGGAAATGGGTCCTTAC 2299
Qy 721 ArgValProAspAenAenLeuProIleProGIuArgTYrLeuSerProAspAlaThrVal 740
Db 2300 CGGGTCCCAACAATACCTTGGCCATCCCTGGAACGCTTACCTTGGCCAGATGCCAGGTA 2359
Qy 741 SerTherGIuValAgaAlaIleIleAlaTPMeGIuYlAspProPheValLeuGIyAla 760
Db 2360 TCCACGAGAGTCCCGGCGCATCATCTGTGATGAGAAACCCCTTCGTCTGGAGCA 2419
Qy 761 AsnLeuAenGIyGIyGIuArgLeuValSerTYrProTYrAspMetAlaArgTPhrProThr 780
Db 2420 AATCTGAAGCGGCGGAGGCTGATCTTACCTTACCTTACCTTACCTTACCTTACCTTAC 2479
Qy 781 GlnGIuGIuLeuLeuValAaIaIaMetAlaAaIaArgGIyGIuAspGIuAspGIuVal 800
Db 2480 CAGGAGCAGCTGGTGGCGGAGCCATGGAGCAGCCCGGGGGAGAGTGAAGAGAGTTC 2539
Qy 801 SerGIuAlaGIuGIuTPhrProAspPheAlaIlePheArgTPLeuAlaIleSerPheAla 820
Db 2540 TCCGAGGCGGAGGAGCTCCAGACAGCCATCTTCCGCTGGCTTCCATCTTCCGCTG 2599
Qy 821 SerAlaIleSerTherTherTherTherTherTherTherTherTherTherTherTher 840
Db 2600 TCCGACACCTTACCTTGAAGCGGAGCTTACCGCGGAGGCTGCGCAAGCGGAGTACAC 2659
Qy 841 GlnGIyMetGIyIleValAenGIyAlaIleTPhrAspProArgTPhrGIyTherIleAspAsp 860
Db 2660 GGGGCGATGGGCACTGTCACAGCGGCGCAAGTGAAGAGCCCGGAGCGGAGCTATCAAGAC 2719
Qy 861 PheSerTYrLeuHleTherAenCYLeuGIuLeuSerPheTYrLeuGIyCYAspLYsPhe 880
Db 2720 TTCAGTACCTGCTACCACTGCTGAGCTCTCTTCACTGAGGCTGTGACCAAGTTC 2779
Qy 881 ProHleGIuSerGIuLeuProArgGIuTPhrGIuAenAenIleValaIleuLeuTherPhe 900
Db 2780 CCTCAAGAGTGAAGTGGCGGAGTGGAGAAACAAGAGGCGTGTCTACCTTC 2839
Qy 901 MetGIuGIuValHleArgGIyIleYleGIyValValTherAspGIuGIuIleProIle 920
Db 2840 ATGGAGCAGGTGCACCGGCGCATTAAGGGGTGTGTGCGAGCAGCAAGGCAATCCCAT 2899
Qy 921 AlaAenAlaTherIleSerValSerGIyIleAsnHleGIyValIleTherAlaSerGIyGIy 940
Db 2900 GCCAAGCGGCACTCTGTGAGTGGCATTAATCAAGCGGTGAAGACAGCAGGTGGT 2959
Qy 941 AspTYrTPhrArgIleLeuAenProGIyGIuTYrArgValTherAlaHleAlaGIuGIyTYr 960
Db 2960 GATTACTGGGAATCTTGAACCGGAGTGAATCGCTGACAGCCGCGGAGGGGTAC 3019
Qy 961 ThrProSerAlaIleYlTherCYAspAenValAspTYrAspIleGIyAlaTherGIuCYAspPhe 980
Db 3020 ACCCGAGCGGCGCAAGCTTCATATGTGATGATACCTGGGGCACTGATGCAATTC 3079
Qy 981 IleLeuAlaArgSerAenTPlyAspGIleArgGIuIleMetAlaMetAenGIyAenArg 1000
Db 3080 ATCTGTGCTGCTTCACTGGAAGCGCATCCGGGAGATCATGGCCATGAACGGGAAACCG 3139
Qy 1001 ProIleProHleIleAspProSerArgProMetTherProGIuGIuArgLeuGIuGIu 1020
Db 3140 CCTATCCCAACATGACCTGCGGCTGATGACCCCGCAACAGGAGCAGCCCTGAGCAG 3199
Qy 1021 ArgArgLeuGIuHleIleArgLeuArgLeuArgAlaIleMetArgLeuArgLeuAsnAla 1040
Db 3200 CGAGCGCTTACAAACCGGCTTGGGCGTGGGAGCAAGTGGGCTGGGCGCTTCAAGCC 3259

Qy 1041 ThrTherTherLeuGIyProHleIleTherValProProTherLeuProProAlaPProAlaTher 1060
Db 3260 ACCACCACTTACGAGGCGGCGGAGCTGTGCTCCCAAGCTGGCGCTGCGCACACCC 3319
Qy 1061 LeuSerTherTherIleGIuProTPPGIyLeuIleProProTherTherAlaGIyTPGIuGIu 1080
Db 3320 CTGAGCACTTCCATGAGGCTTGGGCTGTATACCCCAACACCGCTGCTGGAGAGAG 3379
Qy 1081 SerGIuTherGIuTherTYrTherGIuValTherGIuPheGIyTherGIuValGIuProGIu 1100
Db 3380 TCGGAGACTAGACTTACACAGAGGTGTGACAGAGTTTGGAGCCAGGAGGAGCCGAG 3439
Qy 1101 PheGIyTherYlValGIuProGIuPheGIuTherGIuLeuGIuProGIuPheGIuTherGIu 1120
Db 3440 TTTGGGACCAAGGTGAGCGGCGGAGTTTGAAGACCAAGTTGAGCGCTGATCGAGCCAG 3499
Qy 1121 LeuGIuProGIuPheGIuGIuGIuGIuGIuGIuGIuGIuGIuGIuGIuGIuGIuGIu 1140
Db 3500 CTGGAACCGAGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGATGACCTGGC 3559
Qy 1141 GlnAlaPheProPheTherTherValGIuTherTYrTherValAspPheGIyAspPhe 1158
Db 3560 CAGGCAATCCCTTCAACAAGAGAGACTTACAGGTGAATTTGGGAGCTTC 3613

RESULT 3
US-10-159-563-288
; Sequence 288, Application US/10159563
; Publication No. US2004009154A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Melzer, Paul
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
; TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS
; FILE REFERENCE: 11613.5US11
; CURRENT APPLICATION NUMBER: US/10/159, 563
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 10/133, 937
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 288
; LENGTH: 3935
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-159-563-288

Alignment Scores:
Pred. No.: 0 Length: 3935
Score: 6272.00 Matches: 1158
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-10-642-946-3 (1-1158) x US-10-159-563-288 (1-3935)

Qy 1 MetAlaIleValArgGIyAlaProLeuLeuSerCYLeuLeuAlaLeuLeuAlaLeuCYe 20
Db 140 ATGGCGCGGTGGCGGCGGCGGCGGCTGTGCTGAGCTGCTGCGGTGGCGGCTGTGCTG 199
Qy 21 ProGIyGIyArgProGIuTherValLeuTherAspAspGIuIleGIuGIuPheLeuGIuGIy 40
Db 200 CTTGAGGAGGCGGCGGAGCGGTGTGACCGAGCAGAGATGAGGAGGAGTTCTCGAGGGC 259
Qy 41 PheLeuSerGIuLeuGIuProGIuProArgGIuAspAspValGIuAlaProProProPro 60
Db 260 TTCCTGTCAAGCTTAAACCTGAGCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 319
Qy 61 GluProTherProArgValArgLYsAlaGIuGIyIleAspProGIyLYsArgProGIy 80

Db 320 GAGCCACCCCGGGTCCGAAAGCCAGCGGGGGGCAAGCAGGAGGCGCACGGG 379
Qy 81 ThrAlaAlaGluValProProGluLysThrLysAspLysGlyLysLysGlyLysLysAsp 100
Db 380 AGGGCCGGAGAAAGTGTCTCCGGAAAGAACCAAGAGGAGAAAGAAAGAAAGAAC 439
Qy 101 LysGlyProLysValProLysGlySerLeuGluGlySerProAspProProLysGly 120
Db 440 AAAGGCCCAAGGTGCTCAAGAGTCTTGAGGGGTCTCCCAAGGCGCGCCCAAGAAAGGG 499
Qy 121 LysGlyLysProProLysAlaThrLysLysProLysGlyLysProProLysAlaThrLys 140
Db 500 AAGGAGAACCCACCCAGGCCACCAAGAGCCCAAGAGAGGCACTTAAGGCCACCAAG 559
Qy 141 LysProLysGluLysProProLysAlaThrLysLysProLysGlyLysProProLysAla 160
Db 560 AAGCCCAAGAGAGGAGCCCAAGGCCACCAAGAACCCCAAGAGAGGACCCCAAGGGCC 619
Qy 161 ThrLysLysProProSerGlyLysAspProProLysLeuAlaProSerGluThrLeuGlu 180
Db 620 ACCAAGAGCCCGCTCAGAGGAAAGGCCCGCCCATTTGGCTCTCCAGAAACCTGGAG 679
Qy 181 TrpProLysProProProProSerProGlyProGluGluLeuProGluGluGlyAla 200
Db 680 TGGCCACTGCCCCACCCCGAGCCCTGGCGCCGAGAGACTACCCAGAGAGGAGGGCG 739
Qy 201 ProLysSerAspAsnTrpGlnAsnProGluGluGluThrHisValGluAlaGlnGluHis 220
Db 740 CCCCTTCAAAATTAATCGGAGAAATCCAGAGAGAACCACTGTGAGGACACAGGAGCAC 799
Qy 221 GlnProGluProGluGluGluThrGluGluProThrLeuAspTrpAsnAspGlnLeuGlu 240
Db 800 CAGCTGAGCCGGAGAGAGAGACCGAGAACCCACACTGAGCTACAAATCAAGATCGAG 859
Qy 241 ArgGluAspTrpGluAspPheGluTrpLeuArgGlnLysGluAspProAspProPro 260
Db 860 AAGGAGAGACTATAGAGACTTGAATCATTCGGCGCCAGAGCAACCCAGGCCACCCCA 919
Qy 261 SerArgArgArgArgProGluValTrpProGluProProGluGluLysAlaProAla 280
Db 920 AGAGAGAGAGAGGCGCCGAGCGGTCTGGCCAGACCCCTGAGAGAGAGGCCCGCGCC 979
Qy 281 ProAlaProGluGluGluGluLeuProProValLysProLeuLeuProProLeuProPro 300
Db 980 CCAAGCCCGGAGAGAGAGATTGAGCTCTGTGAACCTCTGTCGCCCGCGCGCCCT 1039
Qy 301 AspTrpGlyAspGlyTrpValLysProAsnTrpAspAspMetAspTrpTrpPheGlyPro 320
Db 1040 GACTATGATGATGATTACGTGATCCCAACTAGATGACATGAGACTATTACTTTGGGCT 1099
Qy 321 ProProProGluLysProAspAlaGluValArgGluThrAspGluGluLysGluLeuLys 340
Db 1100 CTTCCCGCCCAAGAGCCGATGCTGAGCGCCAGACGACGAAAGAGAGAGGAGCTGAAG 1159
Qy 341 LysProLysLysGluAspSerSerProLysGluGluThrAspLysTrpAlaValGluLys 360
Db 1160 AAACCCAAAGAGAGAGACAGCAGCCCAAGAGAGAGACCAAGATGGGCAATGGAGAG 1219
Qy 361 GlyLysAspHisLysGluProArgLysGlyGluLeuGluGluGluLysTrpThrProThr 380
Db 1220 GGGAAAGAGCAAAAGAGCCCGAAAGGGGAGAGATGGAGAGAGAGAGAGCTGACG 1279
Qy 381 GlnLysValLysLysProProLysGlyMetGluSerHisArgLysLeuAspAsnGlnLeu 400
Db 1280 GAAAGAGTCAAGTGTCCCATTTGGATGAGATCAACCGTATTAGAGCAACCAAGATC 1339
Qy 401 ArgAlaSerSerMetLeuArgHisGlyLeuGlyAlaGlnArgGlyLysLeuAsnMetGln 420
Db 1340 CGAGCTCTCTCCATGTCTGCCCAAGGCTGGGGGCAAGGGCGCGGCTCAACATGCGAG 1399
Qy 421 ThrGlyAlaThrGluAspAspTrpTrpAspGlyAlaTrpCysAlaGluAspAspAlaArg 440
Db 1400 ACCGGTGCCTAGAGAGCACTACTATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1459

Qy 441 ThrGlnTrpLysGluValAspThrArgArgThrThrArgPheThrGlyValLysThrGln 460
Db 1460 ACCAGTGAATGAGAGTGAACCCAGAGAGACTACCGGTTCAAGGGCTCTACCCAG 1519
Qy 461 GlyArgAspSerSerLysAspAspPheValThrTrpPhePheValGlyPheSerAsn 480
Db 1520 GGCAGAGACTCAGATCATGAGATTTGTGACCACTTCTGTGGGCTTCAGCAAT 1579
Qy 481 AspSerGlnThrTrpValMetTrpThrAsnGlyTrpGluGluMetThrPheHisGlyAsn 500
Db 1580 GACAGCCAGACATGGGTATGACCAACCGCTATGAGAAATACCTTTCATGGGAAC 1639
Qy 501 ValAspLysAspThrProValLeuSerGluLeuProGluProValAlaArgPheLeu 520
Db 1640 GTGACAGAGACACACCGCTGTAGTAGTCTCCAGAGCGGGTGTGGCTTTCATC 1699
Qy 521 ArgLysTrpProLysThrTrpAsnGlySerLeuCysMetArgLeuGluValLeuGlyCys 540
Db 1700 CGCATCTACCACTCAGCTGGAAATGGCAGCTGTGATGCGCTGGAGGTGCTGGGGTGC 1759
Qy 541 SerValAlaProValTrpSerTrpTrpAlaGlnAsnGluValAlaThrAspAspLeu 560
Db 1760 TCTGTGGCCCTGTCTACAGCTACGACAGATGAGGTGTGGCCACCATGACTG 1819
Qy 561 AspPheArgHisHisSerTrpLysAspMetArgGlnLeuMetLysValAlaAsnGluGlu 580
Db 1820 GATTTCCGGACACACAGCTACAGAGCATGGCCAGCTCATAGAGTGTGTAACAGAG 1879
Qy 581 CysProThrLysThrArgTrpTrpSerLeuGlyLysSerSerArgGlyLeuLysLysLeu 600
Db 1880 TGCCCAACATCACCCGACCTTACAGCTGGGCAAGAGCTCAGAGGCTCAAGATCTAT 1939
Qy 601 AlaMetGluLysSerAspAsnProGluGluHisGluLeuGluGluProGluLysLeuArgTrp 620
Db 1940 GCCATGAGATCTCAGAACCTGTGGAGACATGAACTGGGGGAGCCCGAGTTCCGCTAC 1999
Qy 621 ThrAlaGlyLysGlyAsnGluValLeuGlyArgGluLeuLeuLeuLeuLeuMetGln 640
Db 2000 ACTGCTGGGATCATGGCAAGAGTGTGGCCAGAGCTTGTGCTGCTCATGAG 2059
Qy 641 TyrLeuCysArgGluTrpArgAspGlyAsnProArgValArgSerLeuValGlnAspThr 660
Db 2060 TACCTGTGCCAGAGATCACCGGATGAGAACCCAGCTGTGCGCAGCTGACAGACACA 2119
Qy 661 ArgLysHisLeuValProSerLeuAsnProAspGlyTrpGluValAlaAlaGlnMetGly 680
Db 2120 CGCATTCACCTGTGCTCCCTCACTGAACCTGATGGCTACGAGGTGACGACGATGGGC 2179
Qy 681 SerGluPheGlyAsnTrpAlaLeuGlyLeuTrpTrpGluGluGlyPheAspLysPheGlu 700
Db 2180 TCAAGTTTGGGAATCGGGCGCTGGGACTGTGATGAGAGAGGCTTGTACATCTTTGA 2239
Qy 701 AspPheProAspLeuAsnSerValLeuTrpGlyAlaGluGluValArgLysTrpValProTrp 720
Db 2240 GATTTCCGGATCTCAACTGTGCTGGGAGCTGAGAGAAAGAGAGAGTGTCCCTAC 2299
Qy 721 ArgValProAsnAsnAsnLeuProLysProGluValGlyTrpLysSerProAspAlaThrVal 740
Db 2300 CGGGTCCCAACAAATTAATTCGCACTCCAGAACTCTTTCGCAATGCCAGGTA 2359
Qy 741 SerThrGluValArgAlaLysLeuAlaTrpMetGluLysAsnProPheValLeuGlyAla 760
Db 2360 TTCACGAGAGTCCGGCCATCTTTCCTGATGAGAAAGAACCTTCTGCTGGAGAGA 2419
Qy 761 AsnLeuAsnGlyGlyLysGluLeuValSerTrpTrpAspMetAlaArgThrProThr 780
Db 2420 AATCTGAACGGCGGAGGGCTAGATCTCACTCACTCAATATGAGCCGCGCAGCTTAC 2479
Qy 781 GlnGluGlnLeuLeuAlaAlaAlaMetAlaAlaAlaArgGlyGluAspGluAspGluVal 800
Db 2480 CAGAGACAGCTGTGCGCGCACCATGACAGGCCCGGGGGAGAGTGAAGACAGAGTC 2539

QY 801 SerGlu1aInglu1uThrProAspHisAla1lePheArgTrpLeuAla1leSerPheAla 820
DB 2540 TCGAGGCCCAAGAGACTCCAGACCAAGCCACTTCGGAGGCTTGCACTCTTCGACC 2599
QY 821 SerAla1leLeuThrLeuThrGluProTyrArgGlyGlyCyseGln1aInglu1aPheTyrThr 840
DB 2600 TCCGCACACTCACTTGACCGAGCCCTTACCGCGAGAGCTGCCAAGCCAGCACTACACC 2659
QY 841 GlyGly1aMetGly1aLeu1aInglu1aAlaTyrTrpAsnProArgThrGlyTyr1leAsnAsp 860
DB 2660 GGGGCGATGGGCACTCGCAACGGGGCCAAAGTGAACCCCGGAGCTTACATGAC 2719
QY 861 PheSerTyrLeuHisThrAsnCyseGluLeuSerPheTyrLeuGlyCyseAspLysPhe 880
DB 2720 TTACGTTACTCGATACCAACTGCTGAGCTCTCTTCTTACTTGAGCTGACAGTTC 2779
QY 881 ProHisGluSerGluLeuProArgGluTyrGlu1aAsnAlaGlyGln1aLeuLeuThrPhe 900
DB 2780 CTTCAAGAGAGTGAAGTGGCCCGGAGTGGAGAACAAAGAGGGGCTGCTCACCTTC 2839
QY 901 MetGluGlnValHisArgGly1leuGlyVal1ThrAspGluGlnGly1lePro1le 920
DB 2840 ATGAGAGAGGTGACCCGCGCATTAAGGGGTGTGACGAGCAAGGCAATCCCATTC 2899
QY 921 AlaAsnAlaThr1leSerValSerGly1leAsnHisGlyVal1LysThrAlaSerGlyGly 940
DB 2900 GCCAAGCCACCACTCTGAGAGTGCATTAATCACGGCTGTGAAGAGACCACTGGTGCT 2959
QY 941 AspTyrTrpArg1leLeuAsnProGlyGlyTyrArgVal1ThrAlaHisAlaGluGlyTyr 960
DB 2960 GATTACTGGCGAATCTTGAAACCGGGGTGACTACCGCTGACACCCACGCGAGAGGCTAC 3019
QY 961 ThrProSerAlaLysThrCyseAsnVal1AspTyrAsp1leGly1aThrGlnCyseAsnPhe 980
DB 3020 ACCCCAGCGCCCAAGACTGTGCAATGTATGACATCGGGGCCACTGACTGCAACTTC 3079
QY 981 IleLeuAlaArgSerAsnTrpLysArg1leArgGlu1leMetAlaMetAsnGlyAsnArg 1000
DB 3080 ATCTGAGCTGCTCCAACTGGAAGCGCATCGGAGAGTCATGGCCATGAACGGGAAACCG 3139
QY 1001 Pro1leProHis1leAspProSerArgProMetThrProGlnGlnArgArgLeuGlnGln 1020
DB 3140 CCAATCCCAACATAAGCCCATCGCGCTCATATGACCCCAACAGGAGCCCTGAGAGAG 3199
QY 1021 ArgArgLeuGlnHisArgLeuArgLeuArgAlaGlnMetArgLeuArgArgLeuAsnAla 1040
DB 3200 CGACGCTTACAAACCGCGCTGCGGCTTCCGGGCAAGATGCGGCTGCGGCCCTCAACGCG 3259
QY 1041 ThrThrThrLeuGlyProHisThrVal1ProProThrLeuProProAlaProAlaThrThr 1060
DB 3260 ACCACACCTTAGGCCCCCACTGCTGCTCCACAGCTGCCCCCTGCTGCTGACACACC 3319
QY 1061 LeuSerThrThr1leGluProTyrGlyLeu1leProProThrThrAlaGlyTyrGluGlu 1080
DB 3320 CTGAGCACTACCAATAGGCTCGGGGCTCATACCGCAACACCCCTGCTGCGAGAGAG 3379
QY 1081 SerGluThrGluThrTyrThrGluVal1Val1ThrGluPheGlyThrGluVal1GluProGlu 1100
DB 3380 TCGGAAGACTGAGACTTACACAGAGGTGTGACAGAGTTTGGAGCCAGGTGGAGCCGAG 3439
QY 1101 PheGlyThrThrVal1GluProGluPheGluThrGluGluGluProGluPheGluThrGln 1120
DB 3440 TTGGGACCAAGGTGGAGCGGAGTTTGAGACCCAGTTGAGGCTTGAAGGACCCAG 3499
QY 1121 LeuGluProGluPheGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 1140
DB 3500 CTGGAAGCCGAGTTTGAAG 3559
QY 1141 GluAlaPheProPheThrThrVal1GluThrTyrThrVal1AsnPheGlyAspPhe 1158
DB 3560 CAGGCAATCCCTTCAACACAGTAGAGACTTACACAGTGAACCTTGGGGAGCTTC 3613
RESULT 4

US-10-775-920-194
; Sequence 194, Application US/10775920
; Publication No. US2004017574A1
; GENERAL INFORMATION:
; APPLICANT: Merzen Ltd
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCES AND CORRESPONDING ENCODED POLYPEPTIDES
; TITLE OF INVENTION: OF PARTICULAR SECRETED AND MEMBRANE-BOUND PROTEINS OVEREXPRESSED
; TITLE OF INVENTION: IN CERTAIN CANCERS
; FILE REFERENCE: Merzen - 0010B
; CURRENT APPLICATION NUMBER: US/10/775,920
; PRIOR FILING DATE: 2004-02-10
; PRIOR FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 385
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 194
; LENGTH: 3935
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-920-194
Alignment Scores:
Pred. No.: 0 Length: 3935
Score: 6272.00 Matches: 1158
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 9 Gaps: 0
US-10-642-946-3 (1-1158) x US-10-775-920-194 (1-3935)
QY 1 MetAla1aVal1aArgGly1aPro1leuLeuSerCyseLeuLeuAla1leuLeuAlaLeuCyse 20
DB 140 ATGGCCGGCGGTGGCGGGCGGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 199
QY 21 ProGly1aArgProGlnThrVal1leuThrAspAspGlu1leGluGluPheLeuGluGly 40
DB 200 CCGAGAGGGCGCGCGAGCGGTGCTGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 259
QY 41 PheLeuSerGluLeuGluProGluProArgGluAspAspVal1Glu1aProProProPro 60
DB 260 TTCCTGTCAAGAGTGAACCTGAGCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 319
QY 61 GluProThrProArgVal1aArgGly1aGlnAlaGlyGlyLysProGlyLysArgProGly 80
DB 320 GAGCCCAACCCCGGGTCCGAAAGCCAGGGGGGGGAGAGAGAGAGAGAGAGAGAGAGAG 379
QY 81 ThrAla1aGluVal1aProProGluLysThrLysAspLysGlyLysLysGlyLysLysAsp 100
DB 380 ACGGCCGAGAGAGTCTCCGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 439
QY 101 LysGlyProLysVal1aProLysGluSerLeuGluGlySerProArgProProLysLysGly 120
DB 440 AAAAGGCCCAAGAGTGCCTGAGAGAGTCTTGGAGGGGTCCCAAGGCGCCCAAGAGAGAG 499
QY 121 LysGluLysProProLysAlaThrLysLysProLysLysGluLysProProLysAlaThrLys 140
DB 500 AAGGAG 559
QY 141 LysProLysGluGluProProLysAlaThrLysLysProLysGluLysProProLysAla 160
DB 560 AAGCCCAAG 619
QY 161 ThrLysLysProProSerGlyLysArgProPro1leuAlaProSerGluThrLeuGlu 180
DB 620 ACCAAG 679
QY 181 TrpProLeuProProProProSerProGlyProGluGluLeuProGlnGluGlyGlyAla 200
DB 680 TGGCCACTGCCCCCAACCCCGAGCTGCGCCCGAGAGAGTACCCACAGAGAGAGAGAGAGAG 739
QY 201 ProLeuSerAsnAspTrpGluAsnProGlyGluGluThrHisVal1aGlu1aIngluHis 220

Dd		740	CCCCTCTCAATTACTGGCAGAAATTCAGAGAGAGAACCATTTGGAGGACACAGAGACAC	799
Oy		221	GlnProGluPProGluGluGluThrGluGlnProThrLeuAspTyrAsnAspGlnIleGlu	240
Dd		800	CAGCTTGACC GGAGAGAGAGACCGAGCAACCCACCTGGACTTCAATTAATGCAGATGGAG	859
Oy		241	ArgGluAspTyrGluAspPheGluTyrIleArgArgGlnGlySerProAlaGlyPro	260
Dd		860	AGGGAGGACTATGAGGACTTTGAGTACATTCGGCGCCAGAAAGCAACCGAGGCCACCCCA	919
Oy		261	SerArgArgArgArgProGluArgValThrProGluPProProGluGluValAlaProAla	280
Dd		920	AGCAAAAGAGAGAGCCCGACGGGTCTGGCCAGAGCCCCCTTGAGAGAGAGAGCCCGGAC	979
Oy		281	ProAlaProGluGluArgIleGluProProValLysProLeuLeuProProLeuProPro	300
Dd		980	CCAGCCCCGGAGAGAGAGATTTAGCGCTCTGTGAAGCCTCTGCTGCCCGCTGCCCT	1039
Oy		301	AspTyrGlyAspGlyTyrValIleProAsnTyrAspAspMetAspTyrTyrPheGlyPro	320
Dd		1040	GACTATGGTATGTTAGTTAAGTATCCCAACTACATGACATGACATTAATCTTTGGGCT	1099
Oy		321	ProProProGluLysProAspAlaGluArgGlnThrAspGluGluLysGluGluLys	340
Dd		1100	CCTCGCCCCAGAAACCCGATGCTGAGCCAGACGAGCGAAGAGAGAGAGAGACTTAG	1159
Oy		341	LysProLysLysGluAspSerSerProLysGluGluThrAspLysTrpAlaValAlaGluLys	360
Dd		1160	AACCCAAAAGAGAGAGACAGCACGCCCCACAGAGAGAGACCGACMA GTGGGCGTGGAGAG	1219
Oy		361	GlyLysAspHisLysGluProArgLysGlyGluGluGluGluGluGluThrProThr	380
Dd		1220	GGCAAGAGACCAACAAGAGACCCCGAAGGGCGAGGTTGGAGAGAGATGACCCCTTAG	1279
Oy		381	GluLysValLysCysProProIleGlyMetGluSerHisArgIleGluAspAsnGlnIle	400
Dd		1280	GAGAAAGTCAATGTCTCCCGCATTTGGATGAGATCACCGTATTGAGACACCAATTC	1339
Oy		401	ArgAlaSerSerMetLeuArgHisGlyLeuGlyAlaGlnArgGlyArgLeuAspMetGln	420
Dd		1340	CGAGCTCTCTCATCTCTGCGCACCGCTTGGGGGCGACGCGCGCTCAATGCAG	1399
Oy		421	ThrGlyAlaThrGluAspAspTyrTyrAspGlyAlaTyrCysAlaGluAspAspAlaArg	440
Dd		1400	ACCGGTGCCACTGAGGAGGACACTATGATGATGGTGGTGGTGGCCAGAGATGCCAGG	1459
Oy		441	ThrGlnTrrPileGluValAspThrArgArgThrThrArgPheThrGlyValIleThrGln	460
Dd		1460	ACCCAGTGGATGAGGTGAGACCCGAGAGACTACCCGGTTCACAGGGCTCATACCCAG	1519
Oy		461	GlyArgAspSerSerIleHisAspAspPheValThrThrPhePheValGlyPheSerAsn	480
Dd		1520	GCGAAGACTCCAGCATCATATGCATTTTGTGACCACTTCTTCGTGGGCTTACGCAAT	1579
Oy		481	AspSerGlnThrTrrValMetTyrThrAsnGlyTyrGluGluMetThrPheHisGlyAsn	500
Dd		1580	GACACCGACATGTGGTGTATGTACACCAACGGCTATGAGAATAATGACCTTTCATGGGAC	1639
Oy		501	ValAspLysAspThrProValLeuSerGluLeuProGluPProValAlaAlaArgPheIle	520
Dd		1640	GGGACAGAGACACCCGTGTGATGAGCTCCAGAGCCGGTGGTGGCTCGTTTCATC	1699
Oy		521	ArgGlyeTyrProLeuThrThrAsnGlySerLeuCysMetArgLeuGluValLeuGlyCys	540
Dd		1700	CGCATCTACCACTCACTCGAATGGCAGCTGTGCATGCCCTTGGAGTCTGGGGTGC	1759
Oy		541	SerValAlaProValTyrSerTyrTyrAlaGlnAsnGluValAlaIleThrAspAspLeu	560
Dd		1760	TCTGTGGCCCTGTCTACAGCTAATACGACAGATGAGGTGGTGGCCACCGATGACCTG	1819
Oy		561	AspPheAspGlnHisSerTyrLysAspMetArgGlnLeuMetLysValAlaAsnGluGlu	580
Dd		1820	GATTTTCCGGCACACAGCTACACAGACATGGCCCGCTCAATGAGGTGGTAAAGAGAG	1879

QY	581	CysProThrIlethraGthrTyrSerLeuGlyLysSerSerArgGlyLeuLysIleTyr	600
Db	1880	TGCCCCACCAATCACCCGCACTTACAGCCTCGGGCAAGAGCTCACAGAGCCCTCAAGATCTAT	1939
QY	601	AlaMetGluIleSerAspAsnProGlyGlyNH ₂ ArgLeuGlyGluProGluPheArgTyr	620
Db	1940	GCCATGAGATCTCAGACAAACCTCGGGGAGCATCAACTGGGGGAGCCGAGTTCGGCTAC	1999
QY	621	ThrIaGlyIleHisGlyAsnGluValLeuGlyValArgGluLeuLeuLeuLeuMetGln	640
Db	2000	ACTCTGGGATCCATGCGCAACGAGGTCTGGGCGGAGAGCTGTGCTGCTCATCTCAG	2059
QY	641	TyrLeuCysArgGlyLysTyrArgAsnGlyAsnProArgValArgSerLeuValGlnAsnThr	660
Db	2060	TACCTGTGCGAGAGTACCGGATGGGAGCCACAGTGTGGCGACCTGTGTGACGACACA	2119
QY	661	ArgIleHisLeuValProSerLeuAsnProAspGlyTyrGluValAlaIleAsnMetGly	680
Db	2120	CGCATCCACCTGGTGCCCTCACTGAACCTGATGGCTACAGGGGTGGCAGCGCAGATGGCG	2179
QY	681	SerGluPheGlyAsnTrpAlaLeuGlyLeuTrpThrGluGluGlyPheAspIlePheGlu	700
Db	2180	TCGAAGTTTGGAACTGGGGCTGGAGCTGGACTAGAGAGGCTTTGACATTTGAA	2239
QY	701	AspPheProAspLeuAsnSerValLeuTrpGlyValaGluGluValArgLysTrpValProTyr	720
Db	2240	GATTTCCCGGATCTCAACTCTGTGTCTGGGGAGCTGAGGAGAGAAATGGGTCCCTAC	2299
QY	721	ArgValProAsnAsnAsnLeuProIleProGluValArgTyrLeuSerProAspAlaThrVal	740
Db	2300	CGGGTCCCAACAATACTGGCCATCCCTGAAAGCTACCTTTGCGCAGATGCCACGGTA	2359
QY	741	SerThrGluValArgAlaIleIleAlaTrpMetGluLysAsnProPheValLeuGlyAla	760
Db	2360	TCCACGAGAGTCCGGGCCATCATTTGCCGTGATGAGAAAGAACCCCTTCGTGTGGAGCA	2419
QY	761	AsnLeuAsnGlyGlyGluValArgLeuValSerTyrProTyrAspMetAlaArgThrProThr	780
Db	2420	AATCTGAACGGCGCGAGCGGCTGTGTCTCAACCCCTCAACGATTAAGGCCCGCACCCCTAC	2479
QY	781	GlnGluGluLeuLeuAlaIleAlaMetAlaAlaIleArgGlyGluAsnGluVala	800
Db	2480	CAGAGACAGCTGTGGCCGACGACCATGAGCAGACACCCGGGGGAGCATGAGACAGAGTC	2539
QY	801	SerGluAlaGlnGluThrProAspHisAlaIlePheAspArgTrpLeuAlaIleSerPheAla	820
Db	2540	TCCGAGGCCAGAGAGACTCCAGACACAGCCACTCTTCGGGTGGCTTGGCATCTCTTCGCC	2599
QY	821	SerAlaHisIleLeuThrLeuThrGluProTyrArgGlyGlyCysGlnAlaGlnAspTyrThr	840
Db	2600	TCCGACACCTCACCTTGAACGAGCCCTCAACGCGAGAGCTGCAGAGCCACAGACTACACC	2659
QY	841	GlyGlyMetGlyIleValaAsnGlyAlaIleAspTrpAsnProArgThrArgTyrIleAsnAsp	860
Db	2660	GGCGGCATGGGCATCTGTCAAGGGGCCAAGTGAACCCCGGACGGGACATCAATGAC	2719
QY	861	PheSerTyrLeuNH ₂ TrpThrAsnCysLeuGluGluLeuSerPheTyrLeuGlyCysAspLysPhe	880
Db	2720	TTCAAGTTACCTGCATACCAACTGGCTGTAGCTCTCTTCACTCTGGGCTGTGACAAAGTTC	2779
QY	881	ProHisGluSerGluLeuProArgGluTrpGluAsnAsnArgGluAlaLeuLeuThrPhe	900
Db	2780	CCTATGAGATGAGCTGCCCGGAGTGGAGAAACAACAGAGGGGCTGTCACTTC	2839
QY	901	MetGluGluValHisArgGlyTyrLeuArgIleValaIleThrAspGluGlnGlyIleProIle	920
Db	2840	ATGGAGCAGGTGACCCGGCGATTAAAGGGGTGTGTGACGCGCAGCAAGCATCCCATTT	2899
QY	921	AlaAsnAlaTrpTrpIleSerValSerGlyTyrLeuHisGlyValLysTrpAlaSerGlyGly	940
Db	2900	GCCACGGCCACATCTGTGTAGTGGCAATTATACGGCGGGAAGACAGCCAGTGGTGT	2959

QY 941 AsptYrThpArGlIleuAenProGlYglUyArYValThrAlaHlaGlUglYThr 960
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QY 961 ThProSeRaIaYsThrCySaSnVaIAspTyArAspIleGlYalATHrGlNcySaSnPhe 980
Db ACCCGAGCGGCAAGACTGGAAATGTTGACTATGACATCGGGGCACTCACTGCACTTC 3079
QY 981 IleuAaIaArGSeRaenTTPYsArGlIleArGlUlleMeCaIaMeCaenGlYsArNaY 1000
Db ATCTGCTGCTCCCACTGGAAAGCGCATCCGGAGATCATGCGCAATGAACCGG 3139
QY 1001 ProIleProHsIleAaProSeRaYgProMeThrProGlNglNaYsArGlUglN 1020
Db CCTATCCCAACATAGAACCCATGCGCTTATGACCCCAAGCAAGCAAGCGCTGCAAG 3199
QY 1021 ArYsArGlUglNlIaArGlUeArYsArGlIleArGlUlleMeCaIaMeCaenGlYsArNaIa 1040
Db CGAGCGCTTACACACCGCTGCGCTTCGGGCAAGATGCGGCGCGCCCTCAACGCC 3259
QY 1041 ThrThrThrLeuGlYProHsIsthValProProThrLeuProProAlaProAlaThrThr 1060
Db ACCACCAACCTAGGCCCCCACTGTGCTCCCAAGCTGCGCCCTGCGCCCAACACC 3319
QY 1061 LeuSeRThrThrIleGlUProTTPGlYleuIleProProThrThrAlaGlYTPGlUglU 1080
Db CTGAGCACTACATAGAGCCCTGGGGCTCTATACCGCAACACCGCTGCTGGAGAG 3379
QY 1081 SerGlUThrGlUThrYrThrThrGlUValIThrGlUThrGlYThrGlUValIglUProGlU 1100
Db TCGGAGCTGAGACTTACACAGAGTGTGTACAGAGTTTGGAGCCGAGGTGAGCCGAG 3439
QY 1101 PheGlYThrIlyValIglUProGlUThrGlUThrGlUglUProGlUThrGlUThrGlU 1120
Db TTGGGAGCAAGGTGAGCGCGAGTTGAGACCACTGAGAGCTGAGTTGAGACCCAG 3499
QY 1121 LeuGlUProGlUThrGlUglUglUglUglUglUglUglUglUglUglUglUglUglU 1140
Db CTGGAACTCGAGTTTGGAG 3559
QY 1141 GlAlaIaPheProPheThrThrValIglUThrYrThrValIaenPheGlYsArPhe 1158
Db 3560 CAGGCACTCCCTTCAACAGATGAGACCTACACATGAACTTTGGGACTTC 3613

RESULT 5
US-10-775-920-195
; Sequence 195, Application US/10775920
; Publication No. US20040175744A1
; GENERAL INFORMATION:
; APPLICANT: Merzen Ltd
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCES AND CORRESPONDING ENCODED POLYPEPTIDES
; TITLE OF INVENTION: OF PARTICULAR SECRETED AND MEMBRANE-BOUND PROTEINS OVEREXPRESSED
; FILE REFERENCE: Merzen - 00108
; CURRENT APPLICATION NUMBER: US/10/775,920
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 60/447,900
; NUMBER OF SEQ ID NOS: 385
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 195
; LENGTH: 3935
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-920-195

Alignment Scores:
Pred. No.: 0 Length: 3935
Score: 6272.00 Matches: 1158
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 9 Gaps: 0

US-10-642-946-3 (1-1158) x US-10-775-920-195 (1-3935)
QY 1 MeCaIaAlaValArGlYalAProLeuLeuSeRcySeIleuAaIaLeuAaIaLeuCyS 20
Db ATGGCGGCGGTGGCGGGGGCGCCCTGCTCAGCTGCTCTGCGGTGGCGGTGGCG 199
QY 21 ProGlYGlYArGProGlNThrValIleuThrAspAspGlUlleGlUglUThrLeuGlUglY 40
Db CTGGAGGGGGCGCGGAGAGGCTGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 259
QY 41 PheLeuSeRglUleuGlUProGlUProArYsGlUAspAspValIglUAlaProProPro 60
Db TTCTGTGAGAGCTTGAACCTTAGAGCCCGGAGAGAGAGAGAGAGAGAGAGAGAG 319
QY 61 GlUProThrProArYsValArGlYsAlaGlIleGlYlYsArProGlYlYsArProGlY 80
Db GAGCCCAACCGCGGGGTCCGAAAGCCAGGCGGGGGGCAAGCCAGGAGAGAGAG 379
QY 81 ThrAlaAlaGlUValProProGlUlyThrIlyAspIlyGlYlYsArProGlYlYsAr 100
Db ACCGCGCAGAAATGCTCTCGGAAAGCAACAAAGAGAGAGAGAGAGAGAGAGAG 439
QY 101 lYsGlYProIlysValProIlysGlUSeRLeuGlUglYSerProArYsProProIlysGlY 120
Db AAAGCCCCAAGGTGCCAAGAGAGTCTTGGAGGGTCCCCAGGCGCCCAAGAGGG 499
QY 121 lYsGlUlysArProProIlysAlaThrIlylYsArProIlysGlUlysArProIlysAlaThrIlyS 140
Db AAGAGAGAGCAACCAAGGCAACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 559
QY 141 lYsArProIlysGlUglUProProIlysAlaThrIlylYsArProIlysGlUlysArProIlysAla 160
Db AAGCCCAAG 619
QY 161 ThrIlylYsArProProSeRglYlYsArGProProIleuAlaProSeRglUThrLeuGlU 180
Db ACCAAG 679
QY 181 TrpProLeuProProProProSeRProGlYProGlUglUleuProGlUglYglYAla 200
Db TGCGCACTGCCCCCAACCCCGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 739
QY 201 ProLeuSeRaSnAsnTTPGlNAsnProGlYglUglUThrIlyValIglUglUThrIlyS 220
Db CCCCTCTCAATTAATGAGAGATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 799
QY 221 GlNProGlUProGlUglUglUglUglUglUglUglUglUglUglUglUglUglUglU 240
Db CAGCTGAGCGGAG 859
QY 241 ArGlUAspTyRglUAspPheGlUyRlIeArYsArGlUlySglNProArYsProPro 260
Db AGGAGAGACTATAGAGACTTGTAGTACATTCGGCGCAAGAGAGAGAGAGAGAGAG 919
QY 261 SerArYsArYsArYsProGlUArYsValITPProGlUProProGlUglUlySAlaProAla 280
Db AGCAG 979
QY 281 ProAlaProGlUglUglUglUglUglUglUglUglUglUglUglUglUglUglUglUglU 300
Db CAGGCCCCGAG 1039
QY 301 AspTyRglYAspIlyRValIleProAsnTyRAspAspMeCaAspTyRThrPheGlYPro 320
Db GACTATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1099
QY 321 ProProProGlUlysProAspAlaGlUArYsGlUThrAspGlUglUlySglUglUleuIlyS 340
Db CTTCGCGCCCAAG 1159
QY 341 lYsArProIlylYsGlUlysArSeRProIlysGlUglUThrAspIlyRThrAlaValIglUlyS 360

Db 1160 AAACCCAAAAGGAGGACAGACGCCCAAGAGAGACCGACAAGTGGGCGATGGAGAG 1219
QY 361 G1YLYASPHILelygluProAlglyG1YgluGluLeuGluGluGluTrpThrProThr 380
Db 1220 GGGAAAGACACAAAGAGCCCGAAGAGGAGAGAGTGAAGAGAGAGGAGCTTAG 1279
QY 381 G1uLYeValLYeCySPProFolleg1YMeG1uSeH1;AArg11eg1uAspAeng1u1e 400
Db 1280 GAGAAAGTCAGAGTCCCCCAATTGGGATGAGTCAACCGTATTAGAGACAAACGAGTC 1339
QY 401 ArgAlSeSerSeMetLeuAArgH1sg1YLeuG1YAlaG1nAArg1YhArgLeuAenMeG1n 420
Db 1340 CGAGCTCTCTCCATGCTGGCGCACGGCGCTGGGGGCAACGCGCGGCGCTCAACATGCA 1399
QY 421 ThrG1YAlaThrG1uAspAArgTYTYTAAArg1YAlaTrpCYAlaG1uAspAAlaArg 440
Db 1400 ACCGGTGCCACTGAGAGACGACTATGATGATGGTGCGTGTCAGAGACGATGCGAG 1459
QY 441 ThrG1nTrp11eg1uValAspThrArgArgThrThrArgPheThrG1YAla11eThrG1n 460
Db 1460 ACCCAATGATAGAGGTGAGACACAGAGGACTACCCGGTTCACAGCGCTCATCACCG 1519
QY 461 G1YArgAspSeSer11eH1sAspAAspAheValThrThrPhePheValG1YPheSeAra 480
Db 1520 GGCAGAGACTCCAGCATCCATGACGATTTTGTGACCACTTCTTGGTGGGCTTCAGCAAT 1579
QY 481 AspSeSerG1nThrTrpValMetTYTTrpAeng1YTYG1uGluMetThrPheH1sg1Yan 500
Db 1580 GACAGCGACAGCATGGGTGATGATACACCAACGGCTATGAGAAATGACCTTCATGGGAAC 1639
QY 501 ValAspLYeAspThrProValLeuSeSerG1uLeuProG1uProValAla1AArgPhe1le 520
Db 1640 GTGGACAGAGACACACCGGTGATGAGTCCCAAGCGCGGTGGTGGCTCGTTTCAAC 1699
QY 521 Arg11eTYrProLeuThrTrpAeng1YSeSerLeuCYeMetArgLeuG1uValLeuG1YCy 540
Db 1700 CGCATCTACCCACTCACTCGGAATGGCAGCGCTGTGATGCGCTGAGAGGTGCGGGGTGC 1759
QY 541 SerValAlaProValTYrSeSerTYTYTAlaG1nAsnG1uValAla1AthrAspAAspLeu 560
Db 1760 TCTGTGGCCCTGTCTACAGCTACTACGACAGAAAGAGGTGGTGCCACCGATGACCTG 1819
QY 561 AspPheArgH1;H1sSeTYrLYeAspAAspAArg11eLeuMetLYeValVal1Aeng1uG1u 580
Db 1820 GATTTCGGGACACACAGCTACAGACATGCGGCACTCATGAAAGTGGTGAACGAGAG 1879
QY 581 CySPProThr11eThrArgThrTYrSeSerLeuG1YLeSeSerArgG1YLeuLYe11eTYr 600
Db 1880 TGGCCCAACCATCACCCGCACTTACAGCTGGGCAAGAGCTCAAGAGGCTCAAGATCTAT 1939
QY 601 AlaMetGlu11eSerAspAAspProG1YG1uH1sg1uLeuG1YgluProG1uPheArgTYr 620
Db 1940 GCCATGAGATCTCAACAAACCTGGGAGACATGAATGGGGAGGCCGAGATTCCTCCATAC 1999
QY 621 ThrAlaG1Y11eH1sg1YAsnG1uVal1LeuG1YArgG1uLeuLeuLeuLeuMeG1n 640
Db 2000 ACTGCTGGGATCGATGGCAACGAGGTGCTGGGCGGAGAGCTGTGTGCTGCTCATGCGAG 2059
QY 641 TYrLeuCYeArgG1uTYrArgAAspG1YAsnProArgVal1AArgSeSerLeuValG1nAspThr 660
Db 2060 TACCTGTGGCGAAGATACCGCGATGGGAACCCACGTGTGCGGACCTGGTGCGAGGACACA 2119
QY 661 Arg11eH1;leuVal1ProSeSerLeuAAspProAAspG1YTYrG1uVal1Ala1Agn1MeG1Y 680
Db 2120 CGCATCACTGGTGGCTCTACTGAACCTGATGGCTACAGAGGTGGAGGCGAGATGGCG 2179
QY 681 SerG1uPheG1YAsnTrpAlaLeuG1YLeuTrpThrG1uG1uG1YPheAsp11ePheG1u 700
Db 2180 TCAGAGTTGGGAATCGGGGCTGGGACTGTGAGATGAGAGAGGCTTTGACATCTTTGA 2239
QY 701 AspPheProAspLeuAAsnSerVal1LeuTrpG1YAlaG1uG1uArg1YTrpValProTYr 720
Db 2240 GATTCCCGGATCTCAACTGTGTCTGTGGGAGCTGAGAGAGAAATGGGTCCCTTAC 2299

QY 721 ArgVal1ProAAsnAAsnLeuPro11eProG1uArgTYrLeuSeSerProAspAlaThrVal 740
Db 2300 CGGGTCCCAACAAATACATGCTCATCTCTGAACCTACTTTCGCAAGATCCACGGTA 2359
QY 741 SerThrG1uVal1ArgAla11e11eAlaTrpMeG1uLYeAsnProPheVal1eug1YAla 760
Db 2360 TTCACGAGAGGTCCGGGCTCATCTTGCATGAGAGAAAGAACCTTGTGCTGGGAGCA 2419
QY 761 AsnLeuAeng1YgluG1uArgLeuVal1SeTYrProTYrAAspAAlaArgThrProThr 780
Db 2420 AATCTGAACGGGGGAGAGCGGTACTATCTCAACCTCTAGATGAGCCGCGACGCTTACC 2479
QY 781 G1nG1uG1nLeuLeuAla1AAlaMetAla1AAspG1YG1uAspG1uAspG1uVal 800
Db 2480 CAGGACAGCTGCTGGCGGACCACTGGCAGAGCGCCGGGGGAGATGAGACAGAGTC 2539
QY 801 SerG1uAlaG1nG1uThrProAspH1sAla11ePheArgTrpLeuAla11eSerPheAla 820
Db 2540 TTCAGAGCCCAAGGAGACTCCAGACCAAGCATCTTCCGGTGGCTTGCCATCTCTTCGCC 2599
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Db 2600 TCCGACACCTCACCTTGACCGAGCCCTACCGCGAGGCTGCGCAAGCCAGAGACTACAC 2659
QY 841 G1YLYeMetG1Y11eValAsnG1YAlaLYeTrpAAspProArgThrG1YThr11eAsnAAsp 860
Db 2660 GCGGCGATGGGATGCTGTCACGGGGCCAAAGTGAAACCCCGGACCGGACATTCATAGAC 2719
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QY 921 AlaAsnAlaThr11eSerValSeSerG1Y11eAsnH1sg1YVal1YeThrAlaSeSerG1Yg1Y 940
Db 2900 GCCAAGCCACCATCTCTGTGATGATTAATACAGGGGTGAAGACAGCCAGTGGTGT 2959
QY 941 AspTYrTrpArg11eLeuAAspProG1YgluTYrArgVal1ThrAlaH1sAlaG1uG1YTYr 960
Db 2960 GATTACTGGCGAATCTTGAACCGGGGTAGTACCGGTGACAGCCACCGGAGGGCTAC 3019
QY 961 ThrProSeSerAlaLYeThrCYeAsnValAspTYrAAsp11eG1YAla1eThrG1nCYeAsnPhe 980
Db 3020 ACCCGAGCGCCAAACCTGCAATGTGACTATGACATGAGGGCCACTCAAGTCAATTC 3079
QY 981 11eLeuAlaArgSeSerAsnTrpLYeArg11eArgG1u11eMetAlaMetAAsnG1YAsnArg 1000
Db 3080 ATCTGGGCTCGCTCCAACTGMAAGCGCATCCGGAGATGATAGCCATGAACGGGAACCG 3139
QY 1001 Pro11eProH1;e11eAspProSeSerArgProMetThrProG1nG1uArgArgLeuG1nG1n 1020
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QY 1021 ArgArgLeuG1nH1;AArgLeuArgLeuArgAlaG1MeTAArgLeuArgArgLeuAsnAla 1040
Db 3200 CGAGCGCTACAAACCGCGCTGGGCTTGGGCGACAGATCGGCTCGGCGCTCAAGCGC 3259
QY 1041 ThrThrThrLeuG1YProH1;eThrVal1ProProThrLeuProProAlaProAlaThrThr 1060
Db 3260 ACCACACCTTAGGCCCCCACTGCTGCCAGCGCTGCCCGCTGCGCTCCACACAC 3319
QY 1061 LeuSeSerThrThr11eG1uProTrpG1YLeu11eProProThrThrAlaG1YTrpG1uG1u 1080
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QY	1081	sergIuThrGluThrThyThrcGluValAlaThrGluPheGlyThrGluValGluProGlu	1100
Db	3380	TCGGAGACTGAGACCTTACACAGAGGTGTGAGACGATTGGACCGAGTGGAGCCGAG	34339
QY	1101	PheGlyThrIlyValGluProGluPheGluThrGluLeuGluProGluPheGluIlyrGln	1120
Db	3440	TTTGGGACCAAGCTGGAGCCGAGTTTGAAGCCAGTTGGAGCTTGAATTCGAGCCAG	34359
QY	1121	LeuGluProGluPheGluGluGluGluGluGluGluGluGluGluGluGluIleAlaThrGly	1140
Db	3500	CTGGAAACCCGAGTTTGAGAGAGAGAGAGAGAGAGAGAGAGAGATAGCCACTGCG	35559
QY	1141	GlnAlaPheProPheThrThrValGluThrTrpThrValaenPheGlyAspPhe	1158
Db	3560	CAGGCATTCCCTTCACACAGTAAAGAGACTTACAGATGAACCTTGGGGGACTTC	3613
RESULT 6			
US-10-473-974-128			
; Sequence 128, Application US/10473974			
; Publication No. US20040265808A1			
; GENERAL INFORMATION:			
; APPLICANT: GARCIA, TERESA			
; APPLICANT: ROMAN ROMAN, SERGIO			
; APPLICANT: BARON, ROLAND			
; APPLICANT: CALL, KATHERINE			
; APPLICANT: THEILHABER, JOACHIM			
; APPLICANT: CONNOLLY, TIMOTHY			
; APPLICANT: JACKSON, AMANDA			
; APPLICANT: BUSHNELL, STEVEN			
; APPLICANT: RAMADI, GEORGES			
; TITLE OF INVENTION: GENES INVOLVED IN OSTEOGENESIS, AND METHODS OF USE			
; FILE REFERENCE: 37991-0023			
; CURRENT APPLICATION NUMBER: US/10/473,974			
; CURRENT FILING DATE: 2003-10-03			
; PRIOR APPLICATION NUMBER: PCT/IB02/02211			
; PRIOR FILING DATE: 2002-04-05			
; PRIOR APPLICATION NUMBER: 60/281,400			
; PRIOR FILING DATE: 2001-04-05			
; NUMBER OF SEQ ID NOS: 246			
; SOFTWARE: PatentIn Ver. 3.2			
; SEQ ID NO 128			
; LENGTH: 3935			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-473-974-128			
Alignment Scores:			
Pred. No.: 0			
Score: 6272.00			
Best Local Similarity: 100.0%			
Query Match: 100.0%			
DB: 9			
Gaps: 0			
US-10-642-946-3 (1-1158) x US-10-473-974-128 (1-3935)			
QY	1	MetAlaAlaValAlaGlyAlaProLeuLeuSerCysLeuAlaAlaLeuAlaLeuCys	20
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QY	21	ProGlyGlyArgProGluIlyrValLeuThrAspAspGluIleGluGluPheLeuGluGly	40
Db	200	CCTGAGGGGCGGCCGACAGCGGTGTCGACCGACGACGAGATCGAGGATCTCGAAGGC	259
QY	41	PheLeuSerGluLeuGluProGluProAlaArgIleAspAspValGluAlaProProPro	60
Db	260	TTCCGTGAGACTGAGAACTGAGCCCGGGGAGCGACGTGAGAGCCCGCCGCTTCC	319
QY	61	GluProThrProArgValArgIlyValAlaGluGlyIlyAspProGlyIlyAspProGly	80
Db	320	GAGCCACCCCGCGGGTCCGAAAGACCCAGGCGGGGGGACGACGAGGAGCGGCGAGG	379
QY	81	ThrAlaAlaGluValProProGluIlyrThrIlyAspIlyGlyIlyGlyIlyAsp	100

Db	360	ACGCGCGCAGAGTGCCTCCGAAAAAGCCAAAGCCAAAGGAGAAAGCCAAAGAAAC	439
Qy	101	LysGIyProLysValProLysGIuSerLeuGIuGISeProArGIProProLysLysGIy	120
Db	440	AAAGCCCCCAAGGTGCCCCAAGAGTCTTGGAGGGGTCCCCAGGCCCCCAAGAGAGGG	499
Qy	121	LysGIuLysProProLysAlaThrLysLysProLysGIuLysProProLysAlaThrLys	140
Db	500	AAGGAGAAAGCCACCAGAGCCACCAAGAGGCCAAAGAGAAAGCCACTAAGGCCACCAAG	559
Qy	141	LysPProLysGIuGIuLysProProLysAlaThrLysLysProLysGIuLysProProLysAla	160
Db	560	AAGCCCAAGAGAGAGCCACCAGGCCACCAAGAGGCCCAAGAGAACCCACCCCAAGGCC	619
Qy	161	ThrLysLysProProSerGIyLysArgProProLysLeuAlaProSerGIuThrLeuGIu	180
Db	620	ACCAAGAAAGCCCCCCTCAGAGAGAGGGCCCCCATCTGGGCTCCCTCAGAAACCTTGAG	679
Qy	181	TrpProLeuProProProProSerProGIyProGIuLeuProGIuGIuGIyAla	200
Db	680	TGGCCACTGCCCCCACCCCCGCCCTGGCCCCGAGGAGCTAACCCAGAGAGAGGGGGG	739
Qy	201	ProLeuSerAenAenTrpGIuAsnProGIyGIuGIuTrHLeuAlaGIuGIuHLeu	220
Db	740	CCCCCTCAAAATAACTGGCAGAAATCCAGAGAGGAGACCAATGTGGAGGCACAGAGAC	799
Qy	221	GIuProGIuLysProGIuGIuGIuThGIuGIuLysProThLeuAspTrpAsnAspGIuLysGIu	240
Db	800	CAGCTTGAGCCGAGAGAGAGAGCCAGAGAACCCACACTGAGCTACAAATGACCAAGATCGAG	859
Qy	241	ArgGIuAspTrpArgGIuAspPheGIuTrLysLeuArgArgGIuLysGIuProArgProProPro	260
Db	860	AGGAGAGACTATAGAGACTTTGAGTACTTGGCGCCAGAGAGCAACCAAGGCACCCCA	919
Qy	261	SerArgArgArgArgProGIuArgValTrpProGIuLysProLeuLeuProProLeuProAla	280
Db	920	AGCAGAAAGAGAGGCCCGGAGCGGGGTCTGGCCAGAGCCCTGTAGAGAAAGGCCCGGCC	979
Qy	281	ProAlaProGIuGIuArgTrLysGIuProProValLysProLeuLeuProProLeuProPro	300
Db	980	CCAGCCCCGAGAGAGAGATGAGCTCTGTGAAGCCTCTGTGTCGCCCCCGTGGCCCCCT	1033
Qy	301	AspTrpArgIyAspGIyTrpValLysProAsnTrpAspAspMetAspTrpTrpPheGIyPro	320
Db	1040	GACTATGTGTATGGTTATGTATGCCCACTACAGATGACAGACTATTACTTTGGGGCT	1099
Qy	321	ProProProGIuLysProAspAlaGIuArgGIuThrAspGIuLysGIuGIuLeuLys	340
Db	1100	CCTCCGCCCCAGAAAGCCGATGCTGAGGCCAGACGCGACGAAGAGAGAGAGAGCTGAAG	1155
Qy	341	LysPProLysLysGIuAspSerSerProLysGIuGIuTrpAspLysTrpAlaValGIuLys	360
Db	1160	AAACCCAAAAAGAGAGACAGAGCCCCCAAGAGAGAGACCGACAAGTGGCGAGTGAAG	1215
Qy	361	GIyLysAspHLeuLysGIuProArgLysGIyGIuGIuLeuGIuGIuGIuTrpThrProThr	380
Db	1220	GGCAAGAGCCACAAAGAGCCCCCGAAAGGCCAGAGAGTTGGAGAGAGAGTGAACGCTTACG	1275
Qy	381	GIuLysValLysCysProProLysGIyMetGIuSerHLeuArgIyLeuAspAsnGIuLe	400
Db	1280	GAGAAAGTCAGTGTCCCCCATTTGGATGAGTCACACCGTATTTGAGGACAAACAGATTC	1339
Qy	401	ArgAlaSerSerMetLeuArgHLeuGIyLeuGIyAlaGIuArgGIyAlaGIuLeuAsnMetGIu	420
Db	1340	CGAGGCTCTCTCAATGCTGCGCCAGCGGCTGGGGGACACGCCCGGCTCAACATGAG	1399
Qy	421	ThrGIyAlaThrGIuAspAspTrpTrpAspGIyAlaTrpCysAlaGIuAspAspAlaArg	440
Db	1400	ACCGGTCCACTGAGAGAGACTACTATGATGTGCGTGTGTCGCGAGAGACGATGCCAGG	1455
Qy	441	ThrGIuTrpIyLeuGIuValAspThrArgArgThrArgPheThrGIyValIyLeuThrGIu	460

Db 1460 ACCGATGGATAGAGGTGACACACGAGGAACTACCGGGTTCACAGCGCTCATCACCGAG 1519
QY 461 G1YAAGASPSerSer11eh1sAspAspPheVal1Thr1ThrPhePheVal1Gly1PheSerAsn 480
Db 1520 GCGAGAGATCCGAGCATCATGACATGAGATTTGTGACCACTTCTCTGGGCTTCACAGCAAT 1579
QY 481 AAspSerG1Thr1Thr1Val1Met1Ty1Thr1Asn1Gly1Ty1Glu1Glu1Met1Thr1Phe1Ile1Asn 500
Db 1580 GACAGCAGACATGGGTGATGATACACCAACGGCTTATGAGAAATGACCTTTTCATGGGAAC 1639
QY 501 Val1Asp1Lys1Asp1Thr1Pro1Val1Leu1Ser1Glu1Leu1Pro1Glu1Pro1Val1Ala1Arg1Phe1Ile 520
Db 1640 GTGGACAAAGGACACACCGGTGCTGAGTGAAGCTCCAGAGCGGTGGTGGCTGGTTTCATC 1699
QY 521 Arg1Le1Ty1P1Pro1Leu1Thr1Thr1Asn1Gly1Ser1Leu1Cys1Met1Arg1Leu1Glu1Val1Leu1Gly1Cys 540
Db 1700 CGCATCTACCCACTCATCCTGAGTGAATGCGAGCTGTGTGATCGCTGTGAGGTGTCTGGGGGTGC 1759
QY 541 Ser1Val1Ala1Pro1Val1Ty1Ser1Ty1Ty1Arg1Asn1Glu1Val1Val1Ala1Thr1Asp1Asp1Leu 560
Db 1760 TCTGTGGCCCTCTGTCTACAGCTTCTACGACACGAAATGAGGTGTGGCCACCTGATGACCTG 1819
QY 561 Asp1Phe1Arg1His1Ser1Ty1Lys1Asp1Met1Arg1Glu1Leu1Met1Lys1Val1Ala1Asn1Glu1 580
Db 1820 GATTTCCGGACACACAGCTATCAAGACATGCGCCAGCTCATGAAAGGTGTGAACGAGAG 1879
QY 581 Cys1Pro1Thr1Ile1Thr1Arg1Thr1Ty1Ser1Leu1Gly1Lys1Ser1Ser1Arg1Gly1Leu1Lys1Ile1Ty1 600
Db 1880 TGGCCCAACATCACCCGCACTTACAGCTGTGGGCAAGAGCTCACAGAGCCCTCAAGATCTAT 1939
QY 601 Ala1Met1Glu1Ile1Ser1Asp1Asn1Pro1Gly1Glu1His1Gly1Leu1Gly1Glu1Pro1Glu1Phe1Arg1Ty1 620
Db 1940 GCCATGGAATCTCTCAACAAACCTGGGGACATGAACCTGGGGAGGCCCAAGTTCCCTTAC 1999
QY 621 Thr1Ala1Gly1Ile1His1Gly1Asn1Glu1Val1Leu1Gly1Arg1Glu1Leu1Leu1Leu1Met1Gln 640
Db 2000 ACTGCTGGGATCCATGGCAACGAGGTGTGGCCGAGAGCTGTGTCTGCTGCTCATAGCAG 2059
QY 641 Tyr1Leu1Cys1Arg1Glu1Ty1Arg1Asp1Gly1Asn1Pro1Arg1Val1Arg1Ser1Leu1Val1Glu1Asp1Thr 660
Db 2060 TACCTTGCCGAGAGTACCGCGATGGGAAACCCACGTTGTGGCAGCTGTGGTCAGGAGACAA 2119
QY 661 Arg1Ile1His1Leu1Val1Pro1Ser1Leu1Asn1Pro1Asp1Gly1Ty1Gly1Val1Ala1Ala1Glu1Met1Gly 680
Db 2120 CGCATCACTGGTGGCTCTCATCTGAACCTGTAGTGGTATGAGGTGGCAGCGCAGATGGGC 2179
QY 681 Ser1Glu1Phe1Gly1Asn1Thr1Ala1Leu1Gly1Leu1Thr1Thr1Glu1Glu1Gly1Phe1Asp1Ile1Phe1Glu 700
Db 2180 TCAGAGTTTGGGAACGTGGGCGCTGGGACTGTGAGACTGAGGAGGGCTTTTGACATCTTTGAA 2239
QY 701 Asp1Phe1Pro1Asp1Leu1Asn1Ser1Val1Leu1Thr1Gly1Ala1Glu1Glu1Arg1Lys1Thr1Val1Pro1Ty1 720
Db 2240 GATTTCCCGGATCTCAACTGTGCTGTGGGAGCTGAGGAGGAGAAATGGGCTCCCTTAC 2299
QY 721 Arg1Val1Pro1Asn1Asn1Leu1Pro1Ile1Pro1Glu1Arg1Ty1Leu1Ser1Pro1Asp1Ala1Thr1Val 740
Db 2300 CGGGTCCCCAACAATTAATCTTGCCCATCCCTGAACCGCTACTCTTCCGCAATGCCACGGTA 2359
QY 741 Ser1Thr1Glu1Val1Arg1Ala1Ile1Ile1Ala1Thr1Met1Glu1Lys1Asn1Pro1Phe1Val1Leu1Gly1Ala 760
Db 2360 TCACAGGAGGTCCGGGCGCATCTTGGCTGTGATGAGAGAAACCCCTTCCGTGGGAGAGA 2419
QY 761 Asn1Leu1Asn1Gly1Gly1Glu1Arg1Leu1Val1Ser1Ty1Pro1Ty1Asp1Met1Ala1Arg1Thr1Pro1Thr 780
Db 2420 AACTTAACGCGCGGCGAGCGGTAGTATCTTACCCCTACGATATGCGCCGACGAGCTTACC 2479
QY 781 Gln1Glu1Gln1Leu1Leu1Ala1Ala1Met1Ala1Ala1Arg1Gly1Lys1Asp1Glu1Asp1Glu1Val 800
Db 2480 CAGGACAGAGTGTGTGGCGGACGACATGCGACGAGCCCGGGGGAGGATGAGGACGAGT 2539
QY 801 Ser1Glu1Ala1Gln1Lys1Thr1Pro1Asp1His1Ala1Ile1Phe1Arg1Thr1Leu1Ala1Ile1Ser1Phe1Ala 820
Db 2540 TCCGAGGCGCCAGGAGACTCCAGACCAAGCATCTTCCGGTGGCTTCCATCTCTTCCGCG 2599

QY 821 Ser1Ala1His1Leu1Thr1Leu1Thr1Glu1Pro1Thr1Arg1Gly1Cys1Gln1Ala1Glu1Asp1Ty1Thr 840
Db 2600 TCCGCACACCTTACCTTATACCGAGCTTACCGCGGAGGCTGTGCAAGCCCAAGACTTACAC 2659
QY 841 Gly1Gly1Met1Gly1Ile1Val1Asn1Gly1Ala1Lys1Thr1Asn1Pro1Arg1Thr1Gly1Thr1Ile1Asn1Asp 860
Db 2660 GCGGCGCATGGGATGTCTCAACGGGGCCAAATGGAAACCCCGGACCGGGAGCTATCATATGAC 2719
QY 861 Phe1Ser1Ty1Leu1His1Thr1Asn1Cys1Leu1Glu1Leu1Ser1Phe1Ty1Leu1Gly1Cys1Asp1Lys1Phe 880
Db 2720 TTCAGTACTCTGCATACCAACAGCTGTGAGGCTCTCTTCTACTCTGGCTGTGTACAAATTC 2779
QY 881 Pro1His1Gly1Ser1Glu1Leu1Pro1Arg1Glu1Thr1Glu1Asn1Lys1Glu1Ala1Leu1Leu1Thr1Phe 900
Db 2780 CCTCATGAGAGTGAAGTCTCCCGGAGTGGGAGAAACAAACAGAGGCGGTGCTTCACTTC 2839
QY 901 Met1Glu1Gln1Val1His1Arg1Gly1Ile1Lys1Gly1Val1Val1Thr1Asp1Glu1Gln1Gly1Ile1Pro1Ile 920
Db 2840 ATGGAGCAGAGTGCACCGCGGACTTAAAGGGGGTGTGACGAGACAGACAAAGGATCCCAATT 2899
QY 921 Ala1Asn1Ala1Thr1Ile1Ser1Val1Ser1Gly1Ile1Asn1His1Gly1Val1Lys1Thr1Ala1Ser1Gly1 940
Db 2900 GCCAACGCGCACCATCTGTGTGATGTCATTTATACCGCGCTGAACAGACAGCCAGTGTGTGT 2959
QY 941 Asp1Ty1Thr1PArg1Ile1Leu1Asn1Pro1Gly1Glu1Ty1Arg1Val1Thr1Ala1His1Ala1Glu1Gly1Ty1 960
Db 2960 GATTTCTGGCGCAATTTTGAACCGGGTGTAGTACCTCGGGGACATCGGGGACATCAAGTGCATTC 3019
QY 961 Thr1Pro1Ser1Ala1Lys1Thr1Cys1Asn1Val1Asp1Ty1Asp1Ile1Gly1Ala1Thr1Gln1Cys1Asn1Phe 980
Db 3020 ACCCGAGGCGCAAGACTTGCATATGTTGACTATGACATCGGGGACATCAAGTGCATTC 3079
QY 981 Ile1Leu1Ala1Arg1Ser1Asn1Thr1Lys1Arg1Ile1Arg1Glu1Ile1Met1Ala1Met1Asn1Gly1Asn1Arg 1000
Db 3080 ATCTGGGTCTCGCTCCACATGGAGGCGCATCCGGGAGATCAATGCGCATGAACGGGAAACCGG 3139
QY 1001 Pro1Ile1Pro1His1Ile1Asp1Pro1Ser1Arg1Pro1Met1Thr1Pro1Gln1Ala1Arg1Leu1Gln1 1020
Db 3140 CCTATTCACACATATGACATCCATCGGCTGTATGACCCCGCAACAGCAGCCTGACAGCAG 3199
QY 1021 Arg1Arg1Leu1Gln1His1Arg1Leu1Arg1Leu1Arg1Ala1Glu1Met1Arg1Leu1Arg1Arg1Leu1Asn1Ala 1040
Db 3200 CGAGCGCTAACAAACACCGCTGGCGCTTCGGGACAGATGCGGCTCGGGGCTTCAACCGCC 3259
QY 1041 Thr1Thr1Thr1Leu1Gly1Pro1His1Thr1Val1Pro1Pro1Thr1Leu1Pro1Pro1Ala1Thr1Thr 1060
Db 3260 ACCACACCGCTTAGGCGCCCGCACATGTGCTCCACAGCTGCGCCCTGCGCTGCCACACCC 3319
QY 1061 Leu1Ser1Thr1Thr1Ile1Glu1Pro1Thr1Gly1Leu1Ile1Pro1Pro1Thr1Thr1Ala1Gly1Thr1Glu1Glu 1080
Db 3320 CTGAGCATCTACATGAGACCGCTGGGGCTCTCATCCGCCAACACACCGCTGTGGAGAGAG 3379
QY 1081 Ser1Glu1Thr1Glu1Thr1Ty1Thr1Glu1Val1Val1Thr1Glu1Phe1Gly1Thr1Glu1Val1Glu1Pro1Glu 1100
Db 3380 TCGGAGACTGAGACCTTACACAGAGGTGTGACAGAGTTTGGAGCCGAGGTGAGCCCGAG 3439
QY 1101 Phe1Gly1Thr1Lys1Val1Glu1Pro1Glu1Phe1Glu1Thr1Gln1Leu1Glu1Pro1Glu1Phe1Glu1Thr1Gln 1120
Db 3440 TTTGGGACCAAGTGTGAAGCCGAGTTTGAAGACCCAGTTGAGACCTGTAGTTGACAGACCCAG 3499
QY 1121 Leu1Glu1Pro1Glu1Phe1Glu1Glu1Glu1Glu1Glu1Glu1Lys1Glu1Glu1Glu1Ile1Ala1Thr1Gly 1140
Db 3500 CTGGAACCGGATTTGAGGAGAGAGAGAGAGAGAGAGAGAGAGATACCACTGCGC 3559
QY 1141 Gln1Ala1Phe1Pro1Phe1Thr1Thr1Val1Glu1Thr1Ty1Thr1Val1Asn1Phe1Gly1Asp1Phe 1158
Db 3560 CAGGCAATCCCTTACAAACAGTAGAGACTTACAGAGTAAGTCTTGGGGAGCTTC 3613

RESULT 7
US-10-956-157-561
; Sequence 561, Application US/10956157
; Publication No. US20050118625A1

QY 601 A|A|MetG|U|L|Ser|Asp|Asn|Pro|G|Y|G|U|H|I|E|G|L|U|E|U|G|L|U|P|Pro|G|U|P|He|A|T|T|Y| 620
 Db 1940 GCCAAGGAGATCTCAGACAAACCTGGGGAGCATGAACTGGGGAGAGCCAGATTCCGCTAC 1999
 QY 621 Thr|A|G|L|Y|I|E|H|I|E|G|Y|A|N|G|I|U|V|A|L|E|U|G|I|A|Y|G|L|U|L|U|E|U|E|U|E|U|E|G|I|N 640
 Db 2000 ACTGCTGGGATCTCATGGCAACGAGGTGCTGGGCCGAGAGCTGTGCTGCTCATGGCAG 2059
 QY 641 Tyr|L|E|U|C|Y|A|X|G|L|U|T|Y|A|G|A|B|G|I|Y|A|N|P|O|A|T|G|V|A|I|A|S|E|U|L|U|I|G|I|N|A|P|H|T|H| 660
 Db 2060 TACCTGTGCGAGAGACCGGCATGGGAACCCACGCTGCGCAGCTGTGTCAGAGACACA 2119
 QY 661 Arg|I|E|H|L|E|U|V|A|P|O|S|E|U|E|U|A|N|P|O|A|B|G|I|Y|T|Y|G|L|U|V|A|I|A|L|A|G|I|N|E|G|I| 680
 Db 2120 CGATTCACCTGGTGGCTCTCATCTGAACCTGATGGCTACGAGGTGGACGCGCATGGC 2179
 QY 681 Ser|G|U|P|H|E|G|I|Y|A|N|T|P|A|L|E|U|G|I|Y|L|E|U|T|P|H|G|L|U|G|I|Y|P|H|E|A|P|I|E|P|H|E|G|I| 700
 Db 2180 TCAGAGTTTGGGAACCTGGCGGCTGGGACTGTGGACTGAGAGAGGGCTTTGACATCTTTGA 2239
 QY 701 Asp|P|H|E|P|O|A|S|P|L|E|U|A|N|S|E|R|V|A|L|E|U|T|P|G|I|Y|A|G|L|U|H|U|A|Y|T|P|V|A|P|O|T|Y| 720
 Db 2240 GATTTCCCGAATCTCAACTCTGTGCTCTGGGAGCTGAGAGAGGAAATGGGTCCCTTAC 2299
 QY 721 Arg|V|A|P|O|A|N|A|N|A|N|U|P|O|I|E|P|O|G|I|U|A|X|G|I|Y|L|E|U|S|E|P|P|O|A|P|A|T|H|V|A|I| 740
 Db 2300 CGGGTCCCCAACAATACCTTGCCATCCCTGAACGCTTACCTTTCCGCAATGCCACGGA 2359
 QY 741 Ser|T|H|G|L|U|V|A|A|R|G|A|I|E|I|E|A|I|A|T|P|M|E|G|L|U|Y|A|S|N|P|O|B|H|E|V|A|I|E|U|G|I|Y|A| 760
 Db 2360 TTCACGGAAGTCCGGGCGCATTCATGCTGGAATGGAGAAACCCCTCGTGGGGAGCA 2419
 QY 761 Asn|L|E|U|A|N|G|I|Y|G|L|U|A|T|G|L|E|U|V|A|S|E|T|Y|P|O|T|Y|A|S|P|M|E|C|A|A|A|T|H|P|O|H| 780
 Db 2420 AATCTGAAAGCGCGCGCAGCGGCTAGTATCCTACCCCTACGATATGGCCGCGACCTTAC 2479
 QY 781 G|N|G|L|U|L|E|U|A|I|A|A|I|A|E|C|A|A|A|A|A|A|A|A|A|A|A|A|A|A|A|A|A|A|A|A|A|A|A|A|A|A|A|A| 800
 Db 2480 CAGAGACAGTGTGCTGGCCGACCATGGACAGACCCCGGGGGAGGATAGACAGAGT 2539
 QY 801 Ser|G|U|A|I|G|N|I|U|T|H|P|O|A|P|H|I|A|I|E|P|H|E|A|T|T|P|H|E|U|A|I|E|S|E|P|H|E|A|I| 820
 Db 2540 TCGAGAGCCCAAGAGACTCCAGACCAACGCATCTTCGGGGGCTTCCATCTCTCGCC 2599
 QY 821 Ser|A|H|I|S|E|U|T|H|E|U|T|H|G|U|P|O|T|Y|A|Y|G|I|Y|G|Y|A|G|I|N|A|I|A|S|P|Y|T|H| 840
 Db 2600 TCGCACACCTCACTTGAACCGACCTTACCCGGAAGGCTGCGCAACCCAGACTTACACC 2659
 QY 841 G|Y|G|L|U|E|G|Y|I|E|V|A|I|A|N|G|I|Y|A|L|Y|T|P|A|N|P|O|A|T|G|V|A|I|A|S|E|U|L|U|I|G|I|N|A|P|H|T|H| 860
 Db 2660 GGGGCGATGGCATCTCATCGGGGCGCAAGTGAACCCCGGACCGGACTTACATGAC 2719
 QY 861 P|H|E|S|E|T|Y|L|E|U|H|I|A|T|H|A|N|C|Y|L|E|U|G|L|U|E|S|E|P|H|E|T|Y|L|E|U|G|I|Y|C|Y|A|S|P|Y|S|P|H|E| 880
 Db 2720 TTCAGTTACCTGCATACCAACTCCTGAGCTCTCTTCACTCGGGCTGTGACAAGTTC 2779
 QY 881 Pro|H|I|S|E|U|S|E|U|C|U|E|U|P|O|A|T|G|U|T|P|G|L|U|A|N|A|N|U|S|E|U|L|A|L|E|U|E|U|T|H|P|H|E| 900
 Db 2780 CCTCATGAGATGATGCTGCCCGCGAGTGGGAACAACAGAGGCGCTGCTCACCTTC 2839
 QY 901 Met|G|L|U|I|V|A|H|I|A|R|G|I|Y|L|E|Y|G|L|V|A|I|V|A|I|T|H|A|S|P|G|L|U|N|G|I|N|G|I|L|E|P|O|I|E| 920
 Db 2840 ATGGACAGGTGACCGCGGCATTTAAGGGGTGTGTACGACGACGACGACATCCCAT 2899
 QY 921 A|A|A|A|N|A|L|A|T|H|I|L|E|S|E|U|V|A|S|E|G|I|Y|I|E|A|N|H|I|E|G|I|Y|V|A|I|Y|S|E|U|T|H|A|S|E|G|I|Y|G|I| 940
 Db 2900 GCCAAGCCCAACATCTCTGTGAGTGGCATTAATCAACGCGCTGAAGACAGCCAGTGGTGGT 2959
 QY 941 Asp|T|Y|T|P|A|G|I|L|E|U|A|N|P|O|G|I|Y|G|L|U|T|Y|A|G|V|A|I|T|H|A|I|H|A|A|G|I|N|G|I|Y|T|Y| 960
 Db 2960 GATTACTGGGAATCTTGAAACCGGGGTAGTACCGGTGACACCCACGCGGAGGGCTTAC 3019
 QY 961 Thr|P|O|S|E|U|A|L|Y|E|U|T|H|C|Y|A|S|N|V|A|A|S|P|T|Y|A|S|P|I|E|G|I|Y|A|L|T|H|G|I|N|C|Y|A|S|N|P|H|E| 980

Db 3020 ACCCGAGCGCCAGAGACTGCAATGTTGACATATGACATCGGGGCCACTCAGTGCACCTTC 3079
 QY 981 I|L|E|U|A|I|A|A|G|S|E|A|N|T|P|L|Y|A|G|I|L|E|A|R|G|I|L|E|A|I|A|E|C|A|N|G|I|Y|A|N|A|G| 1000
 Db 3080 ATCTGGCTGCTCCCACTGGAAGGCGATCCGGGAGATCAATGCGCATTAACCGGAACCGG 3139
 QY 1001 Pro|I|E|P|H|I|S|I|E|A|N|P|O|S|E|U|A|P|O|M|E|T|H|P|O|G|I|N|G|I|N|A|Y|A|G|L|E|U|G|I|N|G|I| 1020
 Db 3140 CCTATCCACATATGACCATTCGCGCTTATGACCCCGCAACGACGACGCTGACGACG 3199
 QY 1021 Arg|A|G|L|E|U|G|I|N|H|I|A|R|G|L|E|U|A|Y|A|A|G|I|N|E|C|A|R|G|L|E|U|A|Y|A|G|L|E|U|A|N|A| 1040
 Db 3200 CGAGCCCTTACAACACCGCTCGGCTTCGGGACAGATGGCGCTGCGGCTTCAACGCC 3259
 QY 1041 Thr|T|H|T|H|L|E|U|G|I|Y|P|H|I|S|T|H|V|A|I|P|O|P|O|T|H|L|E|U|P|O|P|O|A|I|A|P|O|A|L|A|T|H|T|H| 1060
 Db 3260 ACCACACCTTAAAGGCCCCACACTGTGCTCCACAGCTGCCCCCTGCGCCACACAC 3319
 QY 1061 Leu|S|E|T|H|T|H|I|E|G|L|U|P|O|T|P|O|I|Y|L|E|U|I|E|P|O|P|O|T|H|T|H|A|I|G|I|Y|T|P|S|I|U|G|I| 1080
 Db 3320 CTGACACTTACCATATGACCTCTGGGCTCATACCGCAACCGCTGCTGGAGAG 3379
 QY 1081 Ser|G|U|T|H|G|L|U|T|H|T|Y|T|H|G|L|U|V|A|I|T|H|G|L|U|P|H|E|G|I|Y|T|H|G|L|U|V|A|I|U|P|O|G|I| 1100
 Db 3380 TCGAGACTGAGACTTACACAGAGGTGTGACAGAGTTTGGGACCGAGGTGAGCCGAG 3439
 QY 1101 P|H|E|G|I|Y|T|H|Y|V|A|I|U|P|O|G|L|U|P|H|E|G|I|U|T|H|G|I|N|L|E|U|G|I|P|O|G|L|U|P|H|E|G|I|U|T|H|G|I|N| 1120
 Db 3440 TTTGGGACCAAGTGTGAACCCGAGTTTGAACCCAGTTGGAGCTGAGTTTCAAGCCAG 3499
 QY 1121 Leu|G|U|P|O|G|L|U|P|H|E|G|L|U|G|I|U|G|L|U|G|I|U|G|L|U|Y|S|G|L|U|G|I|U|G|I|L|E|A|T|H|G|I| 1140
 Db 3500 CTGGAACCGAGTTTGAAGGAAGAGAGAGAGAGAGAGAGAGAGAGAGATTAACCACTGGC 3559
 QY 1141 G|I|N|A|I|A|P|H|E|P|O|H|E|T|H|T|H|V|A|I|G|L|U|T|H|T|Y|T|H|V|A|I|A|N|P|H|E|G|I|Y|A|S|P|H|E| 1158
 Db 3560 CAGGACTTCCCTTACAAACAGTAGAGACTTCAAGTGAAGTCTTGGGACTTC 3613

RESULT 8
 US-10-947-249-162
 ; Sequence 162, Application US/10947249
 ; Publication No. US20050287541A1
 ; GENERAL INFORMATION:
 ; APPLICANT: AKIRA NAKAGAWARA
 ; APPLICANT: MIKI OHIRA
 ; APPLICANT: Shin ISHII
 ; APPLICANT: Takeshi GOTO
 ; APPLICANT: Hiroyuki KUBO
 ; APPLICANT: Takahiro HIRATA
 ; APPLICANT: Yasuko YOSHIDA
 ; APPLICANT: Saichi YAMADA
 ; TITLE OF INVENTION: Microarray for Predicting the Prognosis of Neuroblastoma and Mech
 ; FILE REFERENCE: 117007
 ; CURRENT APPLICATION NUMBER: US/10/947,249
 ; PRIOR FILING DATE: 2004-09-23
 ; PRIOR APPLICATION NUMBER: US 60/505,614
 ; NUMBER OF SEQ ID NOS: 200
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 162
 ; LENGTH: 3935
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-947-249-162

Alignment Scores:
 Pred. No.: 0
 Score: 6272.00
 Percent Similarity: 100.0%
 Best Local Similarity: 100.0%
 Query Match: 100.0%

Length: 3935
 Matches: 1158
 Conservative: 0
 Mismatches: 0
 Indels: 0

DB: 10 Gaps: 0
US-10-642-946-3 (1-1158) x US-10-947-249-162 (1-3935)
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QY 21 ProGlyGlyArgProGlnThrValLeuThrAspAspGluIleGluGluPheLeuGluGly 40
DB 200 CCGAGAGGGCGCCCGCAGACGGTGTGACCGACGACAGATCGAGGGATTCCTCGAGGGC 239
QY 41 PheLeuSerGluLeuGluProGluProArgGluAspAspValGluAlaProProProPro 60
DB 260 TTCTCTGACAGCTAGACCTTAGACCCCGGGAGGACACCTGAGGCCCCCGCTCTCC 319
QY 61 GluProThrProArgValArgValArgValArgValArgValArgValArgValArgVal 80
DB 320 GAGCCCAACCCCGGGGTCCGAAAAGCCAGCGGGGGGCAAGCCAGGGAAGCGGCAAGG 379
QY 81 ThrAlaAlaGluValProProGluGluArgThrLeuAspLeuGlyLeuGlyGlyLeuGlyAsp 100
DB 380 ACCGCGCGCAAAAGTGGCTCCGGAAGAAGCAAAAGACAAAGGAAAGAAAGCAAGAAAGAC 439
QY 101 LysGlyProLysValProLysGluSerLeuGluGlySerProArgProProLysGly 120
DB 440 AAAAGCCCCCAAGGTGCCCAAGAGTCTTGAAGGGATCCCCAGGCGCCCAAGAGGGG 439
QY 121 LysGluLysProLysValArgValArgValArgValArgValArgValArgValArgVal 140
DB 500 AAGGAGAGGCAACCAAGGCAACCAAGAGCCCAAGAGAGAGCACTTAAGGCAACCAAG 559
QY 141 LysProLysGluGluProLysValArgValArgValArgValArgValArgValArgVal 160
DB 560 AAGCCCAAGAGAGGCAACCAAGGCAACCAAGAGCCCAAGAGAGAGCAACCAAGAGGCG 619
QY 161 ThrLysLysProProSerGlyLysArgProProIleLeuAlaProSerGluThrLeuGlu 180
DB 620 ACCAAGAGCCCCGCTCAGGAGAGAGCCCCCAATCTGCTCTCAGAGAACCTCGAGG 679
QY 181 TrpProLeuProProProProSerProGlyProGluGluLeuProGluGluGlyAla 200
DB 680 TGGCCACTGCCCCACCCCCAGCCCGGCGCCGAGAGCTACCCAGAGAGGAGGGGG 739
QY 201 ProLeuSerAspAsnTrpGlnAsnProGlyGluGluThrIleValGluAlaGluGlu 220
DB 740 CCCCTCTCAATTAATCGGAGATCCAGAGAGAGAGCCCATGTGAGGAGCAGAGAGC 799
QY 221 GlnProGluProGluGluGluThrGluGluProThrLeuAspTrpAsnAspGluIleGlu 240
DB 800 CAGCTGAGCCGAG 859
QY 241 ArgGluAspTrpGluAspPheGluTrpIleArgArgGluLysGlnProArgProProPro 260
DB 860 AAGGAGAGCATAGAGACTTGAATCATTTCCGCGCAGAGAGAGAGAGAGAGAGAGAG 919
QY 261 SerArgArgArgArgProGluArgValTrpProGluProProGluGluGlyAlaProAla 280
DB 920 ACCAG 979
QY 281 ProAlaProGluGluGluGluGluProProValLysProLeuLeuProProLeuProPro 300
DB 980 CCAAGCCCCGAG 1039
QY 301 AspTrpGlyAspGlyTrpValIleProAsnTrpAspAspMetAspTrpTrpPheGlyPro 320
DB 1040 GACTAATGATGATGATACGTGATCCCACTAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1099
QY 321 ProProProGluLysProAspAlaGluArgGlnThrAspGluGluGlyGluGluLys 340
DB 1100 CCTCCCGCCCGAG 1159
QY 341 LysProLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 360

DB 1160 AAAACCAAAAG 1219
QY 361 GlyLysAspHisLysGluProArgLysGlyGluGluLeuGluGluGluGluGluGluGlu 380
DB 1220 GGCAG 1279
QY 381 GluLysValLysLysProProIleGlyMetGluSerHisArgIleGluLysAspAsnIle 400
DB 1280 GAGAAAGTCAAAGTGTCCCCCATTTGGATGAGACTCACCGATATTAGAGCAACCGAGTC 1339
QY 401 ArgAlaSerSerMetLeuArgHisGlyLeuGlyValGluArgGlyLysLeuAsnMetGln 420
DB 1340 CGAGCTCTCTCCATGCTGCGCCACCGGCTGGGGGACACGCGGCGCGCTCAACATCGAC 1399
QY 421 ThrGlyAlaThrGluAspAspTrpTrpAspGlyAlaTrpCysAlaGluAspAspAlaArg 440
DB 1400 ACCGTGACCATGAG 1459
QY 441 ThrGlnTrpIleGluValAspThrArgArgThrArgPheThrGlyValIleThrGln 460
DB 1460 ACCAGTGAATGAG 1519
QY 461 GlyArgAspSerSerIleHisAspAspPheValThrThrPhePheValGlyPheSerAsn 480
DB 1520 GGCAGAGACTCCAGCATCCATGACGATTTTGACCACTTCTTGGGGCTTCAGCAAT 1579
QY 481 AspSerGlnThrTrpValMetTrpTrpAsnGlyTrpGluGluMetThrPheHisGlyAsn 500
DB 1580 GACAGCCAGACATGGGTGATGATACCAACGGCTATAGAGAAATGACCTTTATGGAGAC 1639
QY 501 ValAspLysAspThrProValLeuSerGluLeuProGluProValValAlaArgPheIle 520
DB 1640 GTGGACAAAGAGACACCGGTGTGAGTGAAGCTCCAGAGCCGATGTGTGCTGTTTCATC 1699
QY 521 ArgIleTrpProLeuThrTrpAsnGlySerLeuCysMetArgLeuGluValLeuGlyCys 540
DB 1700 CGCATTTACCATCTACCTGGAATGGACAGCTGTGATCGCTGAGAGGTGCTGGGGTTC 1759
QY 541 SerValAlaProValTrpSerTrpTrpAlaGlnAsnGluValValAlaThrAspAspLeu 560
DB 1760 TGTGTGGCCCTGTGTACAGCTTACGACAGAGAAAGAGTGGTGGCCAGATGACCTG 1819
QY 561 AspPheArgHisHisSerTrpLysAspMetArgGlnLeuMetLysValValAsnGluGlu 580
DB 1820 GATTTCCGACACACAGCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1879
QY 581 CysProThrIleThrArgThrTrpSerLeuGlyLysSerSerArgGlyLeuLysIleTrp 600
DB 1880 TGCCCAACATCACCCGACCTTACAGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1939
QY 601 AlaMetGluIleSerAspAsnProGlyGluHisGluLeuGlyGluProGluPheArgTrp 620
DB 1940 GCCATGAGATCTCAGAGAACCCCTGGGAGAGATGAATCGGGGAGCCGAGTTCCGCTAC 1999
QY 621 ThrAlaGlyTrpHisGlyAsnGluValLeuGlyArgGluLeuLeuLeuLeuLeuMetGln 640
DB 2000 ACTGTGGGATCATAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2059
QY 641 TrpLeuCysArgGluTrpArgAspGlyAsnProArgValArgSerLeuValGlnAspThr 660
DB 2060 TACCTGTGCGAGAGATCACCGCATGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2119
QY 661 ArgIleHisLeuValProSerLeuAsnProAspGlyTrpGluValAlaAlaGlnMetGly 680
DB 2120 CGCATTCACCTGTGGCTCACTGAACCTGATGGCTAGAGGTGGAGCGAGATGGCG 2179
QY 681 SerGluPheGlyAsnTrpAlaLeuGlyLeuTrpThrGluGluGlyPheAspIlePheGlu 700
DB 2180 TCAGAGTTGGAGATCGGGCGGTGGAGCTGTGAGCTGAGAGAGAGAGAGAGAGAGAG 2239
QY 701 AspPheProAspLeuAsnSerValLeuTrpGlyValArgGluGluArgLysTrpValProTrp 720

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Db      2240 GATTTCGGGATCTCACTGTGTGCTGGGGAGCTGAGAGAGAAATGGGTCCCTAC 2299
Qy      ArgVal1ProAsnAsnAsnLeuProIleProGluArgTyrLeuSerProAspAlaThrVal1 740
Db      2300 CGGGTCCCCCAACAAATACCTTGCCCATCCCTGAACCTACCTTTCCGCAATGCCCGGTA 2359
Qy      SerThrGluValArgAlaIleIleAlaTrpMetGluValAsnProPheValLeuGlyAla 760
Db      2360 TTCACGAGAGGTCCGGGACCATCTGCTGATGAGAAAGAACCCCTTGCTGCTGGAGCA 2419
Qy      AsnLeuAsnGlyGlyGluArgLeuValSerTyrProTyrAspMetAlaArgThrProThr 780
Db      2420 AATCTGAACGGCGCGGAGGGGTAGATCTTACCCCTTACGATATGCCCCGCGACGCTACC 2479
Qy      GlnGlnGlnLeuLeuAlaAlaAlaMetAlaAlaAlaArgGlyGluAspGluAspGluVal1 800
Db      2480 CAGGAGCAGCTGCTGGCGCGACCATGGCAGCAGCCGGGGGAGAGATGAGACCAAGGTG 2539
Qy      SerGluAlaGlnGluThrProAspHisAlaIlePheArgTyrLeuAlaIleSerPheAla 820
Db      2540 TCCGAGAGCCCAAGAGACTCCAGACCAAGCCATCTTCGGTGGCTTGCCATCTTCGCTC 2599
Qy      SerAlaHisLeuThrLeuThrGluProTyrArgGlyGlyCyseGlnAlaGlnAspTyrThr 840
Db      2600 TCCGACACACTCACCTTGACCGAGCCCTACCGGGAGGCTGCGCAAGCCAGACTACACC 2659
Qy      GlyGlyMetGlyTyrLeuAlaGlnGlyAlaValTyrTrpAsnProArgThrGlyThrIleAsnPro 860
Db      2660 GCGCGCATGGGATCGCTCAACCGGGCGCAAGTGAACCCCGGAGCGGGACTATCATATGAC 2719
Qy      PheSerTyrLeuHisThrAsnCyseGlnGluLeuSerPheTyrLeuGlyCyseAspLysPhe 880
Db      2720 TTCACTGATCTTGATACCACTGCTGAGCTCTCTTCTTACTGGGCTGTACAAAGTTTC 2779
Qy      ProHisGluSerGluLeuProArgGluTyrGluAsnAsnLysGlnAlaLeuLeuThrPhe 900
Db      2780 CCTCATGAGAGTAGAGTGCCTCCGCGAGTGGGAGAACACAAAGAGCGCTGCTCACCTTC 2839
Qy      MetGluGlnValHisArgGlyTyrLeuGlyValAlaThrAspGluGlnGlyIleProIle 920
Db      2840 ATGAGCAGAGTGCACCGCGCATTTAAGGGGTGTGTACGAGCAGAGCAAGCATCCCAT 2899
Qy      AlaAsnAlaThrIleSerValSerGlyIleAsnHisGlyValIleThrAlaSerGlyGly 940
Db      2900 GCCAACGCCACCACTCTGTGAGTGCAATTATCACGGCTGAGACACCCAGTGTGAT 2959
Qy      AspTyrTyrPArgIleLeuAsnProGlyGluTyrArgValThrAlaHisAlaGluGlyTyr 960
Db      2960 GATTACTGGCGAATCTTGAACCGGGGTGAGTACCGGTGACAGCCACCGGAGGGCTAC 3019
Qy      ThrProSerAlaLysThrCyseAsnValAspTyrAspIleGlyAlaThrGlnCyseAsnPro 980
Db      3020 ACCCCGAGGCGCAAGACCTGCAATGTTGACTATGACATCGGGGCCCTCAGTGCACATTC 3079
Qy      IleLeuAlaArgSerAsnTrpLysArgIleArgGlnIleMetAlaMetAsnGlyAsnArg 1000
Db      3080 ATCTGGCTGCTGCCCACTGAAAGCCGCAATCCGGAATCATGTGCCCATGAACGGAAAC 3139
Qy      ProIleProHisIleAspProSerArgProMetThrProGlnGlnArgArgLeuGlnGln 1020
Db      3140 CCTATCCACACATTAACCATCGGCGCTATGACCCCCCAACAGAGGAGCGCTGCAGCAG 3199
Qy      ArgArgLeuGlnHisArgLeuArgLeuArgAlaGlnMetArgLeuArgArgLeuAla 1040
Db      3200 CGAGCGCTACAAACACCGCTGCGGCTTCGGGACACATGCGGTGGGGCGCTCAACCGCC 3259
Qy      ThrThrThrLeuGlyProHisIleThrVal1ProProThrLeuProProAlaProAlaThr 1060
Db      3260 ACCACCACTTAGGCGCCCACTGCTCCCAACGCTGCCCTCCCTGCGCACACAC 3319
Qy      LeuSerThrThrIleGluProTyrGlyLeuIleProProThrThrAlaGlyTyrGluGln 1080
Db      3320 CTGAGCACTACCATAGAGCCCTGGGCTCATATACCGCAACCAACCGCTGGCTGGAGGAG 3379

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Qy      1081 SerGluThrGluThrTyrThrGluValValThrGluPheGlyThrGluValGluProGlu 1100
Db      3380 TTGGAGACTGAGACTTACACAGAGGTGTGACAGATTGGGACCGAGGTGAGGCCGAG 3439
Qy      PheGlyThrLysValGluProGluPheGluThrGlnLeuGluProGluPheGluThrGln 1120
Db      3440 TTGGGACCAAGGTGGAGCCCGAGTTTGAGACCCAGTTGGAGCTGAGTTCGAGACCCAG 3499
Qy      LeuGluProGluPheGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 1140
Db      3500 CTGGAACCCGAGTTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATGAGCCACTGGC 3559
Qy      GlnAlaPheProPheThrThrValGluThrTyrThrValAsnPheGlyAspPhe 1158
Db      3560 CAGGCAATCCCTTCACAAAGTGAAGACTTACACAGTGAATCTTGGGGACTTC 3613

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RESULT 9

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US-11-245-147-128
; Sequence 128, Application US/11245147
; Publication No. US20060030541A1
; GENERAL INFORMATION:
; APPLICANT: GARCIA, TERESA
; APPLICANT: ROMAN ROMAN, SERGIO
; APPLICANT: BARON, ROLAND
; APPLICANT: CALL, KATHERINE
; APPLICANT: THEILHABER, JOACHIM
; APPLICANT: CONNOLLY, TIMOTHY
; APPLICANT: JACKSON, AMANDA
; APPLICANT: BUSHNELL, STEVEN
; APPLICANT: RAMADI, GEORGES
; TITLE OF INVENTION: GENES INVOLVED IN OSTEOGENESIS, AND METHODS OF USE
; FILE REFERENCE: 37891-0023
; CURRENT APPLICATION NUMBER: US/11/245,147
; PRIOR FILING DATE: 2005-10-07
; PRIOR APPLICATION NUMBER: PCT/IB02/02211
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/281,400
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: Patencin Ver. 3.2
; SEQ ID NO 128
; LENGTH: 3935
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-245-147-128

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Alignment Scores:

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Pred. No.: 0 Length: 3935
Score: 6272.00 Matches: 1158
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0

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US-10-642-946-3 (1-1158) x US-11-245-147-128 (1-3935)

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Qy      1 MetAlaAlaValArgGlyAlaProLeuLeuSerCyseLeuLeuAlaLeuLeuAlaLeuCy 20
Db      140 ATGGGGCGCGTGGCGGGGGCGCCCTGCTCAGCTGCTCTGAGCTTGCGCTGCGCTGTC 199
Qy      21 ProGlyGlyArgProGluThrValLeuThrAspAspGluIleGluGluPheLeuGluGly 40
Db      200 CTTGAGGGCGCGCCCGCAGACGGTGTCTGACCGACGACGAGATCGAGAGTTCTCTCAAGGGC 259
Qy      41 PheLeuSerGluLeuGluProGluProArgGluAspAspValGluAlaProProProPro 60
Db      260 TTCTGTGAGACTGAACTGAGCCCGGGAGGAGAGAGTGAAGGCGCCCGCGCTCTCC 319
Qy      61 GluProThrProArgValArgValArgValAlaGlnAlaGlyGlyLysProGlyLysArgProGly 80
Db      320 GAGCCACCCCGCGGTCTCGAAAGCCCAAGCGGGGGGCAAGCCAGGAGAGCGGCGAGG 379

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OY	81	ThrlAlaIaGlValProProGluYbThrIyAspYbGlyVbYbGlyVbYbAsp	100
Db	380	ACGGCCGGCAAGATGCTCTCCGGAAAAAGCCAAAGACAAAGGAAAMAAGCAAGMAAAC	439
OY	101	LybGlyProLYbValProLybGluSerLeuGluYbSerProArXProProLYbLybGly	120
Db	440	AAAGCCCCCAAGGTGCTCCAGAGATCTTTGAGGGGGTCCCCAGGCCCTCCAGAGAGGG	499
OY	121	LybGluLYbProProLYbAlaThrlYbLYbProLYbGluLYbProProLYbAlaThrlYb	140
Db	500	AAGAGAAAGCCACCAGGCGCACCAAGAAAGCCCAAGAGAAAGCCATTAGGCCCAAG	559
OY	141	LYbProLYbGluGluProProLYbAlaThrlYbLYbProLYbGluLYbProProLYbAla	160
Db	560	AAGCCCAAGAGAGAACCCCAAGGCCACCAAGAAAGCCCAAGAGAACCCCAAGGCC	619
OY	161	ThrlYbLYbProProSerGlyLYbArXProProIleuAlaProSerGluThrlLeuGlu	180
Db	620	ACCAAGAAAGCCCCCTCAGGGAGAGAGCCCCCATTTGGGCTCTCCAGAAACCTTGAG	679
OY	181	TrpProLeuProProProProSerProGlyProGluGluLeuProGluGluGlyVala	200
Db	680	TGGCCACTGGCCCCCAGCCCCCGCTGGCCCCCGAGAGCTACCCCAAGAGAGGGCG	739
OY	201	ProLeuSerAbaAbaThrlTrpIbAsbProGlyGluGluThrlbValGluAlaGluIb	220
Db	740	CCCCCTCAAAATACCTGGCAGATCCAGAGAGAGAGACCCCATGTGGAGGCACAGAGAC	799
OY	221	GlnProGluProProGluGluGluThrlGluGlnProThrlLeuAspTrpAbaAspGluIbGlu	240
Db	800	CAGCTTGAGCCGAGAGAGAGACCCAGCAACCACTGACCTACAAAGACCAATCGAG	859
OY	241	ArGluAbaTrpTrpGluAbaAspPheGluTrpIleArGArgGlnLYbGlnProArXProPro	260
Db	860	AGGAGAGACTATAGAGACTTTGATGATCACTTGGGCCCAAGAACCAAGGCCACCCCA	919
OY	261	SerArGArgArgArgProGluArGValTrpProGluProProGluGluLYbAlaProAla	280
Db	920	AGCAGAAAGAGAGGCCCGAGCGGGTCTGGCCAGAGCCCCCTGAGAGAAAGGCCCGGCC	979
OY	281	ProIbAbaProGluGluArGluIbGluProProValLYbProLeuLeuProProLeuProPro	300
Db	980	CCAGCCCCCGAGAGAGAGATTGAGCTCTTGAAAGCTCTGCGCCCCGCTGCCCCCT	1039
OY	301	AspTrpGlyAbaAspGlyTrpValIleProAbaTrpAbaAspPheAspTrpPheGlyPro	320
Db	1040	GACTATGGTATGCTTACTGATATCCCACTACATGACATGACTATTACTTTGGGCT	1099
OY	321	ProProProGluLYbProAbaAlaGluArGlnThrlAbaGluGluLYbGluGluLeuLYb	340
Db	1100	CCTCGGCCCCCAAGAGCCGATGCTGAGCGCCAGACCGACGAAGAGAGAGAGAGACTGAG	1159
OY	341	LYbProLYbLYbLYbAspSerSerProLYbGluGluThrlAbaLYbTrpAlaValGluLYb	360
Db	1160	AAACCCCAAAAGAGAGACAGACCCCAAGAGAGAGACCAAGATGGCGAGTGAAGAAG	1219
OY	361	GlyLYbAbaPheLYbGluProArGlybGlyGluGluLeuGluGluGluGluTrpThrlProThrl	380
Db	1220	GGCAAGGACCACAAAAGACCCCGAAAGGACAGAGTTGGAGAGAGAGATGAGACCTTAG	1279
OY	381	GluLYbValLYbCybProProIleGlyMetGluSerHisArgIleGluAspAsnGlnIle	400
Db	1280	GAGAAAGTCAGATGTCCTCCCATTTGGATGAGTCACACCTATTTGAGGACACACAGATC	1339
OY	401	ArgAlaSerSerMetLeuArGHisGlyLeuGlyValaGlnArGlyValaGluAbaMetGln	420
Db	1340	CGAGCTCTCTCAATGCTCGCCACCGCTGGGGGACAGCCGCGCTCAATCATCTAG	1399
OY	421	ThrlGlyAlaThrlGluAbaAspTrpTrpAbaGlyAlaTrpCybAlaGluAbaAspAlaArg	440
Db	1400	ACCGTGGCACTAGAGACGACTACTATATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1459
OY	441	ThrlGlnTrpIleGluValaAspThrlArGArgThrlThrlArGPhethrlGlyValIleThrlGln	460

Db	1460	ACCGAGTGAATGAGGTGACACCGAGGAGCTAACCGTTCCAGCGCTCATCCGAC	1519
OY	461	GIYARGApSeserIleHisAspAspPheValThrThrphePheValGlyPheSerAan	480
Db	1520	GGCAGAGACTCCAGCATCTCATGACGATTTTGTGACCACTCTTCTGTGGGCTTCAGCAAT	1579
OY	481	AspSerGlnThrTrpValMetTYTrhAsnGlyTYrGluGluMetThrpheHisGlyAan	500
Db	1580	GACAGCCAGACATGGGTGATGTATACCAACGGCTAATGAGGAATGACCTTTTCATGGGAAAC	1639
OY	501	ValAspIysAspThrProValLeuSerGluLeuProGluProValValAaargPheIle	520
Db	1640	GTGACAAAGGACACACCCGTGTGAGTGAAGACTCCGAGACCGGTGTGTGCTCGTTTCATC	1699
OY	521	ArgIleTYrProLeuThrTrpAsnGlySerLeuCYMetArgPheGluValLeuGlyCys	540
Db	1700	CGCATCTACCACTCACCTGGAATGGCAGCCTGTGATGCGCTGGAGGGTGTGGGGTGC	1759
OY	541	SerValAaIapProValTYrSerTYrTYrAlaGlnAsnGluValValAaIaThrAspAspLeu	560
Db	1760	TCTGTGGCCCTGTCTTACAGCTTCTACGCAACAATGAGGTGTGGCCACCGATGACCTG	1819
OY	561	AspPheArgHisHisSerTYrLYsAspMetArgGluLeuMetLYsValValaAngGluGlu	580
Db	1820	GATTTCCGGGACCCAGACTCAAGAGGACATCGCCACACTCATGAAAGGTGTGAAACGAGAG	1879
OY	581	CysProthIleThrArgThrTYrSerLeuGlyLYsSerSerArgIlyLeuLYsIleTYr	600
Db	1880	TGCCCCACACATCACCCGACCTTCAAGCTGTGGGGAAGAGCTCACAGAGGCTTCAGAGATCTAT	1939
OY	601	AlaMetGluIleSerAspAsnProGlyGluHisGluLeuGlyGluProGluPheArgTYr	620
Db	1940	GCCATGAGATCTCTAGACACCTGTGGGAGCAAGAACTGGGGAGGCCAGATTCCGCTTAC	1999
OY	621	ThrAlaGlyIleHisGlyAsnGluValLeuGlyArgGluLeuLeuLeuLeuMetGln	640
Db	2000	ACTCTGGGATCCATGAGCAACGAGGTGTGGGCGCGAGACCTGTGCTGCTGCATGACGAG	2059
OY	641	TYrLeuGlyAspArgIuTYrArgAspGlyAanProArgValArgSerLeuValGlnAspThr	660
Db	2060	TACCTGTGCGAGAGTACCGCAGATGGGAACCCAGTGTGCGCAGCTGTGTGACGAGCACAA	2119
-OY	661	ArgIleHisLeuValProSerLeuAanProAspGlyTYrGluValAaIaGlnMetGly	680
Db	2120	CGCATCACTGTGTGCTTCACTCACTGAAACCTGATGCGTTCAGAGTGGCACCGACAGTGGGC	2179
OY	681	SerGluPheGlyAanTrpAlaLeuGlyLeuTrpThrGluGluGlyPheAspIlePheGlu	700
Db	2180	TCAAGATTGGGAACGTGGCGCTGGGACTGTGAGACGAGAGGGCTTTGACATCTTTGAA	2239
OY	701	AspPheProAspLeuAsnSerValLeuTrpGlyValaGluGluArgLYrTrpValProTYr	720
Db	2240	GATTTCCCGAATCTCAACTGTGCTGTGGGAGCTGAGGAAGGAAGAGGTGTCCCTTAC	2299
OY	721	ArgValProAsnAsnLeuPheProIleProGluArgTYrLeuSerProAspAaIaThrVal	740
Db	2300	CGGGTCCCAACAATACTTGGCCATCTCTGAAACGCTTACTTTTCCGAGATGCCACGGTA	2359
OY	741	SerThrGluValArgAlaIleIleAlaTrpMetGluLYsAsnProPheValLeuGlyAla	760
Db	2360	TCCACGAGGTCCGGGCGCATTTGCTGTGAGATGAGAAACCCCTTGTGTGTGGGAGCA	2419
OY	761	AsnLeuAsnGlyLYsGluArgLeuValSerTYrProTYrAspMetAlaArgThrProThr	780
Db	2420	AATCTGAAACGGCGGACAGCGCTAAGTATCTTACCCCTTAAGATATGGCCCGCACGCTTACC	2479
OY	781	GlnGluGlnLeuLeuAaIaAlaIaMetAlaAlaAlaArgGlyLYsAspGluAspGluVal	800
Db	2480	CAGGAGACGCTGCTGGCCGACGCCATGGCAGCAGCCCGGGGGGAGATGAGGACAGATC	2539
OY	801	SerGluAlaGlnGluThrProAspHisAlaAlaIlePheArgTrpLeuAlaIleSerPheAla	820

[illegible]

QY	601	AlamewGluLlIeserAspAsnProGlyGluHisGlyLeuGlyLysProGluPheArgTyr	620
Db	1940	GCAGAGGAGATCTTCAGACAACTCGGGGAGCATGAACTGGGGGAGACCCGAGTTCGGCTAC	1999
QY	621	ThrAlaGlyLleHisGlyAsnGlyValLeuGlyArgGlyLeuLeuLeuLeuLeuMetGln	640
Db	2000	ACTGCTGGGATTCATAGGCACAGAGTCTGGGCCAGAGCTGTCTCTCTCATGCAg	2055
QY	641	TyrLeuCySarGlyTyrArgAspGlyAsnProArgValArgSerLeuValGlnAspThr	660
Db	2060	TACCTGTCTCCGAGATACCGCGATGGAAACCACTGTGCCACGCTGTGTACAGACACA	2119
QY	661	ArgLleHisLeuValProSerLeuAsnProAspGlyTyrGlyValAlaIleGlyMetCyl	680
Db	2120	CGCATCTCACTGTGTCTCCCTCACTGAACCTGTATGGTACAGAGTGGACGGCAGATGGGAC	2179
QY	681	SerGluPheGlyAsnTyrAlaLeuGlyLeuTyrThrGluGlyGlyPheAspIlePheGlu	700
Db	2180	TCAGAGTTTGGGAACTGGGCGCTGGGACTGTGGACTGAGGAGGGCTTTGACATCTTTGAA	2233
QY	701	AspPheProAspLeuAsnSerValLeuTyrGlyAlaGlyGluValGlySerTyrValProTyr	720
Db	2240	GATTTCCCGGATCTCACTGTGTCTCTGGGGAGCTGAGGAGGAATAGGTGCTCCCTAC	2299
QY	721	ArgValProAsnAsnAsnLeuProIleProGluArgTyrLeuSerProAspAlaThrVal	740
Db	2300	CGGGTCCCCACATACATCTTGCCATCCCTGAACGCTACTTTGGCCAGATGCCAGGTA	2355
QY	741	SerThrGluValArgAlaIleIleAlaTyrMetGluTyrAsnProPheValLeuGlyAla	760
Db	2360	TCCAGGAGAGTCCGGGCGATCATTTGCCGTGATGGAGAAACCCCTGTGTCTGGAGCA	2419
QY	761	AsnLeuAsnGlyGlyGlyValArgLeuValSerTyrProTyrAspMetAlaArgThrProThr	780
Db	2420	AATCTGAACGGGGCGAGCGGGGTAGTATCTTACCCCTTACATATAGGCCCGACGCTAAC	2479
QY	781	GlnGluGlnLeuLeuAlaAlaAlaMetAlaAlaIleArgGlyGluAspGlyAspGlyVal	800
Db	2480	CAGAGGACGCTGTGGCGCGCAGCATAGGCACAGCGCGGGGGAGAGTAGAGACGAGTCT	2539
QY	801	SerGluAlaGlnGluThrProAspHisAlaIlePheArgTyrPheAlaIleSerPheAla	820
Db	2540	TCCGAGGGCCAGGAGACTCCAGACCAACCCATCTTCGGTGGCTTGGCCATCTCTTCCGC	2599
QY	821	SerAlaHisLeuThrLeuThrGluProTyrArgGlyGlyCysGlnAlaGlnAspTyrThr	840
Db	2600	TCCGACACCTCACTTACCCGAGCCCTTACCGCGAGGCTGCCAAGCCCAAGACTTACACC	2655
QY	841	GlyGlyMetGlyIleValAsnGlyAlaLeuTyrTrpAsnProArgThrGlyThrIleAsnAsp	860
Db	2660	GAGCGGCATGGGCATCTGTCAACGGGGGCCAAGTGAACCCCGGACCGGAGCATATCAATAC	2719
QY	861	PheSerTyrIleAsnHisThrAsnCyLeuGluLeuLeuSerPheTyrIleuGlyCyAspIlyPhe	880
Db	2720	TTCAATATCCGCAATACCAACTGCTGGAGCTCTCTTCTTACCTGGGGCTGTGACAAAGTTC	2779
QY	881	ProHisGluSerGluLeuProArgGlyTyrTrpGlyAsnAsnLeuGlyAlaLeuLeuThrPhe	900
Db	2780	CCTATGATGATGAGTGTGCTCCCGGAGGTGGGAGAAACAACAAGAGGGCGCTGTCACTTC	2839
QY	901	MetGluGlnValHisArgGlyIleLeuGlyValValThrAspGluGlnGlyIleProIle	920
Db	2840	ATGAGGCGAGTGCACCGCGGCATTAAAGGGGGTGTGTAGCGGACGAGCAAGCATCCCCATT	2899
QY	921	AlaAsnAlaThrIleSerValSerGlyIleAsnHisGlyValIleThrAlaSerGlyGly	940
Db	2900	GCCAAAGCCACATCTCTGTAGTGGCATTAATACGGCGTGAAGACAGCCAGTGTGTGT	2959
QY	941	AspTyrTyrTrpArgIleLeuAsnProGlyGlyTyrArgValThrAlaHisAlaGlyGlyTyr	960
Db	2960	GATTACTGTGGCAATCTTGTGAACCGGGGTGATGACCGCGTGAAGGCCACGCGGAGGGGTAC	3019

Db 1386 GGCAGAGCACCAAGAGAGCCCGAAGGGGAGGAGTTGGAGGAGGAGTGAGCGCTACG 1445
Qy 381 GILULYVALYVSPROPRIILEGLYMERGLUSERHISARGILEGLUASPANGILILE 400
Db 1446 GAGAAATCAAGTGTCCCGCATTTGGATGAGTCAACCGTATTGGAGCAACAGATC 1505
Qy 401 ARGALASERSEMERLEUARGHISGLYLEUGLYVALAGINARGGLYALUASPANGILIN 420
Db 1506 GAGACCTCTCCATGCTGCGCACGGCTGGGGGACAGCGGGCCGACTCAACATTCAG 1565
Qy 421 THRGLVALATHRGUASPAPTYRTYRASPGLVALATRPCYALAGLUASPAPALARG 440
Db 1566 ACCGGTCCACTGAGGAGACTACTATGATGTGTGCGGTGTGTGCGAGAGAGAGCCAGG 1625
Qy 441 THRGINTPRLIEGLULVALAPGTHARGARGTHRRARGPHEHTRGLVALILETHGLN 460
Db 1626 ACCCAGTGGATGAGGTGGACACCCAGAGAGACTACCCGGTTCCAGAGCGCATCACCCAG 1685
Qy 461 GLYARGAPSERSEITLHISAPAPAPHEVALTHRRPHEPHEVALGYPHSESEPPAN 480
Db 1686 GGCAGACACTCCAGCATTCAGACGATTTGTGACACCTTCTTGTGGGCTTCAGCAAT 1745
Qy 481 ASPSERGINTHRRTPVALMETTYRTHRANGLYTYRGLUGLUMETTHRRPHEHISGLYASN 500
Db 1746 GACAGCCAGCATGGGTGATGTACCAACGGCTATGAGGAATGACCTTTCATGGAGAC 1805
Qy 501 VALASPLYASAPTHRRPROVALLEUSERGLULEUPROGLUPROVALVALAARGPHEILE 520
Db 1806 GTGACACAGAGACACCCGCTGAGTGTAGAGCTCCCAAGCCGGGTGGCTCGTTTCATC 1865
Qy 521 ARGILEYRPROLEUTHRRTPANGLYSERLEUCYMERARGLEUGLYVALILEUGLYCYR 540
Db 1866 GCGATCTACCACTCACCTTGGAATGGACGCTGTGCATGGCTCGGAGGTGTGGGGTGC 1925
Qy 541 SERVALAIPROVALTYRSEITYRTYRALAGINANGILUVALAATHRASPAPLEU 560
Db 1926 TCTGTGGCCCTGTCTACACTACTACGCAACAGATAGGTGTGGCCACGATGACTG 1985
Qy 561 ASPPHEARGHISHISERTYRLYASAPMETARGGLULEUMETLYVALVALANGILULIN 580
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Qy 581 CYSPROTHRIETHRARGTHRRYRSEILEUGLYLYSESESEARGGLYLEULYSLIETRY 600
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Qy 601 ALAMETGLULESERAPAPPROGLYGLUHIISGLULEUGLYGLUPROGLUPHEARGTYR 620
Db 2106 GCCATGGAGATCTCAGACCAACCTCGGGGAGCATGGAACGCCGAGTTCCGCTAC 2165
Qy 621 THRALISGLYILLEHISGLYANGILUVALLEUGLYARGGLULEULEULEULEUMETGLIN 640
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Qy 641 TYRLEUCYARGGLULYRARGAPGLYASAPPROARGVALARGSEILEUVALGINAPGTHR 660
Db 2226 TACCTGTGGGAGAGTACCGGATGGAGACCAAGTGTGCGAGCTGTGGCGAGGACACA 2285
Qy 661 ARGILLEHISLEUVALPROSEILEUASPAPSPGLTYRGLULVALAIAAGINMETGLY 680
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Qy 681 SERGLUPHEGLYANTRPALALEUGLYLEUTRTPHRLUGLUGLYPHEAPGILIEPHEGLIN 700
Db 2346 TCAGAGTTTGGAACTGGGCGCTGGGACTGTGGACTGAGAGGGCTTTGACATCTTTGAA 2405
Qy 701 ASPPHEPROAPAPLEUASERVALLEUTRPGLYVALISGLULUARGLYLSTRPVALPROTYR 720
Db 2406 GATTTCCCGGATCTCACTCTGTGCTGTGGGAGCTGAGGAGAGAAATGGGTCCCTAC 2465
Qy 721 ARGVALPROANBANLEUPROILLEPROGLULARGTYRLEUSERPROAPALATHRVAL 740
Db 2466 CCGGTCCCAACATACTTGCCCATCTCGGAACGCTACTTTGCGCAGATGGCAGGTA 2525

Qy 741 SETRTHGLULVALARGALAILIETLEAATTRPMETGLULYASAPPROPHEVALILEUGLYALA 760
Db 2526 TCCACGAGAGGTCCGGGCAATCATTTGCTGTGATGAGAGAACCCCTTCGTGCTGGAGCA 2585
Qy 761 ASPLUASANGLYGLYGLULUARGLEUVALSERTYRPROTYRASPHEVALAARGTHRRPOTHR 780
Db 2586 AATCTGAACGGCGCGAGCCGCTATGATCTTACCCCTTACGATATGGCCGACGACTTACC 2645
Qy 781 GINGLUGLILEUVALAIAAIAAMEVALAIAAIAARGGLYGLULUASPGLUASPGLULVAL 800
Db 2646 CAGAGAGAGCTGTGGCCGAGCCATGAGCAGAGCCCGGGGGAGGATGAGAGAGAGTCC 2705
Qy 801 SERGLULAGLUGLUTHRRPROAPPHISALAILIEPHEARGTRPLEUAILIESERPHEALA 820
Db 2706 TCCAGAGCCAGAGAGCTCCAGACACCGCATCTTCGCGGTGCTTCCTTCCTTCGCC 2765
Qy 821 SERALHISLEUTHRRLEUTHRRGLUPROTYRARGGLYGLYCYRGLINLAGINAPPTYRTHR 840
Db 2766 TCCGACACCTCACCTTGACCGAGCCCTTACCGGAGGCTGCGAAGCCAGACTACACC 2825
Qy 841 GLYGLYMERGLYILLEVALANGILYALAYSTRPASPAPROARGTHRRGLYTHRIEASAP 860
Db 2826 GCGGCGATGGGCAATCGTCAACGGGGCAAGTGAACCCCGGACCGGACTATCATATGAC 2885
Qy 861 PHESEITYRLEUHIISHRANCYSLUUGLULEUSERPHEITYRLEUGLYCYASAPLYSPHE 880
Db 2886 TTCAGTTACTCTGATACCAATCCCTGAGCTCTCTTCACTCGGCTGTGCAAGATTC 2945
Qy 881 PROHISGLUSERGLULEUPROARGGLUTRPGULUASAPLUSGLULALEULEUTHRRPHE 900
Db 2946 CTTATGAGAGTAAAGCTGCCCCGAGTGGAGAAACAAAGAGGCGCTGTCCACCTTC 3005
Qy 901 METGLULINVALHISARGGLYILEYSGLYVALIATHRASPGLUNGILYILEPROILE 920
Db 3006 ATGACACAGGTGACCCGCGCATTAAGGGGTGTGACGAGACGACAGCAAGCACCATT 3065
Qy 921 ALAASNALATHRILESERVALSERGLYILLEHISGLYVALIYSTRHALASERGLYGLY 940
Db 3066 GCCACAGGCCCACTCTCTGTGAGTGCATTAAATCAGGGGTGAAACAGCCATGTGTGT 3125
Qy 941 ASPTYRTPARGGLILEUASAPPROGLYGLULYRARGVALTHRRALHISALISGLULYTYR 960
Db 3126 GATTTCTGGGAATCTTGAACCCGGGTGAGTACCGGTGACACCCACGCGGGGGCTAC 3185
Qy 961 THRRPSEVALAYSTRHCYASANVALASPITYRASPILIEGLYALATHRGILNCYASAPHE 980
Db 3186 ACCCGAGGCCCAAGACCTGCAATGTGACTATGACATGGGGCCACTGATGCAACTTC 3245
Qy 981 ILEUVALARGSERANTRPLYSARGILLEARGLUILEWETALAMECANGLYASANARG 1000
Db 3246 ATCTGTGCTGCTCCCAACTGGAAGCCCATCCGGAGATCATGCGCTGAACGGGAACCG 3305
Qy 1001 PROILEPROHISILEASAPPROSEARGPROMETTHRRPGLINAGLARGLEUGLINGLIN 1020
Db 3306 CCAATCCACACATTAACCCATGCGCCCTATGAGACCCCAACAGGAGCGCTCGACAG 3365
Qy 1021 ARGARGLEUGLINHISARGLEUARGLEUARGALAGLIMETARGLEUARGLEUASANA 1040
Db 3366 CGACGCTTCAACACACCGCTCGGGCTTCGGGGACANATCGGCTGGGGGCTCAACGCGC 3425
Qy 1041 THRRTHRLEUGLYPROHISSTRVALPROPTHRRLEUPROPROALAPROALATHRR 1060
Db 3426 ACCACACCCCTTGGCCCCCACACTGGCTCCCAACCTGCCCCCTGCGCACACACC 3485
Qy 1061 LEUSERTHRRILEGLUPROTPRGLYLEUUILEPROPTHRRTHRRALAGLYTRPGULGIN 1080
Db 3486 CTGAGACTTACCATTAAGCCCTTGGGCTCTCATACGCCCAACACCGCTGGGGAGAG 3545
Qy 1081 SERGLUTHRGULUTHRRTHRGULUVALTHRGULUPHEGLYTHRGILUVALGLUPROGLIN 1100
Db 3546 TCGAGAGCTGAGACTTACACAGAGGTGTGACAGAGTTTGGAGCGAGGTGAGCCGAG 3605

SOFTWARE: Patentin Ver. 3.1
; SEQ ID NO 490
; LENGTH: 3523
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-264-049-490

Alignment Scores:

Pred. No.:	0	Length:	3523
Score:	5725.00	Matches:	1054
Percent Similarity:	99.8%	Conservative:	2
Best Local Similarity:	99.6%	Mismatches:	0
Query Match:	91.3%	Indels:	2
DB:	7	Gaps:	0

US-10-642-946-3 (1-1158) x US-10-264-049-490 (1-3523)

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Db 2 AAAGGCCCAAGGTGCCAAGAGTCTTGAGGGGTCCCAAGCCGCCCAAGAGGG 61
OY 121 LysGlyLysProProLysAlaThrLysLysProLysGlyLysProProLysAlaThrLys 140
Db 62 AAGGAGAACCCCAAGGCCCAAGAGGCCCAAGAGAACCACTAAGGCCCAAG 121
OY 141 LysProLysGlyLysProProLysAlaThrLysLysProLysGlyLysProProLysAla 160
Db 122 AAGCCCAAGAGAACCCCAAGGCCCAAGAGGCCCAAGAGAACCCCAAGAGGCC 181
OY 161 ThrLysLysProProSerGlyLysArgProLysLeuAlaProSerGlyThrLeuGlu 180
Db 182 ACCAAGAACCCCGTCAGAGGAAGAGGCCCATTCCTGCTCCCTCAGAAACCTGGAG 241
OY 181 TTPProLysProProProSerProSerProGlyProGluLysLeuProGluGluGlyAla 200
Db 242 TGGCCACTGCCCAACCCCAAGCCCTGGCCCGGAGAGCTACCCCAAGAGAGGGCG 301
OY 201 ProLysSerAspAsnTrpGlnAsnProGlyLysGluThrHisValGluLysGluHis 220
Db 302 CCCCTTCAATTAATCTGGAGAACTCAAGAGAGAGAACCACTGTGAGGCAAGAGAC 361
OY 221 GlnProGluProGluGluGluThrGluGluProThrLeuAspTyrAsnAspGlnLeu 240
Db 362 CAGCTGAGCCCGAGAGAGAGAGCCAGCAACCACTGAGCTGAGCTGAGCTGAG 421
OY 241 ArgGluAspTyrGluAspPheGluTyrLeuArgGluLysGlnProArgProPro 260
Db 422 AAGGAGAGCTATGAGAGCTTTGAGTACATTCGGCCGAGAGCAACCCAGGCCCA 481
OY 261 SerArgArgArgArgProGluArgValTTPProGluProProGluGluLysAlaProAla 280
Db 482 AGCAGAGAGAGAGGCCCGAGCCGGGTCTGGCCAGAGCCCTTGAGAGAGAGGCCGCC 541
OY 281 ProAlaProGluGluLysGluLeuGluProProValLysProLeuLeuProPro 300
Db 542 CCAAGCCCGGAGAGAGAGATGAGTTCCTGCTGAACTCTGCTGCCCCCGCTGCCCT 601
OY 301 AspTyrGlyAspGlyTyrValLeuProAsnTyrAspAspMetAspTyrTyrPheGlyPro 320
Db 602 GACTAAGGTGATGCTTACGTGATCCCAACTACGATGACATGACATTAATTTGGGCT 661
OY 321 ProProProGluLysProAspAlaGluLysGluThrAspGluGluLysGluLysLeuLys 340
Db 662 CTTCCGCCCAAGAGGCCGAGTCTGAGGCCCAAGAGAGAGAGAGAGAGAGAGAG 721
OY 341 LysProLysLysGluAspSerSerProLysGluGluThrAspLysTrpAlaValGluLys 360
Db 722 AAACCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 781
OY 361 GlyLysAspHisLysGluProArgLysGlyLysGluLysGluLysGluLysTrpThrProThr 380
Db 782 GGCAGAGACCAAAAGAGCCCGAAAGGGGAGAGAGTGTGAGAGAGAGAGAGAGCTTACG 841
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OY 381 GluLysValLysCysProProLysGlyMetGluSerHisArgLysGluAspAsnGlnLe 400
Db 842 GAGAAAGCTCAAGTGTCCCCCATTTGGATGAGTCAACCGTATTGAGAGACACAGATC 901
OY 401 ArgAlaSerSerMetLeuArgHisGlyLeuGlyAlaGlnArgGlyArgLeuAsnMetGln 420
Db 902 CGAGCTCTCCATGCTCGCCACGGCTGGGGGACAGCGCCGCGCTCAACATGACG 961
OY 421 ThrGlyAlaThrGluAspAspTyrTyrAspGlyAlaTrpCysAlaGluAspAspAlaArg 440
Db 962 ACCGTTGCCCTGAGAGAGAGCTACTATGATGGTGGTGGTGGCCGAGAGACATCCAGG 1021
OY 441 ThrGlnTrpLysGluValAspThrArgArgThrThrArgPheThrGlyValLeuThrGln 460
Db 1022 ACCCATGATGATGAGTGGACACAGAGAGACTACCCGCTTCAACGGGCTATCACCCAG 1081
OY 461 GlyArgAspSerSerLeuHisAspAspPheValThrThrPhePheValGlyPheSerAsn 480
Db 1082 GGCAGAGACTCCAGATCCATGACGATTTTGTGACCACTTCTTGTTGGGCTTCAGCAAT 1141
OY 481 AspSerGlnThrTrpValMetTyrThrAsnGlyTyrGluGluMetThrPheHisGlyAsn 500
Db 1142 GACAGCCAGACATGGGTATGATACCAACGCTATGAGAAATGACCTTTCATGGAAAC 1201
OY 501 ValAspLysAspThrProValLeuSerGluLeuProGluProValAlaAlaArgPheLe 520
Db 1202 GTGGCAAGAGACACCCGCTGTGATGAGCTCCAGAGCCGGTGGTGGCTGTTTCATC 1261
OY 521 ArgLeuTyrProLeuThrTrpAsnGlySerLeuCysMetArgLeuGluValLeuGlyCys 540
Db 1262 CGCATCTACCACTACCTGGAATGGCAGCTGTGCATGCGCTGAGAGTGTGGGGTGC 1321
OY 541 SerValAlaProValTyrSerTyrTyrAlaGlnAsnGluValAlaAlaThrAspAspLeu 560
Db 1322 TGTGGCCCTCTGTACTAGCTACTACCAAGATGAGTGGTGGCCACCATGACCTG 1381
OY 561 AspPheArgHisAspSerTyrLysAspMetArgGlnLeuMetLysValAlaAsnGluGln 580
Db 1382 GATTTTCGGACACACAGCTACAGAGACATGGCCAGCTCATGAGTGGTGAACGAGAG 1441
OY 581 CysProThrLeuThrArgThrTyrSerLeuGlyLysSerSerArgGlyLeuLysAlaLeuTyr 600
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OY 601 AlaMetGluLysSerAspAsnProGlyLysGluLeuGluGluProGluPheArgTyr 620
Db 1502 GCCATGAGATCTCAGACACCTGGGAGCATGAACTGGGGAGCCCGAGTTCGCTAC 1561
OY 621 ThrAlaGlyLeuHisGlyAsnGluValLeuGlyArgGluLeuLeuLeuMetGln 640
Db 1562 ACTGCTGGGATCATGGACAGAGGTGCTGGGCGAGAGCTGTCTGCTCATGACG 1621
OY 641 TyrLeuCysArgGluTyrThrAspGlyAsnProArgValArgSerLeuValGlnAspThr 660
Db 1622 TACTGTGGCCGAGATACCGGATGGAACCCAGCTGTGGAGCTGTGACAGACACA 1681
OY 661 ArgLeuHisLeuValProSerLeuAsnProAspGlyTyrGluValAlaAlaGlnMetGly 680
Db 1682 GCGATCCACCTGTCCTCTCACTGAACCTTGATGGCTACAGAGTGGCAGCGAGATGGC 1741
OY 681 SerGluPheGlyAsnTrpAlaLeuGlyLeuTrpThrGluGluGlyPheAspLeuPheGlu 700
Db 1742 TCAGAGTTTGGGAATGGGGCTGGGACCTGTGATGAGAGAGGCTTTGACATCTTGA 1801
OY 701 AspPheProAspLeuAsnSerValLeuTrpGlyAlaGluGluLysLysTrpValProTyr 720
Db 1802 GATTTCCCGGATCTCACTGTGCTCTGGGAGCTGAGAGAGAGAAAGGGTCTCCCTAC 1861
OY 721 ArgValProAsnAspAsnLeuProLysProGluArgTyrLeuSerProAspAlaThrVal 740
Db 1862 CGGGTCCCAACAAATACCTTGGCCATCCCTGAACCTTCTTCCGACATCCACGAGTA 1921
OY 741 SerThrGluValArgAlaIleIleAlaTrpMetGluLysAsnProPheValLeuGlyAla 760
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Db      1922  TCCACGAGAGTCCGGGCGCATCATTCCTGGATGGAGAAAGAACCCCTTCGTGCTGGAGCA 1981
Qy      761  AAmLeuAnnglylglyluhrgLeuValSerTyProTyraPheMetAlaArgThrProThr 780
Db      1982  AATCTGAACGGCGCGGAGCGGCTAGTATCTTACCCCTACGATATAGGCGCCGACCCCTAC 2041
Qy      781  GlnGlnGlnLeuLeuAlaAlaMetAlaAlaAlaArgGlyValuPheGluuPheGluVal 800
Db      2042  CAGAGAGAGCTGCTGGCGCGAGCGCATGAGACACCCGCGGCGAGAGATGAGAGAGAGTC 2101
Qy      801  SerGluuAlaGlnGlnuThrProAspHisAlaAlaPheArgTrpLeuAlaIleSerPheAla 820
Db      2102  TCCGAGGCCACAGAGAGATCCAGACAGCCATCTCCGGTGCTGGCATCTCTTCCTGGCC 2161
Qy      821  SerAlaHisLeuThrLeuThrGlnuProTyraArgGlyGlyCysGlnuAlaGlnuAspTyThr 840
Db      2162  TCCGCAACCTTCACTTGAACCGAGCCCTACCGCGAGAGCTGCGCAAGCCGAGACTACAC 2221
Qy      841  GlyGlyMetGlyIleValaAnglyAlaIleTyTrpAsnProArgTrpGlyThrIleAsnAsp 860
Db      2222  GGGGCGCATGGGCGCATGTCACCGGGGCGCAAGTGAACCCCGGAGCCGGAGCTATCAAGAC 2281
Qy      861  PheSerTyTrpLeuHisThrAsnCyLeuGlyuLeuSerPheTyTrpLeuGlyCysAspTyPhe 880
Db      2282  TTCAGTTACTGCAATACCACTGCTGAGCTCTCTTCACTGGGCTGTGACAGATTC 2341
Qy      881  ProHisGluSerGluLeuPProArgGlyuTrpGluuAsnAsnGlyValuAlaLeuThrPhe 900
Db      2342  CCTCATGAGAGTGGAGTGGCCCGGAGTGGAGAAACAAGAGGCGCTGCTACCTTC 2401
Qy      901  MetGlnGlnValHisArgGlyIleGlyGlyValValThrAspGlnGlnGlyIleProIle 920
Db      2402  ATGAGAGAGATGACCCGCGCATTTAGGGGTGTGTGCGAGCAGAGCAAGCATCTCCATT 2461
Qy      921  AlaAsnAlaThrIleSerValSerGlyIleAsnHisGlyValIleThrAlaSerGlyGly 940
Db      2462  GCCAAGCGCCACATCTCTGTGAGTGCATATATACCGGCTGAAGACGACATGGTGT 2521
Qy      941  AspTyTrpArgIleLeuAsnProGlyGlyuTyraArgValThrAlaHisAlaGlnGlyTyTr 960
Db      2522  GATTACTGGCGAATCTTGAACCCGCGGTGAAGTACCGCTGACAGCCGCGGAGGGCTAC 2581
Qy      961  ThrProSerAlaIleAsnThrCysAsnValAspTyTrpAspIleGlyAlaThrGlnCysAsnPhe 980
Db      2582  ACCCCGAGCGCCAGAGACTGCAATGTGACTATGACATCGGGCCACTGCTCACTCACTTC 2641
Qy      981  IleLeuAlaArgSerAsnTrpIleArgIleArgGlyuIleMetAlaMetAsnGlyAsnArg 1000
Db      2642  ATCTGGCTGCTCCCACTGGAGCGCATCCGGAGATCATGGCCATGAAACGGAAACGG 2701
Qy      1001  ProIleProHisIleAspProSerArgProMetThrProGlnGlnuArguGlnGln 1020
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Qy      1021  ArgArgGlnGlnHisArgLeuArgLeuArgAlaGlnMetArgLeuArguArgLeuAsnAla 1040
Db      2762  CGAGCGCTACAAACCGCGCTGCGGCTTCGGGCAAGATGCGGCTGCGGCGCCCTCAACG 2821
Qy      1041  ThrThrThrLeuGlyProHisThrValProProThrLeuProProAlaProAlaThrThr 1060
Db      2822  ACCACACCTTACGAGCCCACTGCTGCTCCCAAGCTGCGCCCTGCTGCGCACAC 2881
Qy      1061  LeuSerThrThrIleGluProTrpGlyLeuIleProProThrThrAlaGlyTyTrpGlnGln 1080
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Qy      1081  SerGlnGlnGlnuThrTyThrArgIleValValThrGlnPheGlyThrGlnValuGluProGln 1100
Db      2942  TCGAGAGCTAGAGCTTACAGAGAGTGTGACAGAGTTTGGAGCCGAGGGAGGCCGAG 3001
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Db      3062  CTGGAACCCCAAGTTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATAGCCACTGGC 3121
Qy      1141  GlnAlaPheProPheThrThrValGlnuThrTyThrValAsnPheGlyAspPhe 1158
Db      3122  CAGGCAATTCCTTCAACAGATGAGACCTTACAGTGAATTTGGGAGCTTC 3175

RESULT 14
US-10-101-510-345
; Sequence 345. Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
; APPLICANT: MAN, JACKSON
; APPLICANT: MANG, YIXIN
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
; FILE REFERENCE: 15117.0012
; CURRENT APPLICATION NUMBER: US/10/101,510
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/276,947
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 345
; LENGTH: 3170
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-510-345

Alignment Scores:
Pred. No.: 0 Length: 3170
Score: 4925.50 Matches: 922
Percent Similarity: 94.8% Conservative: 6
Best Local Similarity: 94.2% Mismatches: 14
Query Match: 78.5% Indels: 37
DB: 7 Gaps: 3

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Qy      201  oLeuSerAsnAsnTrpGlnAsnProGlyGlnuThrHisValGluAlaGlnGlnuHisG 221
Db      74  AATGGGCCCATC-----CA 88
Qy      221  nPro-GluProGlnGlnGlnuThrGlnGlnProThrLeuAspTyTrpAsnAspGlnIleGlu 241
Db      89  GCCTTGGGCCCCACTGTGAGCCAGCCTCCCTCTCACTT----- 126
Qy      241  rGlnuAspTyTrpGluAspPheGlnuTyTrIleArgArgGlnGlnGlnProArgProPro 261
Db      127  -----GAGTACATTCGGGCGCGAGAGCAACCAAGCCACCCCA 166
Qy      261  exArgArgArgArgProGluArgValTrpProGluProProGlnGlnuTyAlaProAlaP 281
Db      167  GCGAAGAGAGAGAGCCCGAGCGGGGTGCGCAAGACCCCTGAGAGAGAGAGCCGGGCC 226
Qy      281  roAlaProGlnGlnuArgIleGluProProValIleProLeuLeuProProLeuProPro 301
Db      227  CAGCCCGAGAGAGAGATTTGAGCCCTCTGTGAAGCTCTGCTGCGCCCGCTGCGCCCTG 286
Qy      301  sPTyGlyAspGlyTyValIleProAsnTyAspAspMetAspTyTyTrpPheGlyProP 321
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Qy      321  roProProGlnuTyProAspAlaGluArgGlnuThrAspGlnGlnuTyGlnGlnuLeuTyL 341
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[illegible]

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Db	1547	GGGT	CCCCCA	CAATPA	CTTGCC	CCATCC	CTTGAAC	GTCACT	TTTGCC	AGATGCC	AGGTAT	1606		
Qy	741	erThr	GluVal	ArgAla	IleIle	AlaIle	ArgMet	GluLys	AsnPro	PheVal	LeuGlu	Vala	761	
Db	1607	CCAG	GAGG	CGCC	CGGCAT	ATGCTG	GTGATG	GAGAA	GAACCC	CTTGCTG	TGGACCA	1666		
Qy	761	snLeu	AsnGly	GlyGlu	ArgLeu	ValSer	TyrPro	TyrAsp	MetAla	ArgThr	ProThr	G	781	
Db	1667	ATCT	GAACGG	GGGGAG	CGGCTAG	TATCCT	TACCCCT	TACAT	TATG	CCCGCA	CGCTTACC	1726		
Qy	781	Ingl	GluLeu	LeuAla	IleAla	MetAla	IleArg	GlyGlu	AspGlu	AspGlu	ValS	801		
Db	1727	AGAG	CAGCTG	CTGGCC	CGACCCAT	TGGCAG	CACGCC	CGGGGGAG	AGATGAG	AGACGAG	CTCT	1786		
Qy	801	erGlu	AlaGln	GluThr	ProAsp	HisAla	IlePhe	ArgTyr	PheAla	IleSer	ThrAla	S	821	
Db	1787	CCGAG	GGCCAG	GAACCT	CCACAC	CCGCACT	CTTCTCG	GTGCTT	GCATCT	CTCTTCC	CTCT	1846		
Qy	821	erAla	HisAla	erThr	LysThr	GluPro	TyrArg	TyrGly	CysGln	AlaGly	AspTyr	ThrG	841	
Db	1847	CCGC	ACACCT	CACTTA	CCAGGCC	CTTACCG	CGGAGCTG	CCAGCC	CAAGCA	CGCACT	ACACG	1906		
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OM protein - nucleic search, using frame_plus.p2n model

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.Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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2	3744	59.7	2268	8 US-11-266-748A-184697	Sequence 184697, A
3	3744	59.7	2268	8 US-11-266-748A-192181	Sequence 192181, A
4	3421	54.5	2065	8 US-11-266-748A-184695	Sequence 184695, A
5	3421	54.5	2065	8 US-11-266-748A-192179	Sequence 192179, A
6	2125	33.9	1193	8 US-11-266-748A-98157	Sequence 98157, A
7	2125	33.9	1193	8 US-11-266-748A-150968	Sequence 150968, A

8	2066	32.9	2490	9 US-11-376-589-1	Sequence 1, Appl1
9	1946	31.0	1437	8 US-11-266-748A-192182	Sequence 192182, A
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12	1733	27.6	2388	6 US-10-196-749-457	Sequence 457, Appl
13	1731	27.6	2205	8 US-11-242-505A-23	Sequence 23, Appl
14	1453	23.2	1184	8 US-11-266-748A-226229	Sequence 226229, A
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38	743	11.8	1158	8 US-11-266-748A-189986	Sequence 189986, A
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40	686	10.9	415	8 US-11-266-748A-64109	Sequence 64109, A
41	686	10.9	415	8 US-11-266-748A-66941	Sequence 66941, A
42	636	10.1	2362	6 US-10-539-228-230	Sequence 230, Appl
43	635	10.1	433	8 US-11-266-748A-169326	Sequence 169326, A
44	633.5	9.6	5188	6 US-10-669-920-1128	Sequence 1128, Appl
45	599.5	9.6	2085	6 US-10-511-937-395	Sequence 395, Appl

ALIGNMENTS

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; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkins, Paul
; APPLICANT: Johnson, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266, 748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
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; PRIOR APPLICATION NUMBER: EP 04105483.4
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; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700, 293
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; SOFTWARE: PatentIn version 3.3

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Best Local Similarity: 99.3%
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US-10-642-946-3 (1-1158) x US-11-266-748A-184697 (1-2268)

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DB 165 ATGGCGGCGGTGGCGGGCGCCCTGCTCAGCTGCTCTCGCGTGTGGCGCTGTGC 224
QY 21 ProGLYGLYARGProGLInThrValLeuThrAspAspGLuIleGLuGLuPheLeuGLuGLY 40
DB 225 CCTGGAGGGCGCCCGAGACGGGTCTGACCGACGACGAGATCGAGAGTCTCTCGAGGGC 284
QY 41 PheLeuSerGLuLeuGLuProGLuProARGLVAspAspValGLuAlaProProPro 60
DB 285 TTCCTGTCTCAGAGCTAAGACCTGAGCCCGGAGAGACGCTGAGAGGCCCGCGCTCCC 344
QY 61 GLuProThrProARGValARGLVAlaGLuAlaGLYGLYAspProGLYLYAspProGLY 80
DB 345 GAGCCACCCCGGGGTCCGAAAGCCAGCGGGGGGCAAGCCAGGGAAAGCGGCCAGG 404
QY 81 ThrAlaAlaGLuValProProGLuLYsThrLYsAspLYsGLYLYsLYsGLYLYsLYsAsp 100
DB 405 ACGGCGCGAGAGTGCCTCGGAAAGACCAAGAACAAAGGAGAAAGCAAGAAAGAC 464
QY 101 LYsGLYProLYsValProLYsGLuSerLeuGLuGLYSerProARGProProLYsLYsGLY 120
DB 465 AAAGGCCCAAGGTGCGCAAGAGTCTTGAAGGGTCTCCCGCGCGCCCAAGAGGGG 524
QY 121 LYsGLuLYsProProLYsAlaThrLYsLYsProLYsGLuLYsProProLYsAlaThrLYs 140
DB 525 AAGGAAGAGCACCCAGGCGCACAGAAAGCCCAAGAGAGACCTTAAGGCCACCAAG 584
QY 141 LYsProLYsGLuGLuProProLYsAlaThrLYsLYsProLYsGLuLYsProProLYsAla 160
DB 585 AAGCCCAAGAGAGAGCACCAAGGCCACCAAGAACCCCAAGAGAGCAACCAAGGCC 644
QY 161 ThrLYsLYsProProSerGLYLYsValProProIleLeuAlaProSerGLuThrLeuGLu 180
DB 645 ACCAAGAGGCCCTCTCAGGAGAGAGGCCCTCCATCTGCTCCCTCAAGAACCTCTGGAG 704
QY 181 TrpProLeuProProProProSerProGLYProGLuGLuLeuProGLuGLuGLYValA 200
DB 705 TGGCCACTGCCCCCAGCCCCCAGCCCTGGCCCCGAGAGCTACCCAGAGAGGAGGGG 764
QY 201 ProLeuSerAspAsnTrpGLuAsnProGLYGLuGLuThrHisValGLuAlaGLuGLuHis 220
DB 765 CCCCTCTCAATATACCTGGCAGAT-CCAGAGAGAGAACCCCATGTGAGGAGCGGAGCAC 823
QY 221 GLuProGLuProGLuGLuGLuThrGLuGLuProThrLeuAspTYrAsnAspGLuIleGLu 240
DB 824 CAGCCCTGAGCCGAGAGAGAGAGACCGAGCAACCACTGACTACATGACGATGCGAG 883
QY 241 ARGGLuAspTYrGLuAspPheGLuTYrIleARGARGLYsGLuAsnProARGProPro 260
DB 884 AAGGAAGACTATAGAGACTTGAATCATTTGGGCGCAGAGAACCCAGGCCACCCCA 943
QY 261 SerARGARGARGProGLuARGValITrpProGLuProProGLuGLuLYsAlaProAla 280
DB 944 AGAGAAAGAGAGAGGCCCGAGCGGGTCTGGCCAGAGACCCCTGAGAGAAAGGCCCGG 1003
QY 281 ProAlaProGLuGLuARGIleGLuProProValLYsProLeuLeuProProLeuProPro 300
DB 1004 CCAAGCCCGAGAGAGAGATGAGCTCTGTGAACCTCTGTGCCCCCGCGGCCCT 1063
QY 301 AspTYrGLYAspGLYTYrValIleProAsnTYrAspAspAspTYrTYrPheGLuPro 320
DB 1064 GACTTAAGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1123
QY 321 ProProProGLuLYsProAspAlaGLuARGInThrAspGLuGLuLYsGLuGLuLYs 340

DB 1124 CCTCCGCCCAAGAGCCGATGTGAGCGCCAGACGAGCAAGAGAGAGAGCTGAAG 1183
QY 341 LYsProLYsLYsGLuAspSerSerProLYsGLuGLuThrAspLYsThrAlaGLuLYs 360
DB 1184 AAACCCAAAAG 1243
QY 361 GLYLYsAspHisLYsGLuProARGLYsGLYGLuGLuLeuGLuGLuGLuThrProThr 380
DB 1244 GCGAAGAGACCAAG 1303
QY 381 GLuLYsValLYsCyProProIleGLYMeGLuSerHisARGIleGLuAspAsnGLuIle 400
DB 1304 GAGAAAGTCAAGTGTCCCCCATTTGGATGAGTCAACCGTATGAGAGACAAACAGATC 1363
QY 401 ARGAlaSerSerMetLeuARGHisGLYLeuGLYValAGlnARGLYsARGLeuAsnMetGLn 420
DB 1364 CGAGCTCTCCATGCTCGGCAAGCGCTGGGGGAGAGCGGGCGGCTCAACATGAG 1423
QY 421 ThrGLYAlaThrGLuAspAspTYrTYrAspGLYAlaTrpCYsAlaGLuAspAspAlaARG 440
DB 1424 ACCGTGCGCATGAGAGAGACTACTATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1483
QY 441 ThrGLuInTrpIleGLuValAspThrARGArgThrThrARGPheThrGLYValIleThrGLn 460
DB 1484 ACCCAGTGAATAGAGTGAACACAGAGAGACTACCCGTTCAAGCGGTCAACCCAG 1543
QY 461 GLYARGAspSerSerIleHisAspAspPheValThrThrPhePheValGLYPheSerAsn 480
DB 1544 GGCAGAGACTCAGATCAATGACATTTGTGACACCTTCTTGTGGCTTCAGCAAT 1603
QY 481 AspSerGLuInThrTrpValMetTYrThrAsnGLYTYrGLuGLuMetThrPheHisGLYAsn 500
DB 1604 GACAGCCAGACATGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1663
QY 501 ValAspLYsAspThrProValLeuSerGLuLeuProGLuProValAlaAlaARGPheIle 520
DB 1664 GTGGACAAGAGACACCCGTGTGATGAGTCCAGAGCGGTGTGTGTGTGTGTGTGTGTGT 1723
QY 521 ARGILETYrProLeuThrTrpAsnGLYSerLeuCYsMetARGLeuGLuValLeuGLYCYs 540
DB 1724 CGCATCTACCACTACCTGAGATGAGAGCTGTGACATGCGCTGAGAGTGTGGGGTGC 1783
QY 541 SerValAlaProValTYrSerTYrTYrAlaGLuAsnGLuValAlaAlaThrAspAspLeu 560
DB 1784 TCTGTGGCCCTGTCTACAGCTACACGACAGATGAGTGTGTGTGTGTGTGTGTGTGTGT 1843
QY 561 AspPheARGHisHisSerTYrLYsAspPheARGInLeuMetLYsValValAsnGLuGLu 580
DB 1844 GATTTCCGGCACACAGCTACAGAGACATGCCCGCTCATGATGATGATGATGATGATGATGAT 1903
QY 581 CySProThrIleThrARGThrTYrSerLeuGLYLYsSerSerARGLYLeuLYsIleTYr 600
DB 1904 TCCCCACCATACCCGACCTTACAGCTGTGGCAAGAGTCTCAGAGGCTCTCAAGATCTAT 1963
QY 601 AlaMetGLuIleSerAspAsnProGLYGLuHisGLuLeuGLYGLuProGLuPheARGTYr 620
DB 1964 GCCATGGAGATCTAGACAACTCTGGGAGCATGAACTGGGGAGACCCGAGTTCCGCTAC 2023
QY 621 ThrAlaGLYIleHisGLYAsnGLYValLeuGLYARGLYsGLuLeuLeuLeuLeuMetGLn 640
DB 2024 ACTGCTGGGATCTCAGAGCAACAGGTGTGTGGCCAGAGCTGTGTGTGTGTGTGTGTGTGT 2083
QY 641 TYrLeuCYsARGGLuTYrARGAspGLYAsnProARGValARGSerLeuValGLuAspThr 660
DB 2084 TACCTGTGCGAGAGTACCGCATGAGAAACCATGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2143
QY 661 ARGIleHisLeuValProSerLeuAsnProAspGLYTYrGLuValAlaAlaGLuMetGLY 680
DB 2144 CGCATGCCACTGTGTCCCTCACTGAACCTGATGTGCTAGAGT-GCAGCGCAGATGGGC 2202
QY 681 SerGLuPheGLYAsnTrpAlaLeuGLYLeuTYrThrGLuGLuGLYPheAspIlePheGLu 700
DB 2203 TCAGAGTTTGGAACTGGGCGCTGTGAGCTGTGAGCTGAGAGAGGCTTTGACATCTTTGAG 2262

Db 1544 GGCAGAGACTCCAGCATCCATGACGATTTTGTGACCACTTCTGTGGGCTTCAGCAT 1603
Qy 481 AAPPSEGLTThTTPyAlMeTyrThraAngLYTyrGlulMeThrPheHISglYan 500
Db 1604 GACAGCAGACATGGGTGATGATACCAACGGCTATGAGAAATGACCTTTCATGGAGAC 1663
Qy 501 ValAapLyAspThPProValLeuSerGluLeuProGluProValAlaArpPheLe 520
Db 1664 GTGGACAAAGACACACCGGTGTGAGTGTCCAGACCGGTGTGGCTGTTCATC 1723
Qy 521 ArgLYeTyrProLeuThTTPyAngLYSerLeuCYmeArGLuLeuGLuYys 540
Db 1724 CGCATCTACCACTCACTGGATGAGCAGCTGTGTGATCGCTGGAGGTGTGGGTGC 1783
Qy 541 SerValAlaProValTYrSerTYrTYrAlaGlnSerGluValAlaArpPheLeu 560
Db 1784 TCTGTGGCCCTGTCTACAGACTACGACAGAAAGAGTGTGTGCCACCATGACCG 1843
Qy 561 AAPPpHeArgHISerSerTYrLYsAspMeArGLuLeuMeLYsValValAsnGLu 580
Db 1844 GATTTCGGACACACGCTACAGACAGCATGCCAGCTCATGAGGTGTGAACGAGAG 1903
Qy 581 CysProThrIleThraArgThTYrSerLeuGLYysSerSerArgLYeLeuYsIleTyr 600
Db 1904 TGGCCACCATCACCCGCACTTACAGCTGGGCAAGCTCACAGAGCTCAAGATCAT 1963
Qy 601 AlaMetGluIleSerAspAspProGLYgluHISgluLeuGLYgluProGluPheArgTYr 620
Db 1964 GCCATGAGATCTCAACACACCTGGGAGCAGTGAACCTGGGAGCCCATGTCCTAC 2023
Qy 621 ThrAlaGLYIleHISglYsAngLYuValLeuGLYArgLYeLeuLeuLeuMeTgin 640
Db 2024 ACTGCTGGATCCATGACACAGAGTGTGGGCCGAGACTGTGTCTGCTCATGACG 2083
Qy 641 TYrLeuCYsArgGLuTYrArgAspGLYsAspProArgValArgSerLeuValGlnAspThr 660
Db 2084 TACCTGTCCGAGAGTACCGCGATGGGAACCCAGCTGTGGCGAGCTGTGGCAGACACA 2143
Qy 661 ArgIleHISleuValProSerLeuAspProAspGLYTYrGLuValAlaAlaGlnMeTgin 680
Db 2144 CGCATCACCCTGTGTGCTCTCACTGAACCCCTGATGGCTTACAGAGTGC-GCACGCGAGATGGGC 2202
Qy 681 SerGluPheGLYsAspThPAlaLeuGLYLeuTYrThGLuGLuGLYpHeAspIlePheGlu 700
Db 2203 TCAGATTTGGGAACCTGGCGCTGGAGCTGTGACCTGAGAGGGCTTTGACATTTGAG 2262

RESULT 4
US-11-266-748A-184695
Sequence 184695, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcripome Microarray Technology and
TITLE REFERENCE: Methods of Using the Same
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14

PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: Patent version 3.3
SEQ ID NO 184695
LENGTH: 2065
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (182)..(1884)
OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-184695

Alignment Scores:
Pred. No.: 5,95e-163 Length: 2065
Score: 3421.00 Matches: 647
Percent Similarity: 95.94 Conservative: 0
Best Local Similarity: 95.94 Mismatches: 28
Query Match: 54.54 Indels: 1
DB: Gaps: 0

US-10-642-946-3 (1-1158) x US-11-266-748A-184695 (1-2065)

Qy 447 AAPPThraArgThTThraPheThrGLYValIleThrGlnGLYArgAspSerIle 466
Db 40 GACACACAGAGACATCACCGGTTTACAGGCGTCATCACACAGGCGAGACCTCCAGCATC 99
Qy 467 HISAspAspPheValThTThrPhePheValGLYpHeSerAspAspSerGlnThTTPyAl 486
Db 100 CATGACGATTTGTGTACACACTTCTGTGGGCTTCAGCAATGACAGCCAGCATGGGTG 159
Qy 487 MeTYrThraAsnGLYTYrGLuLeuMeThrPheHISglYAspValAspLYsAspThPPro 506
Db 160 ATGTACACCAAGGCTATGAGAAATGACCTTTCATGGAGCTGACAGACACACCC 219
Qy 507 ValLeuSerGluLeuProGluProValValAlaArgPheIleArgLYeTYrProLeuThr 526
Db 220 GTGCTGAGTGAAGCTCCAGAGCGGTGTGTGCTGTTCATCGCATCACCATCACAC 279
Qy 527 TTPAsnGLYSerLeuCYmeArGLuLeuGLYCYsSerValAlaProValTYr 546
Db 280 TGGATGGCAGCCTGTGCTATGAGTGTGGAGTGTGGGTGTCTGTGCCCCCTGTCTAC 339
Qy 547 SerTYrTYrAlaGlnAsnGLYValAlaArpAspLeuAspPheArgHISHisSer 566
Db 340 ACCTACTACGACAGATGAGGTGTGGCCACGATGACCTGATTTCCGGCACACACG 399
Qy 567 TYrLYsAspMeArGLuLeuMeLYsValValAsnGLuGLYCyAspProThrIleThraArg 586
Db 400 TACAGGACATCGCCAGCTCATGAAGGTGTGAACGAGAGTGGCCCATCACCCGC 459
Qy 587 ThTYrSerLeuGLYysSerSerArgLYeLeuYsIleTYrAlaMeTgluIleSerAsp 606
Db 460 ACTTACAGCTGTGGCAAGGCTCACAGAGCCCTCAAGATTTAGCCATGAGATCTGACG 519
Qy 607 AsnProGLYgluHISgluLeuGLYgluProGluPheArgTYrThraGLYIleHISglY 626
Db 520 AACCTGGGAGACATGAACCTGGGAGGCCGAGTTCCGCTACACTGCTGGATCCATGGC 579
Qy 627 AsnGLuValLeuGLYArgLYeLeuLeuLeuLeuMeTginTYrLeuCYsArgGLYTYr 646
Db 580 AACGAGGTGCTGGGCGAGAGCTGTGTGCTGTCTCATACAGTACCTGTGGCGAGATGAC 639
Qy 647 ArgAspGLYsAspProArgValArgSerLeuValGlnAspThArgIleHISleuValPro 666
Db 640 CGCGATGGGAACCACTGTGTGCGAGCCGTGGCGAGGACACACGCTTCCACCTGGTGGCC 699
Qy 667 SerLeuAspProAspGLYTYrGLuValAlaAlaGlnMeTginSerGluPheGLYsAspThP 686
Db 700 TCACTGAACCTGATGGCTTACAGAGTGTGGCGGCGCATGATGGCTCAGAGTTTGGGAACCTGG 759
Qy 687 AlaLeuGLYLeuTYrThrGLuGLuGLYpHeAspIlePheGluAspPheProAspLeuAsn 706

Db 760 GCCTGGAGCTGTGAGCTGAGAGGCGCTTGACATCTTTGAAGATTCCTCCGAGTCTAC 819
Qy 707 SerValLeuTrpGlyAlaGluGluValArgLeuTrpValProAsnAsn 726
Db 820 TCTGTGCTCTGGAGAGCTGAGAGGAAATGGGTCCCTACCGGGTCCCAACATATAC 879
Qy 727 LeuProIleProGluValArgLeuSerProAspAlaThrValSerThrGluValArgAla 746
Db 880 TTCCCATCCCTGAACCTTACCTTTGCGAGATGCCAGGTATCCAGGAGGTCCGGGCC 939
Qy 747 IleIleAlaTrpMetGluLeuAsnProPheValLeuGlyValAsnLeuAsnGlyGlu 766
Db 940 ATCATTTGCTGGATGGAGAGAACCTCTGTGCTGGAGCAATCTGAACGGCGGAG 999
Qy 767 ArgLeuValSerTrpProTrpAspMetAlaArgThrProThrGluGluLeuVal 786
Db 1000 CGGCTAGTATCTTACCTTACGATATGCGCGCATCCAGAGAGAGCTGTGGCC 1059
Qy 787 AlaAlaMetAlaAlaAlaArgGlyGluAspGluValSerGluValArgGluThr 806
Db 1060 GCAGCAGTGGACAGCCCGGGGGAGATGAGACAGAGTCTCCGAGGCCAGAGACT 1119
Qy 807 ProAspHisAlaIlePheArgTrpLeuAlaIleSerPheAlaSerAlaHisLeuThrLeu 826
Db 1120 CAGACACAGCCCATCTTCCTGGTGGCTTGCATCTCTCCCTCCGACACTCACCTTG 1179
Qy 827 ThrGluProTrpArgGlyGlyGlyGluAlaGluAspTrpThrGlyMetGlyVal 846
Db 1180 ACCGAGCCCTACCGCGAGGCTGCCAAGCCAGAGCTACACCGCGCATGGGATGTC 1239
Qy 847 AsnGlyAlaIleArgTrpAsnProArgThrGlyThrIleAsnAspPheSerTrpLeuHisThr 866
Db 1240 AAGGGGAGCAGAGGAGAACCCCGGAGCGGAGCATATACATTCCTGCTGCAATACC 1299
Qy 867 AsnGlyLeuGluLeuSerPheTrpLeuGlyCysAspLysPheProHisGluSerGluLeu 886
Db 1300 AACTGCTGAGAGCTTCTCTTCTACCTGGCTGTGACAGTCTCCCTCATGAGATGACTG 1359
Qy 887 ProArgGluTrpGluAsnAsnLysGluAlaLeuLeuThrPheMetGluGluValHisArg 906
Db 1360 CCCCAGAGTGGAGAGAACAGAGAGGCGCTGCTCATGAGAGCGTGCACCGC 1419
Qy 907 GlyIleIleGlyValValAlaThrAspGluGluGlyIleProIleAlaAsnAlaThrIleSer 926
Db 1420 GGCATTAAAGGGGTGTGAGCAGAGCAGAGCATCCCATTCGCAACGCGACCATCTCT 1479
Qy 927 ValSerGlyIleAsnHisGlyValLysThrAlaSerGlyGlyAspTrpArgIleLeu 946
Db 1480 GTGAGTGGCATTTATACCGGCTGAAAGACAGCCAGTGGTGTATTACTGGCAATCTTG 1539
Qy 947 AsnProGlyGluTrpArgValThrAlaHisAlaGluGlyTrpThrProSerAlaLysThr 966
Db 1540 AACCCGAGTGAAGTACCGCGTGAACGCCAGCGGAGGCTTACCCGAGCGCGCAAGACC 1599
Qy 967 CysAsnValAspTrpAspIleGlyAlaThrGlnCysAsnPheIleLeuAlaArgSerAsn 986
Db 1600 TCGAATGTTGACTATACATCGGGGCGACATGCAATCTTCTCGGCTCCCTCCAC 1659
Qy 987 TrpLysArgIleArgGluIleMetAlaMetAsnGlyAsnArgProIleProHisLeuArg 1006
Db 1660 TGGAGCGCTTCCGGAGATCATGGCCATTAACGGAGAACCGGCTTATCCACATAGAC 1719
Qy 1007 ProSerArgProMetThrProGluGlnArgArgLeuGlnArgArgLeuGlnHisArg 1026
Db 1720 CCATCCGCGCTTATGACCCCGCAACATCGACGCTGATCAGGAGCGCTTACACACCGC 1779
Qy 1027 LeuArgLeuArgAlaGlnMetArgLeuArgArgLeuAsnAlaThrThrLeuGlyPro 1046
Db 1780 CTGCGGCTTCGGGACAGATGCGCTGCGGCGCTCAACCCNNNNNNNNNNNNNNNNNN 1839
Qy 1047 HisThrValProProThrLeuProProAlaThrThrLeuSerThrThrIleGlu 1066

Db 1840 NNN 1899
Qy 1067 ProTrpGlyLeuIleProProThrThrAlaGlyTrpGluGluSerGluThrGluThrTyr 1086
Db 1900 CCTGGGGCTCATACCGCAACCGCTGCTGGAGAGAGTGAAGACTGAGACTTAC 1959
Qy 1087 ThrGluValValThrGluPheGlyThrGluValGluProGluPheGlyThrLysValGlu 1106
Db 1960 ACAGAGTGTGTGACAGAAATTTGGGACCGAGTGTGACCCGAGTTTGGGACCAAGGTGAA 2019
Qy 1107 ProGluPheGluThrGluLeuGluProGluPheGluThrGluLeu 1121
Db 2020 CCGGATTTGAAACCAAGTTGAGGCTTGAAGTTTGAACCTACTG 2063

RESULT 5
US-11-266-748A-192179
; Sequence 192179, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266, 748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662, 276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700, 293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 192179
; LENGTH: 2065
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc. feature
; LOCATION: (1822)..(1884)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-192179

Alignment Scores:
Pred. No.: 5, 95e-163 Length: 2065
Score: 3421.00 Matches: 647
Percent Similarity: 95.9% Conservative: 0
Best Local Similarity: 95.9% Mismatches: 28
Query Match: 54.5% Indels: 1
DB: 8 Gaps: 0

US-10-642-946-3 (1-1158) x US-11-266-748A-192179 (1-2065)

Qy 447 AspThrArgArgThrThrArgPheThrGlyValIleThrGlnGlyValArgAspSerIle 466
Db 40 GACACCGAGAGGAGCTACCGGTTACAGGCGTATCACCAGGCGAGACTTCACACTC 99
Qy 467 HisAspAspPheValThrThrPhePheValGlyPheSerAsnAspSerGlnThrTrpVal 486
Db 100 CATGACGATTTTGTGACCACTTCTTGTGGGCTTCAGCAATGACGACCATGAGTGGTG 159

QY 487 MetTyrThrAsnGlyTyrGluGluMetPheHisGlyAsnValAspLysAspThrPro 506
 DB 160 ATGTACACCAACGAGCTATGAGAAATGACCTTTCATGGAGACGTGACAAAGACACACCC 219
 QY 507 ValLeuSerGluLeuProGluProValValAlaArgPheIleArgIleTyrProLeuThr 526
 DB 220 GTGGTAGAGGAGCTCCAGAGCGGGTGGTGGCTCGTTTCATCCGATCTACCACTCACCC 279
 QY 527 TrpAsnGlySerLeuCyMetArgLeuGluValLeuGlyCySerValAlaProValTyr 546
 DB 280 TGGAAATGGCAGCCTGTGCTATGGCCCTGGAGGTGCTGGGGTCTCTGTGGCCCCCTGTCTAC 339
 QY 547 SerTyrTyrAlaGluAsnGluValValAlaThrAspAspLeuAspPheArgHisSer 566
 DB 340 ACCTACTACGACACAAATGAGGTGGTGGCCACCGAGTACCTGATTTCCGGACACACAGC 399
 QY 567 TyrLysAspMetArgGluMetLysValValAsnGluGlyCySerProThrIleThrArg 586
 DB 400 TACAAAGACATGCGCAGCTCATGAAAGTGTGAAGAGAGAGTGGCCCCCATCACCCGC 459
 QY 587 ThrTyrSerLeuGlyLysSerSerArgGlyLeuLysIleTyrAlaMetGluIleSerAsp 606
 DB 460 ACTTACAGCCTGGGCAAGAGCTCACAGAGCCTCAAGATCTATGCCATGAGATCTCACAGC 519
 QY 607 AsnProGlyGluHisGluLeuGlyGluProGluPheArgTyrThrAlaGlyIleHisGly 626
 DB 520 AACCCCTGGGAGACATGAACTGGGGGAGCCCGAGTTCCGCTACACGTGGGATTCATGGGC 579
 QY 627 AsnGluValLeuGlyValArgGluLeuLeuLeuLeuMetGluTyrLeuCySerArgGluTyr 646
 DB 580 AACGAGGTGCTGGGCGAGAGAGCTGTGTGCTGCTCATGACAGTACTGTGCCGAGATAC 639
 QY 647 ArgAspGlyAsnProArgValArgSerLeuValGluAspThrArgIleHisLeuValPro 666
 DB 640 CCGCATGGGAAACCAAGTGTGGCAGCTGTGTGCAGACACACGACATCCACTGGTGGCC 699
 QY 667 SerLeuAsnProAspGlyTyrGluValAlaAlaGluMetGlySerGluPheGlyAsnTyr 686
 DB 700 TCACTGAACTCTGATGGCTACAGAGTGGCAGGCGCAGATGGCTCAGAGTTGGGAACTGG 759
 QY 687 AlaLeuGlyLeuTyrPheGluGluGlyPheAspIlePheGluAspPheProAspLeuAsn 706
 DB 760 GGGCTGGGAGCTGTGGAGCTGAGGAGGGCTTTGACATCTTGAAGATTTCCCGGATCTCAC 819
 QY 707 SerValLeuTyrGlyValaGluGluValArgIleTyrValProAsnAsnAsn 726
 DB 820 TCTGTGCTCTGGGAGCTGAGGAGAGAAATGGGTCCCTACCGGGTCCCAACATATAC 879
 QY 727 LeuProIleProGluArgTyrLeuSerProAspAlaThrValSerThrGluValArgAla 746
 DB 880 TTGCCCATCCCTGAAAGCTACCTTTTGGCAGATGCCAGGTATCCAGAGGTCCGGGCC 939
 QY 747 IleIleValIleTyrMetGluLysAsnProPheValLeuGlyAlaAsnLeuAsnGlyGlu 766
 DB 940 ATCATTTGCTGGATGAGAAACCCCTTCGTGCTGGAGCAAAATCTGAACGGCGGCGAG 999
 QY 767 ArgLeuValSerTyrProTyrAspMetAlaArgThrProThrGluGluGluLeuAla 786
 DB 1000 CCGCTAATATCTTACCCCTACGATATGGCCCGACCCCTTACCCAGAGAGAGCTGTGGGCC 1059
 QY 787 AlaAlaMetAlaAlaAlaArgGlyLysAspGluAspGluValSerGluAlaGluGluThr 806
 DB 1060 GCGAGCATGACAGACCCCGGGGGAGATGAGAGAGAGTCTCCAGAGCCCGAGAGACT 1119
 QY 807 ProAspHisAlaIlePheArgTyrLeuValIleSerPheAlaSerAlaHisLeuThrLeu 826
 DB 1120 CCAAGACCAAGCATTTCCGGTGGCTTGCATCTCTTGGCTCCGACACCTCACTGCTG 1179
 QY 827 ThrGluProTyrArgGlyGlyCySerGluAlaGluAspTyrThrGlyLysMetGlyIleVal 846
 DB 1180 ACCGAGCCCTTACCGGAGGCTGCCAAGCCAGACTTACACCGCGGCAATGGCATCGTC 1239
 QY 847 AsnGlyAlaIleTyrAsnProArgThrGlyThrIleAsnAspPheSerTyrLeuHisThr 866

DB 1240 AACGGGCGCAATGGAAACCCCGAGCGGAGCTATCATATGACTTACGTTACTGCATAC 1299
 QY 867 AsnCyLeuGluLeuSerPheTyrLeuGlyCyAspLysPheProHisGluSerGluLeu 886
 DB 1300 AACTGCTGGAGCTCTCTTCTACTCTGGCTGTGCAAGTTCCTCATGAGAGTACGCG 1359
 QY 887 ProArgGluTyrGluAsnAsnLysGluValLeuLeuTyrPheMetGluGluValHisArg 906
 DB 1360 CCGCGAGTGGAGAAACAAGAGGGCTGCTACCTTCATGAGAGAGGTGACCGC 1419
 QY 907 GlyIleLysGlyValValThrAspGluGluGlyIleProIleAlaAsnAlaThrIleSer 926
 DB 1420 GGCATTAAAGGGGTGTGACGAGACAGAGCAATCCCATTTGCCAAGCCACATCTCT 1479
 QY 927 ValSerGlyIleAsnHisGlyValLysThrAlaSerGlyLysAspTyrTyrArgIleLeu 946
 DB 1480 GTGAGTGGCATTTAATCAAGCGGTGAAGACAGCACTGGTGGTGAATTACTGGCGAAATCTTG 1539
 QY 947 AsnProGlyGluTyrArgValThrAlaHisAlaGluGlyTyrThrProSerAlaLysThr 966
 DB 1540 AACCGGGTGGAGTACCGGTGAAGCCACCGGGAGGCTTACACCCGAGCGCCAAAGAC 1599
 QY 967 CyAsnValAspTyrAspIleGlyValaThrGluCyAsnPheIleLeuAlaArgSerAsn 986
 DB 1600 TGCATGTGACTATGACATCGGGGCCACTGACGTCACCTTATCTGCTGCTGCCAAC 1659
 QY 987 TrpLysArgIleArgGluIleMetAlaMetAsnGlyAsnArgProIleProHisIleAsp 1006
 DB 1660 TGGAAAGCCCTTCGGGAAATCATGTGCATGAACGGGAAACCGGCCTATCCACACATAGAC 1719
 QY 1007 ProSerArgProMetThrProGluGluArgArgLeuGluGluArgArgLeuHisArg 1026
 DB 1720 CCATGCGGCTTATATACCCCAACATGACGCTGTGCATCAGCGACGCTTACAAACCGC 1779
 QY 1027 LeuArgLeuArgAlaGluMetArgLeuArgArgLeuAsnAlaThrThrThrLeuGlyPro 1046
 DB 1780 CTGGCGCTTCGGGACAGATGTGGCTGGCGGCTCAACGCGNNNNNNNNNNNNNNNN 1839
 QY 1047 HisThrValProProThrLeuProProAlaProAlaThrThrLeuSerThrThrIleGlu 1066
 DB 1840 NNNAGCTACATATAG 1899
 QY 1067 ProTyrGlyLeuIleProProThrThrAlaGlyTyrGluGluSerGluThrGluThrTyr 1086
 DB 1900 CCTGGGCTCTATATCCGCAACACCGCTGCTGGAGAGATCCGAGCTAGACCTAC 1959
 QY 1087 ThrGluValValThrGluPheGlyThrGluValGluProGluPheGlyThrLysValGlu 1106
 DB 1960 ACAGAGGTGTGACGAATTTGGGACCGAGGTGGAGCCGAGTTTGGACCAAGGTGAA 2019
 QY 1107 ProGluPheGluThrGluLeuGluProGluPheGluThrGluLeu 1121
 DB 2020 CCCGA-TTTGAAACCAAGTTGAGCTTGAATTAACCTTACTG 2063

RESULT 6
 US-11-266-748A-98157
 ; Sequence 98157, Application US/11266748A
 ; Publication No. US2006013463A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harkin, Paul
 ; APPLICANT: Johnston, Patrick
 ; APPLICANT: Mulligan, Karl
 ; TITLE OF INVENTION: Transcriptome Microarray Technology and
 ; FILE REFERENCE: Methods of Using the Same
 ; CURRENT APPLICATION NUMBER: US/11/266,748A
 ; CURRENT FILING DATE: 2005-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105479.2
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105482.6
 ; PRIOR FILING DATE: 2004-11-03
 ; PRIOR APPLICATION NUMBER: EP 04105483.4

Dh 310 TTCTGCGCTTCAATGCATGAAGACCTTAGGGTGGAGGAGCAGAGAACGACGACCGCAC 369
Qy 351 GIUGLUThrAspIySTrPaIaValGIuLeGlyLyLeAspHisIySGLUPrOaRgLySGLy 370
Dh 370 CACACAGGCGCCACGAACTCCCAAGAACGACCATCAAGCCCAAGAAAGGCTCCCAAGAG- 426
Qy 371 GIUGLUTeUGLUGLUTrPTrProThrGluLys----- 382
Dh 427 GAGAACTTGTGCAGAGACCGCTCCACCGATMAAATAGCAACAGAAAAGCAGAGAA 486
Qy 382 ----- 382
Dh 487 AGCAAGATCTTGAAAGCTGCGACAGTATGATACCATGTGTGCTGTGCTCATAGAGAT 546
Qy 383 -----VallyeCySPPrOrolleGlyMeCgluSerHisIaRgIleGluAspAsnGlnIle 400
Dh 547 GTCAGAGAGAGTGGCCACTCTGTGTCTGTAACATTAATAATTCACAGACTTCACAGCTG 606
Qy 401 ArgAlaSerSerMetLeuArgHisIaGlyLeuGlyValaGlnArgGlyValaArgLeuAsnMetGln 420
Dh 607 CATGCTCCCACTCAAGAGCGTTATGGCTGGAGCCACCGGGAGAGACTCAACATTCAG 666
Qy 421 ThrGlyAlaThrGluAspAspTyrTyrAspGlyAlaIleTyrCyAsIaGluAspAspAlaArg 440
Dh 667 GCAGGCAATTAAAGAAATGACTTTTACAGATGGGGCTTGCTGTCTGTGTAGGAACGACTTG 726
Qy 441 ThrGlnTrpIleGluValaAspThrArgArgThrThrArgPheThrGlyValIleThrGln 460
Dh 727 CATCATGTGATCCAAAGGATGCGCCGCGCTGACCAAGTTCCACAGGGGCTCATTAACCA 786
Qy 461 GlyArgAspSerSerIleHisAspAspPheValThrThrPhePheValGlyPheSerAsn 480
Dh 787 GGAAGAACTCTCTGCTGCTGAGTACTGGGTGACATCTTAATAAGTCACTGTGAGCAAT 846
Qy 481 AspSerGlnThrTrpValMetTyrThrAsnGlyTyrGluGluMetThrPheHisGlyAsn 500
Dh 847 GACAGCCACACATGGGTACTGTGAAGAAATGGATCTGGCGACATGATATTGAAGGAAC 906
Qy 501 ValAspLyLeuAspThrProValLeuSerGluLeuProGluProValValaIaArgPheIle 520
Dh 907 AGTGAAGAGAGATCTCTGTGCTCAATGAGCTCCAGTCCCATGTGGGCCCTCAATT 966
Qy 521 ArgIleTyrProLeuThr-----AsnGlySerLeuCyMetArgLeuGluValIle 538
Dh 967 CGCATTAACCTCAAGTCTGTGTTTGAACGGAAGCATCTGCATGAGAGATGAGATCTTG 1026
Qy 539 GlyCySerValaIaProValTyrSerTyrTyr---AlaGlnAsnGluValaIaIaThr 557
Dh 1027 GGCTGCCACTGCGGATCTTAATACTATTATCACCGACGTAAAGATGAGACACACAG 1086
Qy 558 AspAspLeuAspPheArgHisIaSerTyrLyAspMetArgGluLeuMetLyValIaI 577
Dh 1087 GATGACTGATTTTAAAGCACCAACTTAAGAAATGCGCAGTTGATGAAGGTTGTC 1146
Qy 578 AasnGluGlyProThrIleThrArgThrThrTyrSerLeuGlyLySerSerArgGlyLeu 597
Dh 1147 AATGAATATGGCCCAATATTACAGAGATTACAGATTTGCAAAAGCCACAGGCGCTG 1206
Qy 598 LySleTyrAlaMetGluIleSerAspAsnProGlyGluHisGluLeuGlyGluProGlu 617
Dh 1207 AATTATTATGGGTAGATCTCTGACATCTCTGGGGAACATGAATGTGTGAGCCGAG 1266
Qy 618 PheArgTyrThrAlaGlyIleHisGlyAsnGluValaGluValaArgGluLeuLeuLeu 637
Dh 1267 TTCATATACATCCAGGGGCGCCACGCAATGAGGTTCTGGGAGCAAGAACTGCTGCTG 1326
Qy 638 LeuMetGlnTyrLeuCyAsnArgGlyTyrArgAspGlyAsnProArgValaIaArgSerLeuVal 657
Dh 1327 CTGTGCACTTCTCTGCGAGAACTCGGCCAGAGACGACGCACTGCTCGCTTGCTG 1386
Qy 658 GlnAspThrArgIleHisLeuValaProSerLeuAsnProAspGlyTyrGluValaIaIa 677
Dh 1387 GAGAGACTCGAATCCCACTTACCTCTCCATCTGATGTGCTATGAGAAAGGCTTAT 1446

Qy 678 GlnMetGlySerGluPheGlyAsnTrpAlaLeuGlyLeuTrpThrGluGluGlyPheAsp 697
Dh 1447 GAAAGAGGTTCCAGATTGGAGAGGCTGTCTCTGGAGCGTTGGACCATGATGACATCGAT 1506
Qy 698 IlePheGluAspPheProAspLeuAsnSerValIleTrpGlyValaGluGluArgLySTrP 717
Dh 1507 ATCAACAACTTCTCGAGATTAACTGCTGTCTGGAGGACAGACGACGAAAT 1566
Qy 718 ValProTyrArgValaProAsnAsnLeuProIleProGluArgTyrLeuSerProAsp 737
Dh 1567 GCCCAAGAGAGGTTCCCAACCACTACATTCGATCCATGAGTGTCTGTGTGAGAAAT 1626
Qy 738 AlaThrValSerThrGluValaArgAlaIleIleAlaTrpMetGluLyAsnProPheVal 757
Dh 1627 GCCACAGTGGCCACAGAACCAAGAGCGTCATGCTGTGATGAGAAATCCCGTTTGTG 1686
Qy 758 LeuGlyAlaAsnLeuAsnGlyGlyGluArgLeuValSerTyrProTyrAspMetAlaArg 777
Dh 1687 CTGGAGGCACTTCAAGGGGGGTGAGCTGTGTGCTGTGCAATCCCTATGACATGTGCGG 1746
Qy 778 ThrProThrGlnGluLeuLeuValaIaIaIaMetAlaIaIaArgGlyIuAspGlu 797
Dh 1747 TCCCTGTGAGAACCCAG----- 1764
Qy 798 AspGluValSerGluAlaGlnGluThrProAspHisAlaIlePheArgTrpLeuAlaIle 817
Dh 1765 -----GAGCACACCCCAACCTGATGATCATGTGTTCGCTGTGCGGTAT 1812
Qy 818 SerPheAlaSerAlaHisLeuThrLeuThrGluProTyrArgGlyGlyCySGLMaIaGln 837
Dh 1813 TCTTACGCTTCACTACCGCTCATGACAGAGTCCAGAGAGGGAGTGTCCACACGAA 1872
Qy 838 AspTyrThrGlyGlyMetGlyIleValaAsnGlyAlaIleTyrAspProArgThrGlyThr 857
Dh 1873 GATTTTCAGAGAGAGAGGACCGTCATATGGGCTTCTGTGACACAGAGGCTGAAGT 1932
Qy 858 IleAsnAspPheSerTyrLeuHisIaThrAsnCySLeuGluLeuSerPheTyrLeuGlyCyS 877
Dh 1933 CTAAAGATTTCACTCACTCCATCAACAACTGCTTGAAGTGTCCATCAACGTTGAG 1992
Qy 878 AspLyPheProHisGluSerGluLeuProArgGluTrpGluAsnAsnLySGLMaIaLeu 897
Dh 1993 GATTAATACCCACAGAGAGAGCTGCGAGAGAAATGGAGAAATACCGAGTCTCTG 2052
Qy 898 LeuThrPheMetGluGlnValaHisArgGlyIleLySGLyValaIaIaThrAspGluGlnGly 917
Dh 2053 ATTGTCTCATGGAGCAGGTTCTATGAGGCAATCAAGGATGTAGAGATTTACAGAG 2112
Qy 918 IleProIleAlaAsnAlaThrIleSerValSerGlyIleAsnHisGlyValySTrPaIa 937
Dh 2113 AAAGGATTTCAATGCTCTCATCTCTGTGAAGGTGTTAACCATGACATCCGAGACG 2172
Qy 938 SerGlyGlyAspTyrTrpArgIleLeuAsnProGlyGluTyrArgValaIaThrAlaIaIa 957
Dh 2173 AGGATGGGATTAAGTCTGCTCAAGAACCTGGGAAATATGTGTCAACGCAAGGCG 2232
Qy 958 GIUGLYTyrThrProSerAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 977
Dh 2233 GAAAGCTTATCACTTCCACCAAGAACTGCAATGTTGGCTATGATATGGAGTACTCG 2292
Qy 978 CyAsnPheIleLeuAlaArgSerAsnTrpLyArgIleArgGluIleMetAlaMetAsn 997
Dh 2293 TGTGACTTCACTTCCCAAGAACCAACCTGGCTAGGATTAAGAAATTTATGGAGCATTT 2352
Qy 998 GlyAsnArgProIleProHisIleAspProSerArgProMetThrProGlnGlnArgArg 1017
Dh 2353 GGAAGCAGCTGTGAGCTTA-----CCCTCAGG----- 2382
Qy 1018 LeuGlnGlnArgLeuGlnHisIaRgLeuArgLeuArgAlaGlnMetArgLeuArgArg 1037
Dh 2383 -----CGCTGGAAGCTGCGGAGCGAGCAAGAAAGCGGCGAGCT 2418


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QY 1038 LeuAaAlaThrThrThreuglyProHisThrValProProThreupProAlaPro 1057
Db 2419 GGGTAACTCTGCGAAGACCTTGAAGACATAC-----CCCAAGCCG 2457
QY 1058 AlaThrThreuserThrThrile 1065
Db 2458 TCGAAATATAAATCCACTCCAGTA 2481

RESULT 9
US-11-266-748A-192182
; Sequence 192182, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 192182
; LENGTH: 1437
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1065)..(1102)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-192182

Alignment Scores:
Pred. No.: 3,39e-89 length: 1437
Score: 1946.00 Matches: 365
Percent Similarity: 96.3% Conservative: 1
Best Local Similarity: 96.1% Mismatches: 14
Query Match: 31.0% Indels: 0
DB: 8 Gaps: 0

US-10-642-946-3 (1-1158) x US-11-266-748A-192182 (1-1437)
QY 779 ProThgIngluInleuAaAlaAlaMeValAlaAlaArgGlyGluAapGluAap 798
Db 28 CCCCCAAGAGAGAGAGCTGCTGGCGCAGCATGCGAGCAGCCCGGGGGAGATGAGAGC 87
QY 799 GluValSerGluAlaIngluThrProAapHisAlaIlePheArgTrpLeuAlaIleSer 818
Db 88 GAGGTTCGAGAGCCCGAGGAGACTCCAGACAGCAGCATCTTCGGTGGCTTGCCATCTCC 147
QY 819 PheAlaSerAlaHisLeuThrLeuThrGluProTyArgGlyGlyCysGluAlaGluAap 838
Db 148 TTGGCTTCGCGACACTCACTTGAACCGAGCCCTTACCGGAGGCTGCCAAGCCAGAC 207
QY 839 TyThrGlyGlyMetGlyIleValAlaangIyAlaLysTrpAsnProArgTrpThrile 858
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Db 208 TACACGGCGGCGATGGCGATCGTCAACGGGCGCAAGTGAAACCCCGGACCGGCGATATC 267
QY 859 AenAapPheSerTyThrLeuHisThrPasnCysLeuGluLeuSerPheTyLeuGlyCysAap 878
Db 268 AATGACTTCAGTACTCTCATACATACAGTCCCTGGGGCTCTCTTCTTACCTGGAGCTGTAC 327
QY 879 LysPheProHisGluSerGlyLeuProArgGluTrpGluAsnAlaIleGluAlaLeuLeu 898
Db 328 AAGTTCCTCATGAGAGTGAAGTGTGCGCGAGTGGAGAACACACAGAGGCGGCTGCTC 387
QY 899 ThrPheMetGluGluValHisArgGlyIleLysGlyValValThrAapGluInglYIle 918
Db 388 ACCTTCATGAGCAGAGTCAACCGCGCATTAAGGGGGTGTGTACAGCAGCAGAGCAGCATTC 447
QY 919 ProIleAlaAenAlaThrIleSerValSerGlyIleAsnHisGlyValLysThrAlaSer 938
Db 448 CCCATTGGCCAAAGCCACCATCTCTGTAGGTGCATTAAACAGGGGTGAAGACAGCCACT 507
QY 939 GlyGlyAapTyTrpArgIleLeuAapProGlyGlyTyArgValThrAlaHisAlaGlu 958
Db 508 GGTGTGATTAATGCGCAATCTTGAACCGGGTGAATACCGGCTGACAGCCACAGCGGAG 567
QY 959 GlyTyThrProSerAlaLysThrCysAenValAapTyAapIleGlyAlaThrGlyCys 978
Db 568 GGTACACCCCGAGCGCAAGACTGCAATGTGACTATGACATCGGGGCCACTCAGTGC 627
QY 979 AenPheIleuAlaArgSerAsnTrpLysArgIleArgGluIleMetAlaMetAangly 998
Db 628 AACTTATCTCGGTGCTGCTCCAACTGAAAGCCATCGGAGATCATGGCCATGAACGGG 687
QY 999 AenArgProIleProHisIleAapProSerAapPrometThrProGluInaArgLeu 1018
Db 688 AACGGGCTATCCACACATAGACCATCGGCGCTTATGACCCCAACAGAGGAGCGCTG 747
QY 1019 GInGluAlaArgGluGluHisArgLeuArgLeuAlaGluMetArgLeuArgArgLeu 1038
Db 748 CAGCAGCGACGGCTTCAACACCGCTGCGGCTTGGGACAGATCGGTGGCGGCGCTC 807
QY 1039 AenAlaThrThrThreuglyProHisThrValProProThreupProAlaProAla 1058
Db 808 AAGGCCACACACCTTAGGCCCCCACATGTGCTCCACCGCTGCCCTGCCCTGCC 867
QY 1059 ThrThrLeuSerThrThrIleGluProTrpGlyLeuIleProProThrThrAlaGlyTrp 1078
Db 868 ACCACCTGAGACATACATAGAGCCCTGGGGCTCATACGCCCAACACCGCTGGCTG 927
QY 1079 GluGluSerGluThrGluThrTyThrGluValValThrGluPheGlyThrGluValGlu 1098
Db 928 GAGGAGTCGAGACTGAGACTTACACAGAGGTGTGACAGAGTTGGAGCCGAGGTGAG 987
QY 1099 ProGluPheGlyThrLysValGluProGluPheGluThrGluLeuGluProGluPheGlu 1118
Db 988 CCCGAGTTTGGAGCCAGGTGAGGCCGAGTTTGAGACCAAGTTGAGGCTGAGTTTGAG 1047
QY 1119 ThrGluLeuGluProGluPheGluGluGluGluGluGluGluGluGluIleAla 1138
Db 1048 ACCCAGCTGGAACCCGAGTTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTAGCC 1107
QY 1139 ThrGlyGluAlaPheProPheThrThrValGluThrTyThrValAlaAapPheGlyAapPhe 1158
Db 1108 ACTGGCCAGGACTTCCCTTCAACAGTGAAGACCTTACAGAGTGAACCTTGGGAGCTTC 1167

RESULT 10
US-11-266-748A-226230
; Sequence 226230, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
```



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CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ. ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ. ID NO 226230
LENGTH: 1437
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1069)..(1102)
OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-226230

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Alignment Scores:

```

Pred. No.: 3,39e-89 Length: 1437
Score: 1946.00 Matches: 365
Percent Similarity: 96.3% Conservative: 14
Best Local Similarity: 96.1% Mismatches: 1
Query Match: 31.0% Indels: 0
DB: 8 Gaps: 0

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US-10-642-946-3 (1-1158) x US-11-266-748A-226230 (1-1437)

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QY 779 ProThrGlnGluGlnLeuLeuAlaAlaMetAlaAlaArgGluAerGluAer 798
    |||::|||
DB 28 CCCCCAAGAGAGAGAGCTGCGCGCGAGCCATGGAGACCCCGGGGGAGATGAGAG 87
QY 799 GluValSerGluAaGlnGluThrProAspHisAlaIlePheArgTrpLeuAlaIleSer 818
    |||||
DB 88 GAGGTCTCCGAGGCGCCAGAGACTCCAGACCGCATCTTCGCGTGGCTTGCATCTCC 147
QY 819 PheAlaSerAlaHisLeuThrLeuThrGluProTyrArgGlyGlyCysGlnAlaGlnAer 838
    |||||
DB 148 TTCGCTCCGACACCTGACCTTGACCGAGCCCTTACCGCGAGAGCTGCCAAGCCAGAGAC 207
QY 839 TyrThrGlyGlyMetGlyIleValAsnGlyAlaIleTyrAsnProArgTrpGlyTrpIle 858
    |||||
DB 208 TACACGGCGCGCATGGCGCATGTCACAGGGGCCAAGTGGAAACCCCGGACCGGAGCTATC 267
QY 859 AsnAspPheSerTyrLeuHisThrAsnCysLeuGlnLeuSerPheTyrLeuGlyCysAer 878
    |||||
DB 268 AATGACTTCAGTACCTGACATACCACTGCTGGGGCTCTCTTACCTGGGCTGTGAC 327
QY 879 LysPheProHisGluSerGluLeuProArgGluTrpGlnAsnAsnGlyGlyAlaLeuLeu 898
    |||||
DB 328 AAGTTCCTCATAGATGATGAGTGGCCCCCGAGTGGAGAAACAAGAGGGGCTGCTC 387
QY 899 ThrPheMetGluGlnValHisArgGlyIleLeuGlyValValThrAspGluGlnGlyIle 918
    |||||
DB 388 ACCTTCATGAGAGAGGAGCGACCGCGGATTAAGGGGGTGTGACGAGCAGAGAGCATC 447
QY 919 ProIleAlaAsnAlaThrIleSerValSerGlyIleAsnHisGlyValIleThrAlaSer 938
    |||||
DB 448 CCCATTTGCCAACCACCATCTCTGTGAGTGGCATTAATACCGCGGTAAGACAGCCAGT 507
QY 939 GlyGlyAspTyrTrpArgIleLeuAsnProGlyGluTyrArgValThrAlaHisAlaGlu 958

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DB 508 GGTGGCATTAATCTGGGAATCTTGAACCGGGAGAGTACCGCTGACAGCCAGCGGAG 567
QY 959 GlyTyrThrProSerAlaIleThrCysAsnValAspTyrAspIleGlyAlaThrGlnCys 978
    |||||
DB 568 GGTACACCCCGAGCGCGCAAGACTGCAATGTGACATGACATCCGGGGCCTCATGTGTC 627
QY 979 AsnPheIleLeuAlaArgSerAsnTrpLysArgIleArgGluIleMetAlaMetAsnGly 998
    |||||
DB 628 AACTCATCTGCTGCTGCTCAACTGAGCGCATCCGGGAGATCATGCTCATGAACCGGG 687
QY 999 AsnArgProIleProHisIleAspProSerArgProMetThrProGlnGlnArgGluLeu 1018
    |||||
DB 688 AACCGGCTATCCACACATAGACCATGCGGCTTATGACCCCAACAGGAGCCGCTTG 747
QY 1019 GlnGlnArgArgLeuGlnHisArgLeuArgLeuArgAlaGlnMetArgLeuArgArgLeu 1038
    |||||
DB 748 CAGCAGGAGAGCGCTTACACACCGCTGCGCTTCCGGGACAGATGGGCTGCGGCTTC 807
QY 1039 AsnAlaThrThrThrLeuGlyProHisThrValProProThrLeuProProAlaProAla 1058
    |||||
DB 808 AACGCCACACCAACCTAGGCCCCACACTGTGCTCCACAGCTGCCCTGCCCTGCC 867
QY 1059 ThrThrLeuSerThrThrIleGluProTyrGlyLeuIleProProThrThrAlaGlyTrp 1078
    |||||
DB 868 ACCACCTTGAGACTACCTACATAGAGCTTGCGGCTTATACCGGCAACCGCTGCTGG 927
QY 1079 GluGluSerGluThrGluThrTyrTrpGluValValThrGluPheGlyThrGluValGlu 1098
    |||||
DB 928 GAGGATCTGGAGACTAGACTACACAGAGTGTGTACAGAGTTGGAGCCGAGGTGGAG 987
QY 1099 ProGluPheGlyThrTyrValGluProGluPheGluThrGlnLeuGluProGluPheGlu 1118
    |||||
DB 988 CCGGAGTTGGGACCAAGGTGAGCGCGGCTTGAAGACCACTGAGCTGAGTTGAG 1047
QY 1119 ThrGlnLeuGluProGluPheGluGluGluGluGluGluGluGluGluGluGluIleAla 1138
    |||||
DB 1048 ACCGAGCTGAGACCGAGTTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTAGCC 1107
QY 1139 ThrGlyGlnAlaPheProPheThrThrValGluThrTyrThrValAsnPheGlyAspPhe 1158
    |||||
DB 1108 ACTGGCGAGGCAATTCCTTTCACACAGTAGAGACTACAGTAGAATTGGGAGCTTC 1167

RESULT 11
US-11-242-505A-22
Sequence 22, Application US/11242505A
Publication No. US20060099656A1
GENERAL INFORMATION:
APPLICANT: Carroll, Joseph M.
TITLE OF INVENTION: Method and Compositions for Treating
TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
FILE REFERENCE: MP1001-288P1CPIOMINM
CURRENT APPLICATION NUMBER: US/11/242,505A
CURRENT FILING DATE: 2005-10-03
PRIOR APPLICATION NUMBER: US 10/290,078
PRIOR FILING DATE: 2002-11-07
PRIOR APPLICATION NUMBER: US 60/347,949
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: US 10/320,351
PRIOR FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: 60/341,606
PRIOR FILING DATE: 2001-12-17
NUMBER OF SEQ. ID NOS: 48
SOFTWARE: FastSeq for Windows Version 4.0
SEQ. ID NO 22
LENGTH: 2452
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-242-505A-22
Alignment Scores:

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Pred. No.:	1,99E+78	2452
Score:	1735.50	368
Percent Similarity:	59.45	117
Best local Similarity:	45.04	228
Query Match:	27.74	106
DB:	8	16
	Gaps:	106

US-10-642-946-3 (1-1158) X US-11-242-505A-22 (1-2452)

Oy	25	ArGArglnuYgeInlProArGProFo	-----	255
Db	9	CGCCCCCGCGGTAGCCCGCGCCCTTGCACTCAATCCCGCATGTGGGGCTCTGC		68
Oy	260	-----ProSerArgArgArgArgProGluArgValTrp	-----	270
Db	69	TCGCGCTGCGCGCTTGGCGCGCGCGTGGCGCCGGCTCTGGGGGCGCCAGAACTGG		128
Oy	271	-----ProGluProProGluGluYbAla--ProAlaProAlaPro	-----	285
Db	129	TGCTGGGCGCTCGCGAGCCCGGGAGCACCAAGTCCAGAGCTCGACCCCGGCTTGATA		188
Oy	284	GlUGluArgIleGluProValYbPProLeuLeuProProLeuProProAspTyrGly		303
Db	189	GCAAGCCCGGCA-CAGCCGCGCGGAGACAGCT		220
Oy	304	AspGlyTyrValIleProAsnTyrAspAspMetAspTyrTyrPheGlyProProProPro		323
Db	221	-----AACGGAGCCTCAGAAACAG		238
Oy	324	GlnuYbProAspAlaGluArgIlnTrpAspGluGluYbGluGluLeuYbLyseProLyb		343
Db	239	CAGGT-CCGGATTTCAGTCACTAA-----GAAGAAAAAGTCATTATGAAGAAAGCCGAA		291
Oy	344	LyseGluAspSer---SerProLybGluGluGluTrpAspLybTrpAlaValGluYbGlyLyb		362
Db	292	GAACTTAACCTTAATCTGGCCCCACCCCACTGGTACTGCGGGGCCCTTGTGACCCAC		351
Oy	363	AspHisLybGluProArg-LybeGlyGluLeuGluGluGluGluTrpTrpProthrguLy		382
Db	352	TCACAGACGGGACCTCGACCCGCGTAGAA-----CAAGA		387
Oy	382	SValYbCybProProIleGlyMetGluSerHisArgIleGluAspAsnGlnIleArgAl		401
Db	388	AACAGCGTGCCTCTTGGGTCTGAGAGTCCCTGGAGATTTCAGATACCGGCTTGAGGC		447
Oy	402	AspSerMetLeuArgHisGlyLeuGlyValaGlnArgGlyArgLeuAspMetGlnTrnG		422
Db	448	ATCCAGAGACCCAGCTCTTGGTCTTGACCAACCGAGAGCGGCTCAACATTCAGTCAAG		507
Oy	422	YAlaTrhGluAspAspTyrTyrAspGlyValaTrpCybAlaGluAspAspAlaArgTrnG		442
Db	508	CTGGAGAGAGGGGATCTATATATATGAGAGCGTGTGTCTGAGAGCAAGAGCGGATCC		567
Oy	442	nTrpIleGluValAspTrhArgArgTrhTrhArgPheTrnGlyValIleTrnGlnGlyAr		466
Db	568	ATGGTTTCAGGTGAGCGCTGGGACCCACCCGCGCTTCGGGTGTATTATCACAGGGGAG		627
Oy	462	GAspSerSerIleHisAspAspPheValTrhTrpPhePheValGlyPheSerAspAspSe		482
Db	628	GAACTCTGTCTGAGAGTATGACTGGGTACATCATCATCAAGATCCGATTCAGCATGACAG		687
Oy	482	rGlnTrhTrpValMetTyrTrhAsnGlyTyrGluGluMet-----ThrPheHisGlyAs		500
Db	688	TCGGAACCTGGTGGGAAATGAGAAACACAGACGTGGGATGAGACGAGATTTTCTCGCAA		747
Oy	500	nValAspLybAspTrhProValLeuSerGluLeuProGluProValValAlaArgPheI		520
Db	748	TTTCAGACCCAGAAATCTCAATGCTGAACCTCTGCGGAGCCCGAGTGGCCGCTTCAT		807
Oy	520	eArgIleTyrProLeuTrp-----AsnGlySerLeuCybMetArgLeuGluValLe		538
Db	808	TCGGCTCTGCGCCAGACCTGGCTTCAGAGGAGCGGCGCTTACCTTCGCGGAGAGATCT		867

QY	538	IGLYGSeSerValaIaProValaTyTSeTyTylValaInSeIngluValaI--AlaTh	557
Db	868	GCCCTGCCCACTCTCAKACCCCAATGACCTATCTTTAGAGCCCTCGCTGGAGTCCG	927
QY	557	rAspAseLeuAsePheArgHsiASeTyTylAsePheCaArgInLeuMetLeuValA	577
Db	928	TGACCCCTTAGACTTTCCAGCATCTCAATTACAAGCCATGAGGAAGCTGATAMACAGGT	987
QY	577	lAsnIngluCyAseProThrIleThAArgThTyTSeTleuIngluTyTSeSeSerAglYle	597
Db	968	ACAAGAACAATGCCCAACAATACCCGCATCTACAGCATTTGGAGAAAGCTACCAAGCCT	104
QY	597	uLysIleTyAlawetGluIleSeAseAseAseProGlyGluHsiIngluLeuGlyProG1	617
Db	1048	GAAAGCTGATGATGAGAAATGTCGGAACAAGCTGGGAGAGCATGAGCTGGGGAGCTTGA	1108
QY	617	uPheArgTyThrAlaGlyIleHsiAglValaIngluYArgGlyuLeuLeuLeuLeu	637
Db	1108	GATGGCTACAGTGGCTGACATGCAATGGGAACAAGCCCTGGGGGGGGAGTTGCTTGCT	1168
QY	637	uLeuMetGlnTyTleuCyAArgGluTyTArgAsePylAseProAArgValAArgSerLeuA	657
Db	1168	CCTGATGCAAGTTCCGTGTCGATGATGCTCTGGAGAGAACCCAGGGGTGACCCGGCTGT	1228
QY	657	lGlnAsePThrArgIleHsiAgluValProSerLeuAseProAsePylTyTgluValAlAl	677
Db	1228	CTCTAGAGATGGCATTTCACTGTGCTCCCTCCATGAACCTGATGGCTGTGAATGCGCTA	1288
QY	677	agInMetGlySerGluPheGlyAsePThrAlaleuGlyLeuTyTThrIngluGlyPheA	697
Db	1288	CCACCGGGGTTCAGAGCTGTGGGTGGGCGGAGGGCCGCTGGAACAACCAAGACATCA	1348
QY	697	pIlePheGluAsePheProAsePLeuAseSerValleuTyTglYAlaIngluYArgTyT	717
Db	1348	TCTTAACCATTAATTTTGTGCACTCAACAACCACTGTGGAGACAGACAGATGGGA	1408
QY	717	pValProTyTArgValProAseAseAseLeuProIleProGluArgTyTleuSerProA	737
Db	1408	GATGCCCAATCGTCCCAACATACCTGCACTTGCCACTTACTACACCTTGCCAA	1468
QY	737	pAlaThrASeSerThrgluValArgAlaIleIleAlaTyMetGluTyTAsnProPheA	757
Db	1468	TGCCACCGGTGCTGTAAGCGGGAGATATCAAGTGAATGAAGCGGATCCCTTTGT	1528
QY	757	lLeuGlyAlaAseLeuAseInglYleGluArgLeuValSerTyTProTyTAspMetAlAr	777
Db	1528	GCTAAGTGCACACTCCACAGGGGGAGCTCGTGTGTCTTACCAATTTGACATGACTGG	1588
QY	777	gThyrProThrgIngluInleuLeuAlaAlaIleMetAlaAlaIleArgGlyuAseP1	797
Db	1588	CACCCCGTGG-----GCTGCCCG-----1608	1608
QY	797	uAsePgluValSerGluAlaIngluThTyTProAseP1AlaAlaIlePheArgTyTleuAlaI	817
Db	1607	-----GAGCTCACGCCCAACCAAGATATGCTGTGTTCCTGCTGCTCAGCAC	1657
QY	817	eSerPheAlaSerAlaHsiAseThleuThrgInuProTyTArgGlyGlyCyGluAlaIaG1	837
Db	1654	TCTTATGCTGGCAATTAATCTGGCCATAGAGACACCAAGCCCGCACTTGCCACAGCA	1714
QY	837	nAsePylThrgIyGlyMetGlyIleValAseGlyAlaIaTyTAsnProAArgThrgIyTh	857
Db	1714	GGACTTTCCCGTGGCAAGGAAATCATCATCAAGGGGCTGACTGGCACAGGTCCCGGGAG	1774
QY	857	rIleAseAsePheSerTyTleuHsiThTyAseCyAleuGluAseSerPheTyTleuGlyCy	877
Db	1774	CATGATATGCTTCACTACATCAACAACAACGCTTTAGAGTCACTGTGGAGCTGTCTG	1834
QY	877	sAspTySPhPeProHsiAgluSerGluAseProArgInuTyTpgIuAseAseIngluAlaIe	897
Db	1834	TACACAAGTTCCTCAACGAAGAATGCTGCCCAAGAGTGGAGAACACAAGAAGCCCT	1894
QY	897	uLeuThrPheMetGluInValHsiAArgGlyIleLeuGlyAlaValThAsp--GluG1	916

OY	271	-----ProGluProProGluGluVala---ProAlaProAlaProGluGluValaG	286
Db	86	TCGCGCAAGCCCGGAGACACCAAGTCTCCAGGCTCCAGCCCGGCGCATACAGCCCGG	145
OY	287	IIeGluProProValIysProLeuLeuProProLeuProProAspTyrGlyAspGlyTyr	306
Db	146	CA-CAGCGCCCGGCGGAGACACT-----	168
OY	307	ValIleProAsnTyrAspAspMetAspTyrTyrPheGlyProProProGluGluValPro	326
Db	169	-----AACGGAGCCCGAGAACAGCATGT-CCG	194
OY	327	AspAlaGluArgGlnThrAspGluGlyValGluGluLeuValLysProLysIleGluAsp	346
Db	195	GATTGAGATCATCAA-----GAGAGAAAAGGTATTATGAGAGAAAGCGGAAAGCATAC	248
OY	347	Set-----SerProLysGluGluGluThrAspLysTTPAlaValGluLysGlyLysAspHisLys	365
Db	249	TCTAACTGCCCCACCCACCTGATGATCTCCGGGCCCCCTTGACCCCCCATCCAGCAGG	308
OY	366	GluProArg-LysGlyGluGluLeuGluGluGluGluGluGluTTPThrProThrGlnValLysCy	385
Db	309	GACCCCTGACCCCGCGTGAATA-----CAAGAAACAGCGTG	344
OY	385	aProProIleGlyMetGluSerHisArgGlyLeuAspAsnGlnIleArgIleSerSerIle	405
Db	345	TCTCTCTTGGGTCTGAGATCCCTCGAGATTTCAGATACCCGGCTTGAGGCATCCAGCAG	404
OY	405	CLeuArgHisGlyLeuGluValGluLysArgGlyLysArgLysMetGlnThrGlyValAlaThrGly	425
Db	405	CCAGTCTCTTGGTCTTGACACACCCGAGACCGCTCAACATTCAGTCAAGCTGAGGAGA	464
OY	425	uAspAspTyrTyrAspGlyAlaTTPCyValIleGluAspAspAlaArgThrGlnTTPIleGly	445
Db	465	CGGCGATCATATGATGATGAGCCTGCGTCTCTAGAGACAGACCCCGCATTCATGGTTTCA	524
OY	445	uValAspThrArgArgThrThrArgPheThrGlyValIleThrGlnGlyArgAspSerSe	465
Db	525	GGTGACCGCTGGGCAACCCACCGCTTCTCGGGTGTATCACACAGGCGAGGAGACTGTGT	584
OY	465	rIleHisAspAspPheValThrThrPhePheValGlyPheSerAsnAspSerGlnThrTr	485
Db	585	CTGAGGATGATGCTGGGTCACTATCAACAGGTTCAGTTCACAGCAATGACAGTCGAGCTCG	644
OY	485	rValMetTyrThrAsnGlyTyrGluGluMet-----ThrPheHisGlyAspValAspLys	503
Db	645	GTCGGGAGATGAGAACACACAGCAGGGGATGAGACGAGATTCTCTCCCAATTCAGACCC	704
OY	503	aAspThrProValLeuSerGluLeuProGluProValValAlaArgPheIleArgIleTyr	523
Db	705	AGAAGCTCCAGTCTGAGAACCTCTCTCCGGAGCCCAAGGTGGCCGCTTCATTCCGCTGT	764
OY	523	rProLeuThrTrp-----AsnGlySerLeuLysMetArgLeuGluValLeuGlyCysSe	541
Db	765	GCCCCAGACCTGGCTCCAGGAGGGCGGCTTGCTCCGGGCGAGATCTCGGCTGCCC	824
OY	541	rValAlaProValTyrSerTyrTyrAlaGlnAsnGluValVal---AlaThrAspAspLe	560
Db	825	AGTCTCAACCCCAATGACATATCTCTTGAGGCCCTCGCTGGATCTCTTGACCCCTT	884
OY	560	uAspPheArgHisHisSerTyrLysAspMetArgGlnLeuMetLysValValAsnGluGly	580
Db	885	AGACTTTCAGCATCACAATTACAGAGCCATGAGAGCGTATGAGAGCAGGTACAAGAGA	944
OY	580	uCyAspThrThrIleThrArgThrTyrSerLeuGlyLysSerSerArgGlyLeuLysIleTyr	600
Db	945	ATGCCCAACATCACCCCGCATCTACAGCATTTGGAGAAAGCTACACAGGCGCTGAACTGTA	1004
OY	600	rAlaMetGluLysSerAspAsnProGlyValHisGluGluGlyValProGluLysPheArgTyr	620
Db	1005	TGTGATGAGAAATGTCTGCGACAGCTCTGGGAGCATATAGCTGGGGGAGCTTGAGTGGCTTA	1066
OY	620	rThrAlaGlyIleHisGlyAsnGluValLeuGlyValArgLeuLeuLeuLeuMetGly	640

Db	1065	CGTGCCTACACATGCATGGGAAAGAGGCCCTGGGGGGGAGTTGCTTGCCTCGATATGCA	1124
Qy	640	nTYrIeuCySaArggluTYrArGAspGlyAsnProArGValArGserIeuValGlnAspTh	660
Db	1125	GTTCTGTGCGCATGAGTCTCTGCGAGGAGAACCCACGGGTGACCCGGCTGCTCTTGAGAT	1184
Qy	660	rArgIleIbIeuValProSerIeuAsnProAspGlyTYrGluValAlaIaGlnMetG1	680
Db	1185	GGGCATTCACCTGCTGCCCTCATGGAACCTGATGGCTATGAGATGCGCTACACACCGGG	1244
Qy	680	ySerGluPheGlyAsnTPAlaLeuGlyLeuTYrThrGluGluGlyPheAspIlePheG1	700
Db	1245	TYCAAGCTGGTGGGCTGGGCGCGGCGCTGGAACAACACAGAGCATCGATCTTAACA	1304
Qy	700	uAspPheProAspIeuAsnSerValIeuTYrGlyValAlaGluGluuArgysTYrValProTY	720
Db	1305	TAATTTTCTGACCTCAACACACACCATGTGGGAAGCACAGGACATGGGAAGTGGCCCA	1364
Qy	720	rArgValProAsnAsnIeuProIleProGluuArgTYrIeuSerProAspAlaTrnVa	740
Db	1365	CATGCTCCCAACCATATCATCGGCATTTGCCACTTACTACACCTGGCCCATGGCACCGT	1424
Qy	740	ISeThrGluValArgAlaIleIleAlaTYrMetGluYsaSnProPheValIeuGlyAl	760
Db	1425	GGCTCTGTAAACGGGGGAGTAAATCAAGTGAAGAGCGAGATCCCTTTGTGCTAAGTGC	1484
Qy	760	aAsnIeuAsnGlyGlyuArgLeuValSeTYrProTYrAspMetAlaArgThProTh	780
Db	1485	CAACTCCACGAGGGGTGAGCTGGTGGTCTTACCATTGCAACATGACTGCACCCCGTGG	1544
Qy	780	rGlnGluGlnIeuIeuAlaAlaIeMetAlaAlaIaArgGlyGluAspGluVa	800
Db	1545	G-----GCTGCCCG-----	1554
Qy	800	ISeGluAlaGlnGluThrProAspHisAlaIlePheArgTYrIeuAlaIleSerPheAl	820
Db	1555	----GAGCTCAGCCCAACACAGATGATGCTGTGTTGCTGCTCAGCACTGCTCATGTC	1610
Qy	820	aSerAlaHisIeuThrIeuThrgluProTYrArgGlyGlyCyseGlnIaGlnAspTYrTh	840
Db	1611	TGGCAGTATCTGGCCATGCAGACACCAAGCCGCGAGCCCTGCCACAGCCAGACTTCTC	1670
Qy	840	rGlyGlyMetGlyIleValaGnglyAlaTYrTAsnProArgThrGlyThrIleAsnAs	860
Db	1671	CGTGCACGGCAACATCATCAACAGGGGCTGACTGCGACACCGTCCCCGGAGACATGATGA	1730
Qy	860	pPheSerTYrIeuHisrThrAsnCySLeuGluIeuSerPheTYrIeuGlyCySaAspIysPh	880
Db	1731	CTTCAGCTACCTACACACCAACTGCTTTAGAGTCACTGTGAGCTGTGTCGTGCAAGTT	1790
Qy	880	leProHisGluSerGluIeuProArgGluTYrGluuAsnIysGluValaIeuIeuThrPh	900
Db	1791	CCCTCACAGATATGAATTTGCCCGAGGTGGGAACAACAAGCCCTCTCCATCCTA	1850
Qy	900	eMetGluGlnValHisArgGlyIleYsglyValValIThrAsp---GluGlnGlyIlePr	919
Db	1851	CCTGAGCAGAGTGGCCATGGGCAATTGCAGAGTGTGTAGGACAAGAACAGACGAGCTTGG	1910
Qy	919	oIleAlaAsnAlaThrIleSerValSeGlyIleAsnHisGlyValIysThrAlaSerG1	939
Db	1911	GATGTCGTACGCTGTCAATTCGCGTGATGGGATTAACCATGACGTGACCAAGCGGTGGGG	1970
Qy	939	yGlyAspTYrTYrArgIleIeuAsnProGlyGluTYrArgValThrAlaHisAlaGluG1	959
Db	1971	CGGGGATTTATTTGGGTCTGTGACCCCAAGGAGCTAATGATGTGCTCCAGTGGCCGAGGG	2030
Qy	959	YTTrThrProSerAlaIysrThrCySaAsnValaAspTYrAspIleGlyAlaThrGlnCySaS	979
Db	2031	CTACCATTCAGATGACAGGAACGTTCGGGTACCTTTGAAGAAGGCCCCCTTCCCTTCCA	2090
Qy	979	nPheIleIeuAlaArgSerArnTYrIysArgIleArgGluIleMetAlaMetAsnGlyAs	999

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Qy 999 nArProileProHsilleAspProSerArpProMetThrProgIngnArGleuGl 1019
Db 2151 GGTGCC-----CCGAGCTTCCG----- 2169
Qy 1019 nGlnArGleuGlnHleArGleuArGleuArGln 1032
Db 2170 ----AGCGCTGGAG-----CGGCTAAAGGAGCAG 2196
RESULT 14
US-11-266-748A-226229
; Sequence 226229, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 226229
; LENGTH: 1184
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (780)..(813)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-226229
Alignment Scores:
Pred. No.: 1,42e-64 Length: 1184
Score: 1453.00 Matches: 272
Percent Similarity: 94.8% Conservative: 2
Best Local Similarity: 94.1% Mismatches: 15
Query Match: 23.2% Indels: 0
DB: 8 Gaps: 0
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Qy 890 TrpGluAsnAsnLygGluAlaLeuLeuThrPheMetGluGlnValHisArgGlyLeys 909
Db 72 TGGGAACAACAAGAGGCGCTGCTCACCCTTATGAGAGCGTGACCGCGCATTTAAG 131
Qy 910 GlyValValThrArpGluGlnGlyIleProIleAlaAsnAlaThrIleSerValSerGly 929
Db 132 GGGGTGTGACGAGCAGCAAGGCAATCCCATTCGCAACGCCACATCTCTGTGAGTGGC 191

Qy 930 IleAsnHisGlyValLyvThrAlaSerGlyIleArpTyrlTrpArgIleLeuAsnProGly 949
Db 192 ATTAAATCCGGCGGTGACAGACAGCCAGTGGTGTGATTCTGGCAATCTTGAAACCGGGT 251
Qy 950 GluTyrlArgValThrAlaHisAlaGluGlyTyrlThrProSerAlaLyvThrCyAsnVal 969
Db 252 GAGTACCGCGTACAGCCACGCGGAGGGGTACACCCCGAGCGCCAAAGCCTGCATGTT 311
Qy 970 AspTyrlArpIleGlyValThrGlnCyAsnPheIleAsnAlaArgSerAsnTrpLyvArg 989
Db 312 GACTATGACATCGGGGCGCACTTATTCATCTGTGCTGCTCCAACTGGAAAGCGC 371
Qy 990 IleArgGluIleMetAlaMetAsnLyvAsnArpProIleProHsilleAspProSerArg 1009
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Qy 1010 ProMetThrProgIngnArGleuGlnGlnArGleuGlnHleArGleuArGleu 1029
Db 432 CCTATGACCCCGCAACAGAGCGCTGCAGCAGCAGCCTTACACACCGCTCGGCTT 491
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Qy 1050 ProProThrLeuProProAlaProAlaThrThrLeuSerThrThrIleGluProTrpGly 1069
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Qy 1070 IleuIleProProThrThrAlaGlyTyrlGluGluSerGluThrGluThrTyrlGluVal 1089
Db 612 CTCATACCGCCCAACACCGCTGCTGGAGGAGTGGAGACTGAGAACCTTACACAGAGTG 671
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RESULT 15
US-11-266-748A-167870
; Sequence 167870, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcriptome Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: US/11/266,748A
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; PRIOR APPLICATION NUMBER: EP 04105507.0
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; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03


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; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 48396
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 167870
; LENGTH: 950
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (782)..(815)
; OTHER INFORMATION: n l s a, c, g, o r t
US-11-266-748A-167870
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Alignment Scores:

Pred. No.:	2,31e-63	Length:	950
Score:	1427.00	Matches:	275
Percent Similarity:	94.5%	Conservative:	1
Best Local Similarity:	94.2%	Mismatches:	13
Query Match:	22.8%	Indels:	3
DB:	8	Gaps:	0

US-10-642-946-3 (1-1158) x US-11-266-748A-167870 (1-950)

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QY      890  TrpGluAsnAsnLysGluValLeuLeuThrPheMetGluGluValHisArgGlyIleLys 909
       71  TGGGAGAACACAGAGGGGCGCTGCTCATCTTGAGAGCGAGTGACCGCGCATTAAG 130
QY      910  GlyValValThrAspGluGlnGlyIleProIleAlaAsnAlaThrIleSerValSerGly 929
       131  GGGGTGGTGAACGAGCAGCAGGAGGATCCCATTCGCAACCGCACCATCTGTGAGTGGC 190
QY      930  IleAsnHisGlyValLysThrAlaSerGlyGlyAspTyrTrpArgIleLeuAsnProGly 949
       191  ATTAAATCACCGCGTGAAGACAGCAGCGTGTGATTACTGCGCAATCTTGAAACCGCGGT 250
QY      950  GluTyrArgValThrAlaHisAlaGluGlyTyrThrProSerAlaLysThrCysAsnVal 969
       251  GAGTACCGCGTGAACGAGCAGGAGGCTTACACCGCAGCGCAGACCTGCAATGTT 310
QY      970  AspTyrAspIleGlyAlaThrGlnCysAsnPheIleLeuAlaArgSerAsnTrpLysArg 989
       311  GACTATGACATCGGGGCACTCAGTGCATTTCATCTGCTGCTCCACTGGAAGCGC 370
QY      990  IleArgGluIleMetAlaMetAsnGlyAsnArgProIleProHisIleAspProSerArg 1009
       371  ATCCGGGAGATCATGGCCATGAACGGGAAACGGGCTATCCACACATAGACCATCGCGC 430
QY     1010  ProMetThrProGlnGlnArgArgLeuGlnGlnArgArgLeuGlnHisArgLeuArgLeu 1029
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       491  CGGCGACAGATGGCGCTGCGCGGCTCAACGCCACACACCTAGGGCCCCCACTGT 550
QY     1049  LProProThrLeuProProAlaProAlaThrThrLeuSerThrTrileGluProTrpGlu 1069
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QY     1069  YLeu-IleProProThrThrAlaGlyTyrGluGluSerGluThrGluThrTyrThrGluVal 1089
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QY     1089  AlValThrGluPheGlyThrGluValGlu-ProGluPheGlyThrLysValGluProGlu 1108
       671  TGGTACACAGAGTTTGGGACCGAGGTGAGCCCGAGTTTGGGACCAAGGTGAGCCCGAG 730
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QY      1109  PheGluThrGlnLeuGluProGluPheGluThrGlnLeuGluProGluPheGluGlu 1128
       731  TTTGAGACCCAGTGTGGAGCTGTGAGTGTGAGACCCAGCTGGAACCGAGTTTNNNNNNNN 790
QY      1129  GluGluGluGluLysGluGluGluIleAlaThrGlyGlnAlaPheProPheThrTrVal 1148
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QY      1149  GluThrTyrThrValAsnPheGlyAspPhe 1158
       851  GAGACCTACACAGTGAACCTTGGGACTTC 880
Db
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Search completed: October 1, 2006, 00:15:22
Job time : 592 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: September 30, 2006, 23:48:23 : Search time 17677 seconds
(without alignments)
5494.817 Million cell updates/sec

Title: US-10-642-946-3

Perfect score: 6272
Sequence: 1 MAVRGAPLUSCLLALALC.....TGGAFFTYETVTNNGDF 1158

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame+.p2n.model -DEV=x1p
-O=/abes/ABSSMB.spool/US10642946/runat.29092006.125310.12521/app_query.fasta_1
-DB=EST -OPMT=faetap -SUFFIX=p2n.fst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abes06p
-USR=US10642946.OCGN_1.1.9528.0/runat.29092006.125310.12521 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-MAIN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:
1: gb_est1.*
2: gb_est3.*
3: gb_est4.*
4: gb_est5.*
5: gb_est6.*
6: gb_est7.*
7: gb_est8.*
8: gb_est9.*
9: gb_est10.*
10: gb_est11.*
11: gb_est12.*
12: gb_est13.*
13: gb_est14.*
14: gb_est15.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5081.5	81.0	3825	AK159377	Mus muscu
2	5081.5	81.0	3860	AK159409	Mus muscu
3	5077.5	81.0	3840	AK159330	Mus muscu
4	5077.5	81.0	3860	AK159342	Mus muscu

5	5075.5	80.9	3831	AK159957	AK159957 Mus muscu
6	5070.5	80.8	3831	AK159774	AK159774 Mus muscu
7	5009.5	79.9	3854	AK158276	AK158276 Mus muscu
8	4912	78.3	3224	DQ035090	DQ035090 Homo sapi
9	4096	65.3	2836	AK004712	AK004712 Mus muscu
10	2988	47.6	3211	DQ035091	DQ035091 Pan trogl
11	2074	33.4	3499	AK019509	AK019509 Mus muscu
12	2033.5	33.1	2237	DQ051196	DQ051196 Homo sapi
13	1925.5	30.7	2917	HSN805045	AL837372 Homo sapi
14	1789.5	28.5	2169	DQ051197	DQ051197 Pan trogl
15	1751	27.9	2169	AY418886	AY418886 Mus muscu
16	1738	27.7	2199	AY418884	AY418884 Homo sapi
17	1738	27.7	2297	CR621966	CR621966 full-leng
18	1712	27.3	1107	CR598691	CR598691 full-leng
19	1642	26.2	2024	AY418885	AY418885 Pan trogl
20	1603	25.6	936	AL533357	AL533357
21	1590	25.4	908	DV919324	DV919324 LB02915.C
22	1556	24.8	910	AL536370	AL536370
23	1540	24.6	880	DT817537	DT817537 LB0167.CR
24	1513	24.1	863	DT810893	DT810893 LB0163.C
25	1510	24.1	867	DT810026	DT810026 LB01610.C
26	1508	24.0	876	DV817015	DV817015 LB01721.C
27	1501	23.9	894	BQ884305	BQ884305 AGENCOURT
28	1483	23.6	844	DV926117	DV926117 LB0301.CR
29	1476	23.5	862	CD514819	CD514819 AGENCOURT
30	1457.5	23.2	1666	AK132611	AK132611 Mus muscu
31	1455	23.2	972	AL542558	AL542558
32	1452	23.2	834	DV916664	DV916664 LB0292.CR
33	1452	23.2	846	DV923633	DV923633 BX44373.C
34	1444	23.0	1006	BX444373	BX444373
35	1441	23.0	1004	B1410327	B1410327 602966604
36	1439.5	22.9	871	CD359998	CD359998 AGENCOURT
37	1434	22.9	822	DT810385	DT810385 LB01611.C
38	1419.5	22.6	836	BQ897584	BQ897584 AGENCOURT
39	1419	22.6	914	CD245277	CD245277 AGENCOURT
40	1414	22.5	841	BX102854	BX102854
41	1402	22.4	927	DV921162	DV921162 LB02924.C
42	1396	22.3	905	CR852604	CR852604
43	1391	22.2	867	DV768868	DV768868 ILLUMIN
44	1384.5	22.1	797	BM008065	BM008065 603617832
45	1380	22.0	820	B1769923	B1769923 603606192

ALIGNMENTS

RESULT 1	AK159377	3825 bp	mus musculus osteoclast-like cell cDNA, RIKEN full-length enriched library, clone:1420018014 product:AE binding protein 1, full insert sequence.
LOCUS	AK159377		
DEFINITION	AK159377.1	GI:74196951	
ACCESSION	AK159377		
VERSION	AK159377.1		
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	1	Carninci, P., Hayashizaki, Y., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)	
REFERENCE	2	10349636	
REFERENCE	3	Carninci, P., Shibata, Y., Hayashizaki, Y., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)	
REFERENCE	4	11042159	
REFERENCE	5	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,	

Komno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, S., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
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RIKEN Genome Exploration Research Group Phase II Team and the

FANTOM Consortium

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CONSRM
TITLE
JOURNAL PUBLISHED
REFERENCE
AUTHORS
The transcriptional landscape of the mammalian genome
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RIKEN Genome Exploration Research Group

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Direct Submission

Submitted (30-MAR-2004) Yoshinide Hayashizaki, The Institute of

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Exploration Research Group, RIKEN Genomic Sciences Center (GSC),

RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,

Kanagawa, 230-0045, Japan (E-mail: genome-research@riken.jp,

URL: http://genome-gsc.riken.jp/, Tel: 81-45-503-9222,

Fax: 81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.

Tissues were provided by Takashi Ishikawa (Department of Surgery

2 Yokohama City University 3-9 Fukuura, Kanazawa-ku, Yokohama

236-0004 Japan) whose assistance we gratefully acknowledge.

Please visit our web site for further details.

COMMENT

URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/

FEATURES

Source

Location/Qualifiers

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PSAGKSTVALETDLRLPSNPSAQLPKQKDTPPNMQGSETOVAKQK
PEPEEETEMPTLDNDIIEKEDYEDFEYIRKORPTPSRRRLMPERPEKKE
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EGSSPKEDTETDKTKVKNKDKHKGPKRGEELBESMAVEKIKCPGIMESHRIEDNOI
RASSMLRHGLGAQRGLNQAGNEDDYDGAMCADEDSQTIIEVTRTRTFGTGI

Alignment Scores:

Pred. No.:	0	Length:	3825
Score:	5081.50	Matches:	964
Percent Similarity:	87.6%	Conservative:	55
Best Local Similarity:	82.9%	Mismatches:	107
Query Match:	81.0%	Indels:	37
DB:	6	Gaps:	12

US-10-642-946-3 (1-1158) x AK159377 (1-3825)

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QY	21	ProGlyGlyArgProGlnThrValLeuThrAspAspGlnIleGluGluPheLeuGluGly	40
DB	257	CCAGAGGGGAACCCACAGAGGTCGTGACGACGACGATCAGAGGTTCTCGAAGGC	316
QY	41	PheLeuSerGluLeuGluProGlu-----ProArgGluAspAspValGluAlaProPro	58
DB	317	TTCCTTTCCGAGTTGGAGACCCAGTCCCGCCCGGGAAGACACGTGGAGTCCAGCCG	376
QY	59	ProProGluProThrProArgValArgValAlaGlnAlaGlyGlyProGlyLysArg	78
DB	377	CTTCCCGAACCCACCGCGCTCCCGCAATCCAGGCGAGGCGCAG-----	424
QY	79	ProGlyThrAlaAlaGluValProProGluGluThrLysAspLysGlyLysGlyLys	98
DB	425	CAGCGGGCAGATGTAGAGTCCCTCCGAGAAAAACAAAGAACAAAGAAAGAAAG	484
QY	99	LysAspLysGlyProLysValProLysGluSerLeuGlySerProArgProProLys	118
DB	485	AAGGACAAAGGCCCCCAAGGACCAAA-----CCCTGGAGGGCTTACCAAGGCCAC	541
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DB	662	AAGGCCACTAAGAGGCGCTCGGAGAGAAAGAACTCTCACTGGGCCCTTGAAAGC	721
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DB	782	GACACACCTTCCCAATGCTGCGCAAGGTCAAGAGAAAGAGCCAGGTGGAGCCAG	841
QY	219	GluHisGluProGluProGluGluGluThrGluGlnProThrLeuAspTyrAspAspGln	238
DB	842	CAGCCCGGCCCAAGGACAGAGAGAGATCGAGATCCCACTGAGCTACATGACAG	901
QY	239	IleGluArgGluAspTyrGluAspPheGluTyrIleArgArgGluLysGlnProArgPro	258
DB	902	ATAGAGAGAGGATTAACGAGGATTTTGATGATCATCCGTCGACGAGGCCAGGCCA	961
QY	259	ProProSerArgArgArgArgProGluArgValTyrProGluProProGluGluVal	278
DB	962	ACACCCAGCGAGG-----AGGCTGGCGAGAGCGCCCTGAGAGAAAGACT	1009
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QY	377	TyrThrProThrGluLysValLysCysProProIleGluMetGluSerHisArgIleGlu	396
DB	1301	TGGGCCGCTGTGAGAAATCAAGTGCACCTATTGGATGAGTCAACCCCATTTGAG	1360
QY	397	AspAsnGlnIleArgLaseSerMetLeuArgIleGlyLeuGlyAlaGlnArgGlyArg	416
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Db	1781	GTGCTAGGCTGCCCCGTTAACCCCTGCTCTACAGCTCTACGGACAGAAATGAGGTGGTAACT	1840
QY	557	ThiAspApeLeuAspPheArgH1sh1SerTyTyrLyAspMetArgGlnLeuMetLyseVal	576
Db	1841	ACTGACACGCTGGAACCTTCGGGACCCAGAGCTTACAAGAGCATGCGCCAGCTCATGAAAGGCT	1900
QY	577	ValaangluGluCyseProThrTllethrxArgThrTySerLeuGlyLyseSerArgGly	596
Db	1901	GTCAATGGAGGTGGTCCCAACAATCACTGGCACATACAGCTGGGGGAGAAAGTTCCAGAGGG	1960
QY	597	LeuLyseTleTyAlaMetGluLileSerAspAsnProGlyLuh1sgLLeuGlyGluPro	616
Db	1961	CTCAAGATCTACGCAATGGAATCTCAACAACTCTGGGAGTCAATGAATCTGGGGAGGCC	2020
QY	617	GluPheArgTyTThrAlaGlyTlle1sgLyangluValLeuGlyValArgGluLeuLeu	636
Db	2021	GAGTTCGCCCTCACAGCCGGGATCCACGGCATGAGGTGTAGGGCCGAGACTCTGCTC	2080
QY	637	LeuLeuMetGlnTyTLeuCyseArgGluTyTArgAspGlyAsnProArgValArgSerLeu	656
Db	2081	CTGCTCAATGACAAATACCTAATGCCAGGAGTAACCGCATGGGAAACCGAGAGTGGCAACTG	2140
QY	657	ValGlnAspThrArgTlle1shLeuValProSerLeuAsnProAspGlyTyTArgLyuValAla	676
Db	2141	GTGCAGGACACACGCATCCACTGGGTGCCCTCGCTGAACCTCGATGGCTTAGAGGTGGAC	2200
QY	677	AlaGlnMetGlySerGluPheGlyValAsnThrAlaLeuGlyLeuTyTThrGluGluGlyPhe	696
Db	2201	GCGCAGATGGGCTCAGAGTGTGGGAACCTGGGACTGTGGACTGTGAAGAGGGCTTT	2260
QY	697	AspTllePheGluAspPheProAspPheAsnSerValLeuTyTArgLyuValGluGluArgLys	716
Db	2261	GACATCTTCGAGGAACTTCCAGATCTCAACTCTGTGCTCTGGGACGCTGAGAGAGAA	2320
QY	717	TyrValProTyTArgValProAsnAsnAsnLeuProLleProGluArgTyTLeuSerPro	736
Db	2321	TGGGTCCCTTCAGAGGCTCCCAACAAATTAATCTTGCAATCCCTGAACCTTACTCTGCCCA	2380
QY	737	AspAlaThrValSerThrGluValArgLysTlleTlleAlaTyTMetGluLyseAsnProPhe	756
Db	2381	GATGCCAAGGCTCCACAGAAAGTCCGGGCCATTATTTCTGGATGGAGAAAGAACCCCTT	2440
QY	757	ValleuGlyAlaAsnLeuAsnGlyGlyGluArgLeuValSerTyTProTyTAspMetAla	776
Db	2441	GTGCTGGGTGCAAATCTGAACGAGTGTGAGCGGCTTGCTTTATCTTACCTTAGACATGGCC	2500
QY	777	ArgThrProThrGlnGluGluLeuLeuAlaAlaAlaMetAlaAlaAlaArgGlyGluAsp	796
Db	2501	CGGACCACTAAGCAGAGAGAGGTGTGGCCGAGGACCTGGGACGCTGGCCGGGAGAAAGAT	2560
QY	797	GluAspGluValSerGlyAlaGlnGluThrProAspH1saAlaTllePheArgTyrPheAla	816
Db	2561	GATGACGGGGGTGTCTGAGGCCAGGAACTCCAGATCAACGCTATTTTCGGTGGCTGGCC	2620
QY	817	TlleSerPheAlaSerAlaH1shLeuThrTleuThrGluProTyTArgGlyGlyCyseGlnAla	836
Db	2621	ATCTCATTTGCTTCGGCCATCTCAACATGAGGAGCCCTTACCGGGAGGGGTGCCAGGCC	2680
QY	837	GlnAspTyTThrGlyGlyMetGlyTlleValaanglyAlaLysTyTAsnProArgThrGly	856
Db	2681	CAGAGCTACACCAAGGGGATGGGCAATGTCAACGGGGCCAAAGTGAATCTCTGCTCTGGG	2740
QY	857	ThrTlleAsnAspPheSerTyTLeuH1shThrAsnCyseGluGluLeuSerPheTyTLeuGly	876
Db	2741	ACTTTCATATGACTTAACTACTGCACAAACTCTCGAGAGCTCTCCGTATTACTGGGC	2800
QY	877	CysAspLysPheProH1shGluSerGluLeuProArgGlyTyTArgLyuAsnAsnLyseGluAla	896
Db	2801	TGTGCAGAGTTCGCCACAGAGTGAAGTACCCCGAGATGGGAAACAAACAAGACGG	2860

Oy	897	Leu1eu1rhp1heme1gu1n1va1h1sa1rg1y1l1e1ye1gi1y1a1l1t1r1a1p1g1u1g1n1	916
Db	2861	CTGCTCACTCTTCATGAGACAGCGGTGCACCCGTGGCATTTAGAGGTGTGGTGCACAGATGACGA	2920
Oy	917	Gl1y1Le1Pro1le1a1a1na1a1a1r1h1le1Se1r1Va1Se1r1y1Le1a1n1h1S1g1y1a1l1y1e1Th	936
Db	2921	GGCATCCCACTTGGCCATTCGCACCATCTCTGTAGTGGCATCAACCATGTGTGAGACA	2980
Oy	937	Al1a1Se1r1y1G1y1a1r1P1y1r1T1r1P1a1g1l1e1u1a1n1P1r1G1u1y1r1A1r1g1V1a1l1T1r1A1h1S	956
Db	2981	GCAAGTGAAGGTGACTACTGAGCATTCCTAACCCTGGTAGTACCGTGGACAGCTTAC	3040
Oy	957	Ala1g1u1y1y1r1Th1r1P1r1o1Se1r1a1l1y1e1Th1Cy1a1n1a1l1a1S1r1y1a1r1P1l1e1g1y1a1l1a1Th	976
Db	3041	GCAGAGGGCTTACACCTGAAGTGCAGAGATCTGCAGATGTGACATACGATATTTGGGGCCACT	3100
Oy	977	Gl1nC1y1a1n1Phe1l1e1u1a1a1r1g1Se1a1r1T1r1y1a1r1g1l1e1a1r1g1u1l1e1m1e1a1m1e1	996
Db	3101	CAGGCAACTTCATCCCGGTCTGCATTCACACTGGAAAGCGCATTTGGGAGATCTTGGCATATG	3160
Oy	997	Aa1n1y1a1n1a1r1P1r1o1Le1P1r1o1h1a1l1e1a1S1P1r1o1Se1r1y1g1r1P1r1o1m1e1Th1r1P1r1o1G1n1a1r1g	1016
Db	3161	AACGGGAACCGTCCCATTTCTCCAGATTGACCCCTTCACAGACCCATGACCCCCACAGACGG	3220
Oy	1017	Arg1e1u1g1n1a1r1a1r1a1r1g1e1u1g1n1h1sa1r1g1e1u1a1r1g1e1u1a1r1a1g1n1e1r1a1r1g1e1u1a1r1g	1036
Db	3221	CGCATGCAAGACGCCCGCTCTACAGTACCGGCTCCGATGAGGAAACAGATGCGACTGCGT	3280
Oy	1037	Arg1e1u1a1n1a1r1Th1r1T1r1h1r1n1e1G1y1P1r1o1h1e1r1h1a1l1P1r1o1--P1r1o1Th1r1e1u1P1r1o	1055
Db	3281	CGCTCTCAATCTTACCGCA-----GGCCCTGCCACAGACCCCTACTCTTGCCTTAATGCT	3334
Oy	1056	Ala1P1r1o1a1l1a1r1Th1r1Le1u1Se1r1Th1r1l1e1g1u1P1r1o1T1r1P1y1e1u1l1e1P1r1o1Th1r1	1075
Db	3335	CCCCCTTCCCCCTTACACAGCATATTACTTAGAGGCCCTGGGAAGTTTCAACCATACCAT	3394
Oy	1076	Ala1e1y1T1r1P1r1o1G1u1S1e1r1G1u1T1r1G1u1Th1r1Ty1Th1G1u1Va1l1a1Th1r1G1u1P1h1e1g1y1Th	1095
Db	3395	GCAGAGCTGGAGAGGTAGACAGACTGACACTTACAGAGTAAGTACAGAGATT-----	3448
Oy	1096	Gl1u1Va1l1u1P1r1o1G1u1P1h1e1g1y1Th1r1y1Va1l1u1P1r1o1G1u1P1h1e1g1u1Th1r1G1n1e1u1G1u1P1r1o	1115
Db	3449	-----GAGACAGAGTATGGGACTGCACCTAGAGGTGAA-----	3481
Oy	1116	Gl1u1P1h1e1g1u1Th1r1G1n1e1u1G1u1P1r1o1G1u1P1h1e1g1u1G1u1e1g1u1G1u1y1S1g1u1G1u1	1135
Db	3482	GAGGTATGAG-----GAGACAGAGAGAGGAGGAGAGAGAGAA	3520
Oy	1136	Gl1u1Le1a1l1a1Th1r1G1n1a1l1a1P1h1e1P1r1o1P1h1e1Th1r1Va1l1G1u1Th1r1T1r1h1Va1a1n1P1h1e	1155
Db	3521	GAGATGACACAGGCTTACATTTCCATTTCACACAGATGAGACTTACACAGTAACTTT	3580
Oy	1156	Gl1y1a1r1P1h1e11158	
Db	3581	GGGAGACTTC3589	
RESULT 2			
AK159409			
LOCUS	AK159409	3860 bp	mRNA
DEFINITION	Mus musculus osteoclast-like cell cDNA, RIKEN full-length enriched	linear	HTC 21-SEP-2005
	library, clone:I420019106	product:AE binding protein 1, full insert	
		sequence.	
ACCESSION	AK159409		
VERSION	AK159409.1	GI:74197010	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;		
	Sciurionathi; Muridae; Murinae; Mus.		
REFERENCE	1	Carninci, P. and Hayashizaki, Y.	
AUTHORS	High-efficiency full-length cDNA cloning		
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Qy 477 GlyPheSerAenApeSerGlnThrTrpValMetYrThrAenGlyYrGluGluMetThr 496
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Db 1631 GGCTTCAGCAATGACACAGACCTGGGTGATGACCAATGGCTACGAGAAATACC 1690
Qy 497 PheH1eGlyAenAlyApeLyApeThrProValIleuSerGluLeuProGluProVal1 516
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Db 1691 TTCTATGAAATGTGACAAAGACACACTGTGTGACGAGCTCCCGAGCCAGTTGTG 1750
Qy 517 AlaApeHe1leAenGlyYrProLeuThrTrpAenGlySerLeuCyAenAlyGlu 536
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Db 1751 GCCGGTTTCATCCGCATCTATCCACTCAGATGGTGTGCTGTCCATGCGCTTGAG 1810
Qy 537 ValIleuGlyCySerVal1ApeProValYrSerYrYrAlyAenGluVal1A 556
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Db 1811 GTGCTAGGCTGCCCCGAGACCCCTGTCTACAGCTACGACGAATGAGGTGACT 1870
Qy 557 ThrApeAlyApeApeApeApeApeApeApeApeApeApeApeApeApeApeApe 576
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Db 1871 ACTGACAGCTGAGCTCCGACACACAGCTACAGAGACATGGCCGACGTGAGAGCT 1930
Qy 577 ValAenGluGlyCyProThr1leThrAlyThrYrSerLeuGlyYrSerSerAlyGly 596
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Db 1931 GTCAATGAGAGAGTCCCAACATCACTCGCACATACAGCTGGGCAAGATTCAAGAGG 1990
Qy 597 LeuYrGlyYrAlyAmetGlyIleSerApeApeProGlyYrGlyYrGluYrPro 616
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Db 1991 CTCAAGTCTACGCAATGAAATCTCAGACACCTGGGATCATGAACTGGGGAGACCC 2050
Qy 617 GluPheAlyYrThrAlyAlyIleH1eGlyAenGlyValIleuGlyAlyGluLeuLeu 636
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Db 2051 GAGTTCCGCTACACAGCCGGATCCACGGCAATGAGGTGTAGGCCGAGAGCTCTGCTC 2110
Qy 637 LeuLeuMetGlnYrLeuCyAlyGlyYrYrAlyApeGlyAenProAlyVal1AlySerLeu 656
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Db 2111 CTGCTCATGCAATACCTATGACAGAGTACCGCATGGAGAACCGAGACGTCCGACCTG 2170
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Db 2171 GTTCAGGACACAGCATCTCCTGTGTCTCCCTCGCTGAACCTGTAGCTATGAGTGGCA 2230
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Db 2231 GCCAAGATGGGCTCAGAGTTTGGGAACTGGGCACTGGGGCTGTGACTGAGAGAGGCTTT 2290
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Db 2291 GACATCTTCAGAGACTTCAGAGTCTCACTGTGTGTGGGACGCTGAGAGAGAGAA 2350
Qy 717 TrpValProYrAlyAlyProAenAenAenLeuPro1leProGluAlyYrLeuSerPro 736
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Db 2351 TGGGTCCCTACAGAGGTCCCAACAAATACCTGCAATCCCTGAACCTTACTGTCCCA 2410
Qy 737 ApeAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAly 756
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Qy 757 ValIleuGlyAlyAenAenAenGlyYrGlyAlyAlyAlyAlyAlyAlyAlyAlyAly 776
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Qy 777 ArgThrProThrGlnGluGluLeuLeuAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAly 796
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Qy 817 IleSerAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAly 836
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Qy 837 GluApeYrYrThrGlyMetGlyIleValAenGlyAlyAlyAlyAlyAlyAlyAlyAlyAly 856
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Db 2771 ACTTCATAGACTTGTAGCTACTGTGACACAACTGTGTGAGCTCCGATATACCTGGGG 2830
Qy 877 CysApeAlyApeApeApeApeApeApeApeApeApeApeApeApeApeApeApeApeApe 896
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Qy 897 LeuLeuThrApeMetGluGluVal1H1eAlyGlyIleYrGlyVal1AlyAlyAlyAly 916
    |||||
Db 2891 CTGCTACCTTCATGAGAGAGCTGACCGTGGCATTTAAGGTGTGTGACAGATGAGCA 2950
Qy 917 GlyIlePro1leAlyAenAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAly 936
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Qy 937 AlaSerGlyYrAlyApeYrTrpAlyIleLeuAenProGlyYrGluYrAlyAlyAlyAly 956
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Db 3131 CAGTGCAACTTCATCTCGGTGATCCCACTGGAACGCACTTGGGAGATCTTGAGCTATG 3190
Qy 997 AenGlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAly 1016
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Db 3191 AAGGGAACCGTCCATTCCTCCAGATGACCCCTCAAGACCCCAAGACCCCGAGAGCG 3250
Qy 1017 ArgLeuGlnAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAly 1036
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Db 3251 CGCATGACAGAGGCGCTCTACAGTACCGGCTCCGATGAGAGAAACAGATGCACTGGCT 3310
Qy 1037 ArgLeuAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAly 1056
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Db 3311 CGCCTCAATCTTACCGCA-----GGCCCTGCAAGACCCCACTGCTGCTTATGGCT 3364
Qy 1056 AlaProAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAly 1075
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Qy 1076 AlaGlyYrGluGluAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAly 1095
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Db 3425 GCAGGCTGGAGAGTCAAGAGTCAAGACTGAGACTTATACAGAAATGATGACAGATTT----- 3478
Qy 1096 GluValAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAly 1115
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Db 3479 -----GAGACAGAGATGAGGACTGACCTTACAGGTGAG----- 3511
Qy 1116 GluPheGluYrThrAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAly 1135
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Db 3512 GAGATGAG-----GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3550
Qy 1136 GluIleAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAly 1155
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Qy 1156 GlyApeAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAlyAly 1174
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Db 3611 GGGGACTTC 3619

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RESULT 3
AK159330
LOCUS
DEFINITION
AK159330 3840 bp mRNA linear HTC 21-SEP-2005
Mus musculus osteoclast-like cell cDNA, RIKEN full-length enriched
library, clone:1420016E21 product:AE binding protein 1, full insert
sequence.

- ACCESSION AKI59330
VERSION AKI59330.1 GI:74192986
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.
- REFERENCE
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636
- CONSORTM
TITLE
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AUTHORS
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Functional annotation of a full-length mouse cDNA collection
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Nature 420 (6915), 563-573 (2002)
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Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K.,

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COMMENT

FEATURES
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Direct Submission
Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gs.c.riken.jp, URL: http://genome.gs.c.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Takashi Ishikawa (Department of Surgery 2 Yokohama City University 3-9 Fukuura, Kanazawa-ku, Yokohama 236-0004 Japan) whose assistance we gratefully acknowledge.
Please visit our web site for further details.
URL: http://genome.gs.c.riken.jp/
URL: http://fantom.gs.c.riken.jp/
Location/Qualifiers
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CDS

Alignment Scores:

Pred. No.: 0
Score: 5077.50
Percent Similarity: 87.6%
Best Local Similarity: 82.8%
Query Match: 81.0%
DB: 6
Matches: 963
Conservative: 56
Mismatches: 107
Indels: 37
Gaps: 12

US-10-642-946-3 (1-1158) x AK159330 (1-3840)

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QY 21 ProGlyGlyArgProGlnThrValLeuThrAspAspGluIleGluGluPheLeuGluGly 40
DB 267 CTCGAGGGGAAACCCACGACGCTGCTGACGACGACGATCCAGAGTTCCTCGAAGGC 326
QY 41 PheLeuSerGluLeuGluProGlu-----ProArgGluAspAspValGluAlaProPro 58
DB 327 TTCCTTTCGAGTTGGAGACCGATCCCGCCCGGAGAAAGACGACGTAAGTCCAGCCG 386

QY 59 ProProGluProThrProArgValArgIysAlaGluAlaGlyIysProGlyIysArg 78
DB 387 CTTCCGAGACCCACCGACGCTCCCGAATCCAGGCGGGGCAAG----- 434
QY 79 ProGlyThrAlaAlaGluValProProGluIysThrIysAspIysGlyIysGlyIys 98
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QY 99 LysAspIysGlyProIysValPProIysGlySerLeuGluGlySerProArgProIys 118
DB 495 AAGGACAAAGGCCCAAGCCAAAGCAAAA---CCCTGAGGGCTCAAGGCCCAAG 551
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DB 1371 GACAAACCAATCCGCTCTCTCCATGCTGCGCACAGGCTTGGAGCCAGCGGGGCGCG 1430
QY 417 LeuAsnMetGlnThrGlyAlaThrGluAspAspIysTrpAspGlyAlaIleTrpCysAlaGlu 436

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 VERSION
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 HTC; CAP trapper.
 SOURCE
 Mus musculus (house mouse)
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 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.
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 AUTHORS
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PUBMED
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AUTHORS

TITLE
JOURNAL

COMMENT

FEATURES
source

CDS

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Best Local Similarity: 82.8%
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Direct Submision
Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan [E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Takashi Ishikawa (Department of Surgery 2 Yokohama City University 3-9 Fukuura, Kanazawa-ku, Yokohama 236-0004 Japan) whose assistance we gratefully acknowledge.
Please visit our web site for further details.
URL: http://fantom.gsc.riken.jp/
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 LOCUS
 DEFINITION AKI59957 3831 bp mRNA linear HTC 21-SEP-2005
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 ACCESSION AKI59957
 VERSION AKI59957.1 GI:74213392
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.
 REFERENCE
 AUTHORS Carninci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 PUBMED 10349636
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 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
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 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsuami, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
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 TITLE RIKEN Genome Exploration Research Group Phase II Team and the
 JOURNAL FANTOM Consortium
 PUBMED Functional annotation of a full-length mouse cDNA collection
 REFERENCE Nature 409 (6821), 685-690 (2001)
 AUTHORS 11217851
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 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Otsu, N., Saito, R., Suzuki, H., Yamana, T., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bull, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsumoto, H., Batalov, S., Beisel, K.W., Blake, J., Brack, D., Brucic, V., Chochia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fleischer, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Giesi, C., Godzik, A., Gough, J., Grimmond, S., Gueinich, S., Hirokawa, N., Jackson, J.J., Jarvis, E.D., Kane, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Petrea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Rongwald, M., Sandelin, A., Schneider, C., Sempile, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavalan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, I., Aizawa, K., Arahawa, T., Fukuda, S., Hara, A., Hashizume, W., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.
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 TITLE FANTOM Consortium
 JOURNAL Analysis of the mouse transcriptome based on functional annotation
 PUBMED of 60,770 full-length cDNAs
 REFERENCE Nature 420 (6915), 563-573 (2002)
 AUTHORS 12466851
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 Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Fitch, M.C., Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzu, R., Shimokawa, K., Bajic, V.B., Brenner, S.E., Batalov, S., Forrest, A.R., Zavolan, M., Davis, M.J., Wilming, L.G., Adkins, V., Allen, J.E., Ambesi-Implombato, A., Anrather, R., Aruiz, R.N., Bailey, T.L., Banal, M., Baxter, L., Beisel, K.W., Bersano, T., Bono, H., Chalk, A.M., Chin, K.P., Choudhary, V., Christofori, A., Clutterbuck, D.R., Croke, M.L., Dalla, E., Dalrymple, B.P., de Bono, B., Della Gatta, G., di Bernardo, D., Down, T., Engstrom, P., Fagiolini, M., Faulkner, G., Fleischer, C.F., Fukushima, T., Furuno, M., Futaki, S., Gariboldi, M., Georgii-Hemming, P., Gingeras, T.R., Gojobori, T., Green, R.E., Gusella, J.S., Harbers, M., Hayashi, Y., Hensch, T.K., Hirokawa, T., Hill, D., Hummel, L., Iacono, M., Ikeo, K., Iwama, A., Ishikawa, T., Jakt, M., Kanapin, A., Katoh, M., Kawasawa, Y., Kelso, J., Kitamura, H., Kitano, H., Kollias, G., Krishnan, S.P., Kruger, A., Kummerfeld, S.K., Kurochkin, I.V., Lareau, L.F., Lazarevic, D., Lipovich, L., Liu, J., Liuni, S., McWilliam, S., Madan, Babu, M., Madera, M., Marchionni, L., Matsuda, H., Matsuzawa, S., Miki, H., Mignone, F., Miyake, S., Morris, K., Moutagui-Taber, S., Muller, N., Nakano, N., Nakachi, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nozaki, F., Ohara, O., Okazaki, Y., Olando, V., Pang, K.C., Pavan, W.J., Pavese, G., Pesole, G., Petrovsky, N., Piazza, S., Reed, J.F., Reid, J.F., Ring, B.Z., Rongwald, M., Rosi, B., Ruan, Y., Salzberg, S.L., Sandelin, A., Schneider, C., Schonbach, C., Seligson, K., Sempile, C.A., Seno, S., Sessa, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D., Sinclair, B., Spelling, S., Stupka, B., Sugita, K., Sultana, R., Takenaka, Y., Taki, K., Tammoja, K., Tan, S.L., Tang, S., Taylor, M.S., Tegner, J., Teichmann, S.A., Ueda, H.R., van Nimwegen, E., Verardo, R., Wei, C.L., Yang, K., Yamashita, H., Zdobych, E., Zhu, S., Zimmer, A., Hide, W., Bull, C., Grimmond, S.M., Teasdale, R.D., Iju, E.T., Brucic, V., Quackenbush, J., Wahlstedt, C., Mattick, J.S., Hume, D.A., Kai, C., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori-Katayama, M., Suzuki, M., Aoki, J., Arahawa, T., Iida, J., Imamura, K., Itoh, M.,

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16141072

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AUTHORS

CONSTRM
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Science Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-fes@sc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Science Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Takashi Ishikawa (Department of Surgery 2 Yokohama City University 3-9 Fukuura, Kanazawa-ku, Yokohama 236-0004 Japan) whose assistance we gratefully acknowledge.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
Location/Qualifiers

FEATURES

source

CDS

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Alignment Scores:

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Score: 5075.50 Matches: 963
Percent Similarity: 87.5% Conservative: 55
Best Local Similarity: 82.8% Mismatches: 108
Query Match: 80.9% Indels: 37
DB: 6 Gaps: 12

US-10-642-946-3 (1-1158) x AK159957 (1-3831)

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259 ProProSerArgArgArgArgProGlnArgValAlaThrProGlnProProGlnGlnGln 278
963 ACACCCAG 1010
279 ProAlaProAlaProGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 298
1011 GAAAG 1061
299 ProProAspThrGlyAspGlyThrValAlaIleProAsnThrAspAspMetAspThrThr 318
1062 CCTCGGAGATGAG 1121

[illegible]

OY	677	AlaGlnMetGlySerGluPheGlyAsnTrpAlaLeuGlyLeuTrpThrGluGluGlyPhe	696
Db	2202	GCGCAGATGGAGCTTCAGAGTTTGGGAATGGGACATGGGGCTGTGGACTGTGAGAGAGGCTTT	2261
OY	697	AspIlePheGluAspPheProAspLeuAsnSerValLeuTrpGlyIaGluGlnAArgLys	716
Db	2262	GACATCTTCCAGAGACTTCCAGATCTCACTCTGTCTCTGGGCACTGAGAGAAAGAA	2321
OY	717	TrpValProTyrArgValProAsnAsnAsnLeuProIleProGluArgTyrLeuSerPro	736
Db	2322	TGGGTCCCTCAACAGGCTCCCAACAAATPACTTGGCAATCCCTGAACGTTACTGTCCCA	2381
OY	737	AspAlaThrValSerThrGluValArgAlaIleIleAlaTrpMetGlyLysAsnProPhe	756
Db	2382	GATCCCAACGGCTTCCACAGAAATCCGGGCGCATATTCTCGATGGAGAAACCCCTTT	2441
OY	757	ValLeuGlyAlaAsnLeuAsnGlyGlyGluArgLeuValSerTyrProTyrAspMetAla	776
Db	2442	GTCCTGGGTGCMAATCTGAACGGTGTGAGCGGCTTGTGCTTATCCCTATGACATGGCC	2501
OY	777	ArgThrProThrGlnGlnGluLeuLeuAlaAlaIleAlaIlePheArgTrpLeuAla	796
Db	2502	CCGACCACTTGCACGAGAGCAGCTGTTGGCCGAGCACTGGGAGCTGCCCGGAGAAAGAT	2561
OY	797	GluAspGluValSerGluAlaGlnGluThrProAspHisAlaIlePheArgTrpLeuAla	816
Db	2562	GATACCGGGGTGTGGAGGCCACGAGAACCTCCAGATCACCTATTTCCTCGCTGGCTGGC	2621
OY	817	IleSerPheAlaSerAlaHisIleuThrLeuThrGluLysProTyrArgGlyGlyCysGlnAla	836
Db	2622	ATCTCATTTGCTCTCGCCATCTCACATGACGAGCCCTTACCGGGAGGGTGGCCAGGCC	2681
OY	837	GlnAspTyrThrGlyGlyMetGlyIleValAsnGlyAlaLysTrpAsnProArgThrGly	856
Db	2682	CAGACATCAACACAGGGCGATGGGCAATTGTCAACGGGGCCAAATGGAAATCCCTCGCTGGG	2741
OY	857	ThrIleAsnAspPheSerTyrLeuHisThrAsnCysLeuGluLeuSerPheTyrLeuGly	876
Db	2742	ACTTTCATGACTTTTACTCTACTCTGCACACAAACTGTGTGAGGCTCTCCGATACCTGGGC	2801
OY	877	CysAspLysPheProHisGluSerGluLeuProArgLysTrpGluAsnAsnLysGluAla	896
Db	2802	TGTACACAGTCCCCCAGAGAGAGACTACCCCGAAGATGGGAAACAACAAAGAAACG	2861
OY	897	LeuLeuThrPheMetCysGluGlnValHisArgGlyIleLysGlyValValThrAspGluGln	916
Db	2862	CTGCTCACTTCATGAGAGCAGGTGCACCTGTGCATTAAAGGTGTGTGTGACAGATGACGAA	2921
OY	917	GlyIleProIleAlaAsnAlaThrIleSerValSerGlyIleAsnHisGlyValLysThr	936
Db	2922	GGCATCTCCCATATGCCAATGCCACCATCTCTGTGTGGCATCAACCATGTGTGAAGCA	2981
OY	937	AlaSerGlyGlyAspTyrTrpArgIleLeuAsnProGlyGluTyrArgValThrAlaHis	956
Db	2982	GCAATGTGAGGTGACTACTGGCGGATTTGAAACCGGGGTGTGATACCGGTGACAGCTCAC	3041
OY	957	AlaGluGlyTyrThrProSerAlaLysThrCysAsnValAspTyrAspIleGlyAlaThr	976
Db	3042	GCAAGGGCTTACACTTCAGAGCCCAATCTGCACATGTGACTACGATATTGGGGCCACT	3101
OY	977	GlnCysAsnPheIleLeuAlaArgSerAsnTrpLysArgIleArgGluIleMetAlaMet	996
Db	3102	CAGTGCAACTTCATCTGTGCTCGATCCAACTGGAAGCGCAATTCGGGAGATTTGGCTATG	3161
OY	997	AsnGlyAsnArgProIleProHisIleAspProSerLysArgProMetCysTrpGlnGlnArg	1016
Db	3162	AACGGGAACCGTCCCATTTCTCCAGATTGACCCCTCAGACCAACCAAGACCCCAACAGCGG	3221
OY	1017	ArgLeuGlnGlnArgArgLeuGlnHisArgLeuArgLeuArgAlaGlnMetArgLeuArg	1036
Db	3222	CGCATGTACGACGCGCGCTTACAGTACCGGCTCCGCAATGAGGAACAGATCGACTGGT	3281
OY	1037	ArgLeuAsnAlaThrThrThrLeuGlyProHisThrValPro---ProThrLeuProPro	1055

Db 3282 CGCTCATTCATCCGA-----GGCCCTGCCCAAGCCCACTCCTGCCCTTATGCT 3335

Qy 1056 AAlAPrAlaThrThrLeuSerThrThrIleGluProTrpGlyLeuIleProProThrThr 1075

Db 3336 CCCCCCTCCCTACACCACTTACCTTGAGGCCCTGGAGAAAGTACCACATACACT 3395

Qy 1076 AAlaGlyTrpGluGluSerGluThrGluThrThrThrGluValValThrGluGluGlyThr 1095

Db 3396 GCGAGCTGGAGGAGGTAGAGACTGAGAACCTTACAGAAAGTACAGACAGACTTT----- 3449

Qy 1096 GluValGluProGluProGluProGluProGluProGluProGluProGluProGluPro 1115

Db 3450 -----GAGACAGAGTATGGAGCTGAGCTGAGAGTGA----- 3482

Qy 1116 GluPheGluThrGluInLeuGluProGluPheGluGluGluGluGluGluGluGluGlu 1135

Db 3483 GAGATAGAG-----GAG 3521

Qy 1136 GluIleAlaThrGlyGlnAlaPheProPheThrThrValGluThrThrValAlaPhe 1155

Db 3522 GAGATGACACAGGCTTACATTCATTCACACAGTGAAGACTTACAGAGTGAACCTTT 3581

Qy 1156 GlyAspPhe 1158

Db 3582 GGGGACTTC 3590

RESULT 6
AK159774 3831 bp mRNA linear HTC 21-SEP-2005
LOCUS AK159774
DEFINITION Mus musculus osteoclast-like cell cDNA, RIKEN full-length enriched library, clone:1420030M05 product:AE binding protein 1, full insert sequence.

ACCESSION AK159774 GI:74204573
VERSION AK159774.1
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM

REFERENCE 1
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QY	255	ProProSerArgArgArgArgProGluArgValTTrpProGluProProGluGluVal	278
Db	963	ACACCCAGCAGAGG-----AGGCTCTGGCCAGAGCGCCCTGAGAGAAAGACT	1010
QY	279	ProAlaProAlaProGluGluArgTLeGIuProProValProLeuLeuProLeu	298
Db	1011	GAAGAGCCCAAGAGAAAGAGAGAGCGAGCCACTGTGAAGCCCCCTG-----CTG	10651
QY	299	ProProAspTyrGlyAspGlyTyrValIleProAsnTyrAspAspMetAspTyrPhe	318
Db	1062	CCTCGGAGCTATGGGGATAGCTAGCTGATCCCAACTGATGATGACTTGAGACTATATTTC	11221
QY	319	GlyProProProProGluLysProAlaGluArgGlnThrAspGluGluLysGlu	338
Db	1122	CCCCACCCTCCACCCCCAGAGCCCTGATGTGGACAAGAGTGGATGAGAAAGGAAG	1181
QY	339	LeuLysLysProLysLysGluLysAspSerProLysGluGluThr--AspLysTrpAla	357
Db	1182	ATGAAGAAAGCCCCAAAAGAGGGTGTAGCCCCAAGAGAGACACAGAGACAAAGTGACC	1241
QY	358	ValGluLysGlyLysAspHisLysGlu--ProArgLysGlyGluGluLeuGluGlu	376
Db	1242	GTGGAGAAAACAAAGACACCAACACAGAGCCCCCGAAGGGTGAAGACTGGAAGAGAG	1301
QY	377	TrpThrProThrGluLysValLysCysProProIleGlyMetGluSerHisArgTLeu	396
Db	1302	TGGGGCCAGTGAAGAAATCAAGTGCCCACTATTGGAGTGAATCACACCGACTGAG	1361
QY	397	AspAsnGlnIleArgAlaSerSerMetLeuArgHisGlyLeuGlyValGlnArgGlyArg	416
Db	1362	GACAAACCAAGATCCGGCTCTCCATGTGGCCACCGGCTTGGAGCCAGCGGGGCGGG	1421
QY	417	LeuAsnMetGlnThrGlyValArthrGluAspAspTyrTyrAspGlyAlaTrpCysAlaGlu	436
Db	1422	CTCAACATGCAAGCGCTGGTCCCAATGAATGACTCTATGACGGGGCATGTGTGCTGAG	1481
QY	437	AspAspAlaArgThrGlnTrpIleGluValAspThrArgArgThrArgPheThrGly	456
Db	1482	GACGAGTGGCAGACCCAGTGGATCGAGGTGAGCACCCGAGAGACAACCTCGGTTCACGGGC	1541
QY	457	ValIleThrGlnGlyArgAspSerSerIleHisAspAspPheValThrThrPhePheVal	476
Db	1542	GTCACTACCTCAGGGGGCGTGACTCCAGCATTCATGACGACTTCCTGTGTGTG	1601
QY	477	GlyPheSerAsnAspSerGlnThrTyrPheValMetTyrThrAsnGlyTyrGluGluMetThr	496
Db	1602	GGCTTCACCATGACAGCCAGACCACTGGGTGATGTACACCAATGGCTACAGAGAAATGACC	1661
QY	497	PheHisGlyAsnValAspLysAspThrProValLeuSerGluLeuProGluProValVal	516
Db	1662	TTCTATGAAATGTGGACAGGACACACTGTGTGCTGAGCGAGCTCCCGAGCCAGTTGTG	1721
QY	517	AlaArgPheIleArgTLeuTyrProLeuThrTrpAsnGlySerLeuCysMetArgLeuGlu	536
Db	1722	GCCCGTTTCATCCGCATCTATCTCACTCACTCGAGATGTAGCTGTGCATCGCCTGGAG	1781
QY	537	ValLeuGlyCysSerValAlaProValLysSerTyrTyrAlaGlnAsnGluValValAla	556
Db	1782	GTGTAGGCTGCCCCGTGACCCCTGTCTACAGCTACTAGCAGCAAGAAAGAGTGTACT	1841
QY	557	ThrAspAspLeuAspPheArgHisHisSerTyrLysAspMetArgGlnLeuMetLysVal	576
Db	1842	ACTGACACACCTGAGACTTCGGGCAACAAGCACTACAGAGAGAGAGAGAGTGAAGGCT	1901
QY	577	ValAsnGluGluCysProThrTLeThrArgThrTyrSerLeuGlyLysSerSerArgGly	596
Db	1902	GTCAATGAGAGGTGCCCAACAATCACTCGCAATACACCTGGGCAAGAGATTCCAGAGGG	1961
QY	597	LeuLysIleTyrAlaMetGluLysSerAspAsnProGlyGlnHisGluLeuGlyGluPro	616
Db	1962	CTCAAGATCTACGCAATGAATCTCAACAACCTGGGGATCAATGAATGGGGGAGAGCC	2021
QY	617	GluPheArgTyrThrAlaGlyIleHisGlyAsnGluValLeuGlyArgGluLeuLeuLeu	636

Db 2022 GAGTTCGCCCTACACAGCCGGGATCCACGGCAATGAGGTGCTAAGGCCGAGACCTCCTGCTC 2081

QY LeuLeuMetGlnTYrLeuCYsArgGluTYrArgAspGluAsnProArgValAArgSerLeu 656

Db 2082 CTGCTCAATGACAATCTAATGCAAGGAGTACCGCATGTGGAAACCGAGAGTGCGAACCTG 2141

QY 657 ValGlnAspThrArgIleIleLeuValProSerLeuAsnProAspGluTYrGluValAla 676

Db 2142 GTGGCAGGACACACGGATCCACTGGTGGCTTCGGTGAACCTGATGGCTATGAGTGGCA 2201

QY 677 AlaGlnMetGlySerGluPheGlyAsnTPrlaLeuGlyLeuTPrlhGluGluGlyPhe 696

Db 2202 GCGCAGATGGGCTCAGAGTTTGGGAACTGGGCACTGGGGCTGTGGACTGAGAGAGGGCTTT 2261

QY 697 AspIlePheGluAspPheProAspLeuAsnSerValLeuTPrlGluAlaGluArgLeu 716

Db 2262 GACATCTTCGAGGAACTTCCAGATCTCAACTGTGTGCTGTGGGCACTGAGAGAAAGAA 2321

QY 717 TrpValProTYrArgValProAsnAsnAsnLeuProIleProGluArgTYrLeuSerPro 736

Db 2332 TGGTCCCCCTCAGGGTCCCAACAATPACTGGCAATCCTGAACCTTACTCTCCCA 2381

QY 737 AspAlaThrValSerThrGluValArgAlaIleIleAlaTPrlMetGluLeuAsnProPhe 756

Db 2382 GATGCCAGGCTCCACAGAGAGCTCGGGCCATPATTTCCTGATGAGAGAAACCCCTTT 2441

QY 757 ValLeuGlyAlaAsnLeuAsnGlyGlyGluArgLeuValSerTYrProTYrAspMetAla 776

Db 2442 GTGCTGGGTGCAAACTGGAAGGTGTGAGCGGCTTGCTGTATTCCTTGACATGAGC 2501

QY 777 ArgThrProThrGlnGluGlnLeuLeuAlaIleAlaMetAlaIleAlaArgGlyGluAsp 796

Db 2502 CGGACACCTTACCGCAGAGCACTGTGGCCGAGGCACTGGCACTGCCCGCGAGAAAGAT 2561

QY 797 GluAspGluValSerGluAlaGlnGluThrProAspHisAlaIlePheArgTPrlLeuAla 816

Db 2562 GATGACGGGGTGTGAGGCCCAAGAGACTCCAGATCACGCTATTTCCTCGGTGGCTGGC 2621

QY 817 IleSerPheAlaSerAlaHisIleuThrLeuThrGluProTYrArgGlyGlyCYsGlnAla 836

Db 2632 ATCTCATTTGGCTCCGCCCATCTCAATCCAGAGCCCTACCGGGAGGGGTGCCAGAGC 2681

QY 837 GlnAspTYrThrArgGlyMetGlyIleValAsnGlyAlaLeuSTrlAsnProArgThrGly 856

Db 2682 CAGGACTACACACAGCGGATGGGCAATGTCTCAACGGGGCCAGTGGAAATCTCGCTCTGGG 2741

QY 857 ThrIleAsnAspPheSerTYrLeuHisThrAsnCYsLeuGluLeuSerPheTYrLeuGly 876

Db 2742 ACTTTCATATGACTTTAGTACTCTGCACACAAACGTCTGGAGCGCTCCGATATCCTGGC 2801

QY 877 CysAspLeuPheProHisGlnLeuSerGluLeuProArgGluTPrlGluAsnAsnLeuGluAla 896

Db 2802 TGTGCAAGATTCCCCCGAGAGTGTAGCTACCCCGAATATGGGAGAACCAAGAAAGCG 2861

QY 897 LeuLeuThrPheMetGluGlnValHisArgGlyIleLeuGlyValValThrAspGluGln 916

Db 2862 CTGCTCACTTCAGAGACAGAGGTGACCGGTGTGAAGGGTGTGGTGAGACAGTGAACAA 2921

QY 917 GlyIleProIleAlaAsnAlaThrIleSerValSerGlyIleAsnHisGlyValLeuThr 936

Db 2922 GGCATCCCAATGGCAATGCCACATCGTGTGTAGTGGCATCAACATGGTGTGAACACA 2981

QY 937 AlaSerGlyGlyAspTYrTPrlArgIleLeuAsnProGlyGluTYrArgValThrAlaHis 956

Db 2982 GCAAGTGAAGGTGACTACTGGCGCATCTGAACCCGGGTGAGTACCTGTGACAGCTCAC 3041

QY 957 AlaGluGlyTYrThrProSerAlaLeuValThrCysAsnValAspTYrAspIleGlyAlaThr 976

Db 3042 GCAAGGGGCTACACTCAAGTCCAAAGATCTGCATGTGACATACGATATTGGGGCCACT 3101

QY 977 GlnCYsAsnPheIleLeuAlaArgSerAsnTPrlAsArgIleArgGluIleMetAlaMet 996

Db		3102	CAGTGGCAACTTCATCTGCGCTGCATGCCAACACGAAGGCGCATTTGGGAGATCTTGSGCATNG	3161
Oy		997	Aenglyaenatgproilleeprohiellaepproseratgproemethrproglinglathrg	1016
Db		3162	AACGGGAACCGCTCCCATTCCTCCGAGTTTAACCCCCCTCACAACCACATGACCCCCCACAGCGG	3221
Oy		1017	ArgleugnglnaragrargleughnlsarpleumkrgleuaaglaaglimeArgleunarg	1036
Db		3222	CGCATGCGAGCGCGCGTCAACAGTACCGGGCTCCGCATGAGGAAACAGATCGACTGGCT	3281
Oy		1037	ArgtleuanalathrThrThrleuglYProHlsThValPro----ProThrleuProPro	1055
Db		3282	CGCCTCATTTCTACCGCA-----GGCCCTGCACACACCCCACTCCGCCCTTATGCT	3335
Oy		1056	AlaprolathrThrLseSerThrThrilegluProTrpglyLeulleproProThrThr	1075
Db		3336	CCCCCTTCCCCTCACACGACTTACCTTGAGGCGCCTGGGAAGATTCTCACCATCACACT	3395
Oy		1076	AlaaglyTPGjuglusergltuthglnthrlythrthrglvallvalThglnPheglyThr	1095
Db		3396	GCAGGCTGGGGAGACTCAGAGCTGAGACTTATACAGAAGTAGTACAGACTTT-----	3449
Oy		1096	GlulvAlguiprogluPheglyThrLyvalGuiproglugluPheglutHnGlnleugluPro	1115
Db		3450	-----GAGACAGAGTATGGAGCTGACTAAGGTGGA-----	3482
Oy		1116	GlupheglutHnGlnleugluProgluphegluglugluglugluglugluglu	1135
Db		3483	GAGATAGAG-----GAAAGAGAGAGAGAGAGAGAGAGAGAA	3521
Oy		1136	GlutlealathrglyglAlaPhepropherThrValGluThrTyThrValAspHe	1155
Db		3522	GAGATGGACACAGGCGCTTACATTCCTCATTCACAACAGTGAGAGACTTACACAGTAACTTT	3581
Oy		1156	GlyAepHe	1158
Db		3582	GGGACCTTC	3590
RESULT 7				
LOCUS		AKI58276	3854 bp	mRNA linear HTC 21-SEP-2005
DEFINITION			Mus musculus adult inner ear cDNA, RIKEN full-length enriched library, clone:P330049P09 product:AE binding protein 1, full insert sequence.	
ACCESSION		AKI58276		
VERSION		AKI58276.1	GI:74196689	
KEYWORDS		HTC; CAP trapper.		
SOURCE		Mus musculus (house mouse)		
ORGANISM				
REFERENCE				
AUTHORS				
JOURNAL				
PUBMED				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
PUBMED				
REFERENCE				
AUTHORS				
TITLE				
JOURNAL				
PUBMED				
REFERENCE				
AUTHORS				
TITLE				

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RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium

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FANTOM Consortium

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FEATURES
source

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US-10-642-946-3 (1-1158) x AK158276 (1-3854)

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21 ProGlyGlyArgProGlnThrValLeuThrAspAspGlnIleGluGluPheLeuGly 40
286 CCTGAAGGGAACCAACAGACGAGTGAAGGAGAGATGAGAGATGCTCGAAGGC 345
41 PheLeuSerGluLeuGluProGlu-----ProArgGluAspAspValGluAlaProPro 58
346 TTCCTTTGAGAGTTGAGAGACCGATCCCGCCCGCCGAGAGAGACAGATGAGAGCGCCG 405
59 ProProGluProThrProArgValArgGlyAlaGlnAlaGlyGlyProGlyArg 78
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79 ProGlyThrAlaAlaGluValProProGlu-LysThrLysAspGlyGlyLysGly 98
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514 GAAAGCAAAAGGCGCCCAAGACCAACAA--CCCTGAGAGGCTTACAGAGGCCACCA 570
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138 ThrLysLysProLysGluGluProProLysAlaThrLysLysProLysGlyLysProPro 158
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691 CAGGCGCACTAAGAGGCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 750
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198 LysAlaProLeuSerAspAspThrGlnAspProGlyGluGluGluThrHisValGlu 218
811 AGACACACCTTCCCAATGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 870
218 nGluHisGlnProGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 238
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putative"

ORIGIN

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Score:	5009.50	Matches:	957
Percent Similarity:	86.9%	Conservative:	54
Best Local Similarity:	82.2%	Mismatches:	113
Query Match:	79.9%	Indels:	41
DB:	6	Gaps:	10

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QY	298	uProProaPpTYrgLYaPpGLYrYrValIleProaPnTYraPpSeLaPpTYrYrPh	318
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Db	1150	CCCCACCTTCACCGCAGAAAGCCGATGTGGACAAAGAGTGATGAGAGAAAGAAAGA	1209
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Db	1210	GATGAAGAAAGCCCAAAAAGAGGATGATAGCCCCCAAGAGACACAGAGACAAAGTGGA	1269
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QY	576	lValleuGLYlYCyPProThrIleThrArGLYrThrYrSeSeLeuGLYlYsSeSeArGL	596
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QY	596	yLeuLYsIleTYrAlaMeGLYlnleSeSeArAPpProGLYlYhYlYglYleuGLYlYlYr	616
Db	1990	GCTCAAGACTCTAGCAATGAATCTCAGACAACTGGGAGATCAATGAATCTGGGGAGCC	2049

QY	616	UGLUPheArgrYrThrAlaGlyLLeuLeuValLeuGlyValArgGluLeuLeuLeu	636
Db	2050	CGAGTTCGGCTACACAGCGGGGATCTCCAGGCAATGAGGTGTCAAGCCGAGACTCTGT	2100
QY	636	uLeuLeuMetGlnTyLeuLeuCybArgGluTyTArGspAluAspProArGValArgSerLe	656
Db	2110	CCTGCTCATTCGAATTCCTATTGCCAGAGATCACCGGATGGGAATCCGAGAGTCCGCACT	2160
QY	656	uValGlnAspThrArgLLeuLsLeuValProSerLeuAsnProAspGlyTyTArgLValAl	676
Db	2170	GGTGACAGACACAGCATCCACTGTGTGCCCTCGCTGAACCTGTATGGCTATGAGATGGC	2220
QY	676	aAlaGlnMetGlySerGluPheGlyAsnTPAlaLeuGlyLeuTPThrGluGluGlyPh	696
Db	2230	AGCGCAGATGGGCTCAGAGTTTGGAGACTGGGCACTGGGCGCTGTGAGACTGAGAGAGGCTT	2280
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Db	2290	TGACATCTTCAGGACTTCCAGATCTCACTGTGCTTGCGCACTGAGAGAGAGAAAGA	2340
QY	716	sTPValProTyTArGValProAsnAspAsnLeuProLLeProGluArgTyLeuSerPr	736
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QY	736	oAspAlaThrValSerThrGluValArgAlaLLeuAlaTPMetGluLysAsnProPh	756
Db	2410	AGATGCCACGGCTCTCACAGAAAGTCGGGGCCATTATTTCCCGG-ANGGAGAAACACCCCTT	2460
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QY	776	aArgThrProThrGlnGluGlnLeuLeuAlaAlaAlaMetAlaAlaAlaArgGlyGluAs	796
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QY	796	pGluAspGluValSerGluAlaGlnGluThrProAspAlaAlaLLePheArgTPLeuAl	816
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QY	816	aLLeSerPheAlaSerAlaAlaLeuThrLeuThrGluProTyTArArgGlyCybGlnAl	836
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Db	2820	CTGTGACAAATTCCCCCAGAGAGTGAAGCTACCCGAGATGAGAGAACAAACAAACAAAC	2880
QY	896	aLeuLeuThrPheMetGluGlnValAlaHLeArgGlyLLeuGlyValValThrAspGluGl	916
Db	2880	GCTGCTCACTTCATGAGAGAGGTGACACCGTGGCATTAAGGTTGTGTACAGATGAGCA	2940
QY	916	ngLylLeProLLeuAlaAsnAlaThrLLeSerValSerGlyLLeuAsnGlyValLysTh	936
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QY	936	rAlaSerGlyGlyAspTyTTPArgLLeuAsnProGlyGlyTyTArGValThrAlaAl	956
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QY	956	sAlaGluGlyTyTThrProSerAlaLysThrCybAsnValAspTyTArAspLLeuGlyAlaTh	976
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QY	766	GluArgLeuValIleSerTyrProTyrAspMetAlaArgThrProThrGlnGlnIleLeu	785
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QY	786	AlaAlaAlaMetAlaAlaAlaArgGlyGluAspGluAspGluValIleSerGluValGlnGlu	805
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QY	826	LeuThrGluProTyrArgGlyGlyCysGlnAlaGlnAspTyrThrGlyGlyMetGlyIle	845
Db	2223	TTGACCGAGCCCTACCGCGAGGCTGCCAAGCCACGACATCACCGCGCGCATGGCATC	2282
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QY	886	LeuProArgGluTyrTrpGluAsnAsnLysGluValLeuLeuThrPheMetGluGlnValHis	905
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QY	906	ArgGlyIleLysGlyValValThrAspGlnGlnGlyIleProIleAlaAsnAlaThrIle	925
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QY	946	LeuAsnProGlyGluTyrArgValThrAlaHisAlaGluGlyTyrThrProSerAlaLys	965
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QY	966	ThrCysAsnValAspTyrAspIleGlyAlaThrGlnCysAsnPheIleLeuAlaArgSer	985
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[illegible]

JOURNAL Science 309, 1559-1563 (2005)
REFERENCE 8 (bases 1 to 2836)
AUTHORS Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,
Arkawa,T., Bono,H., Carninci,P., Fukuda,S., Fukuuchi,Y.,
Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,
Hirooka,T., Horii,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M.,
Kasakawa,T., Kato,H., Kawai,Y., Kojima,Y., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsumura,T., Miyazaki,A., Nishi,K.,
Nomura,K., Numasaki,R., Ono,M., Okazaki,Y., Okido,T., Owa,C.,
Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Saeki,D.,
Shibata,K., Shibata,Y., Shingawa,A., Shiraki,T., Sogabe,Y.,
Suzuki,H., Tagami,W., Tagawa,A., Takahashi,F., Tanaka,T.,
Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,
Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submision
JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa, 220-0045, Japan (E-mail:genome-gsc@gs.c.riken.jp/
URL:http://genome-gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and genome science laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome-gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/
LOCATION/Qualifiers

FEATURES	1..2836
SOURCE	/organism="Mus musculus"
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	/tissue type="lung"
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	/dev_stage="adult"
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ORIGIN	

Alignment Scores:

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Score:	4096.00	Matches:	765
Percent Similarity:	90.1%	Conservative:	37
Best Local Similarity:	86.0%	Mismatch:	60
Query Match:	65.3%	Indels:	28
DB:	6	Gaps:	6

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ACCESSION AK019509
VERSION AK019509.1 GI:12859761
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
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REFERENCE
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636

REFERENCE
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159

REFERENCE
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, Y., Nishi, K., Ktsunai, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, N., Nishie, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasaiwagi, K., Fujitake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
PUBMED 11076861

REFERENCE
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
PUBMED 11076861

REFERENCE
AUTHORS The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I and II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
PUBMED 11076861

REFERENCE
AUTHORS RIKEN Genome Exploration Research Group, Genome Science Group (Genome Network Core Team) and the FANTOM Consortium.
TITLE Antisense Transcription in the Mammalian Transcriptome
JOURNAL Science 309, 1564-1566 (2005)
PUBMED 15641566

REFERENCE
AUTHORS The FANTOM Consortium, Riken Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group).
TITLE The Transcriptional Landscape of the Mammalian Genome
JOURNAL Science 309, 1559-1563 (2005)
PUBMED 15591563

REFERENCE
AUTHORS Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arikawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hirao, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasaoka, T., Kato, H., Kawai, Y., Kojima, Y., Kono, H., Kouda, M., Koyasu, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Taya, T., Yamamuro, T., Yashinaka, F., Tanaka, T., Tejima, Y., Toyama, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Yamamoto, M. and Hayashizaki, Y.
TITLE Direct Submission
JOURNAL Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@ac.riken.jp, YHR: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,

COMMENT Fax: 81-45-503 -9216)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopaedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site for further details.
 URL: <http://genome.gsc.riken.jp/>
 URL: <http://fantom.gsc.riken.jp/>.
 Location/Qualifiers
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Hominoidea; Homo.
REFERENCE 1 (bases 1 to 2237)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civeello,D.,
White,T.J., Snihsy,J.J., Adams,M.D. and Cargill,M.
A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
JOURNAL (er) PLOS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 2237)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civeello,D.,
White,T.J., Snihsy,J.J., Adams,M.D. and Cargill,M.
Direct Submision
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
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ORGANISM	Homo sapiens			
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ORIGIN				

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Pred. No.: 2,41e-134 Length: 2917
 Score: 1925.50 Matches: 364
 Percent Similarity: 71.2% Conservative: 92
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 Query Match: 30.7% Indels: 35
 DB: 6 Gaps: 4

US-10-642-946-3 (1-1158) x HSM805045 (1-2917)

QY 416 ArgLeuAaMetGlnThrGlyAlaThrGluAspSerThrValProGlyAlaTyrCysAla 435
 DB 2 AGACTCAACATCCAGGGGCGCATTAAGAAATGATTTTATGACGAGCGTGCGCG 61
 QY 436 GluAspAspAlaArgThrGlnTrrPILegluValAspThrArgThrArgPheThr 455
 DB 62 GGAAGAAATGCTCCAGCAGTGGATTGAATGGATCTCGCGCGCCGACAGATTCACT 121
 QY 456 GluValIleThrGlnGlyArgAspSerSerIleHisAspAspPheValThrThrPhePhe 475
 DB 122 GGTGTCATCACTAAGGAGAACTCCCTGCTGCTGAGTACGCGGACATCCTAAAG 181
 QY 476 ValGlyPheSerAspAspSerGlnThrThrValMetThrArgGlyTyrGlnGluMet 495
 DB 182 GTCATGTGACATAGACACACACCTGGGTCACTTAAGATGATCGAGACATG 241
 QY 496 ThrPheHisGlyAsnValAspLysAspThrProValLeuSerGluLeuProGluProVal 515
 DB 242 ATATTGAGGGAACAGTGAAGAGAGATCCCTGTTCTCAATGAGTACCCGTCATG 301
 QY 516 ValAlaArgPheIleArgGlyIleTyrProLeuThrTTP-----AsnGlySerLeuCysMet 533
 DB 302 GTGGCCCGCTACATCCGCATMAACCCCTCAGTCTGTTGATATATGGAGCATCTGCATG 361
 QY 534 ArgLeuGluValLeuGlyCysSerValAlaProValTyrSerTyrTyr---AlaGlnAsn 552
 DB 362 AGAATGAGATCTTGCGCTGCCACCTGCCAGATCCTAATTAATTTATTCACCGCGGAC 421
 QY 553 GluValAlaIleThrAspAspLeuAspPheArgHisIleSerTyrLysAspMetArgGln 572
 DB 422 GAGATGACCAACCACTGATGACCTGGATTTAAGCACACAAATTATAAGAAATGCCGAC 481
 QY 573 LeuMetLysValAlaAsnGlyGluCysProThrIleThrArgThrTyrSerLeuGlyLys 592
 DB 482 TTGATATAAGTTGTGATGATAATGTGTCCCAATATATCCAGAAATTTAACAATTTGAA 541
 QY 593 SerSerArgGlyLeuLysIleTyrAlaMetGluIleSerAspAsnProGluGluIleGlu 612
 DB 542 AGCCACAGGGGCTGAAAGCTGATGCTGTGAGATCTCAGATCAACCTGGGGAGCATGAA 601
 QY 613 LeuGlyGluProGluPheArgTyrThrAlaGlyIleHisGlyAsnGluValLeuGlyArg 632
 DB 602 GTGGGTGAGCCGAGATTCCACTACATCGCGGGGCCACAGCAATGAGGTGCTGGGCGG 661
 QY 633 GluLeuLeuLeuLeuMetGlnTyrLeuCysArgGluTyrArgAspGlyAsnProArg 652
 DB 662 GACCTCTGCTGCTGCTGAGT 721
 QY 653 ValArgSerLeuValGlnAspThrArgIleHisLeuValProSerLeuAsnProArgGly 672
 DB 722 ATGTGTCACCTGGTGAAGAGACGCGATTCAGCTCTCCCTCCCAACCCCGATGGC 781
 QY 673 TyrGluValAlaIleAsnMetGlySerGluPheGlyAsnThrAlaLeuGlyLeuTrrThr 692
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 QY 693 GluGluGlyPheAspIlePheGluAspPheProAspLeuAsnSerValLeuTrrPGLyAla 712
 DB 842 CACGATGAGATTACATCAACAACACTTTCGATTTAAACACGCTGCTCGGAGGCA 901
 QY 713 GluGluArgLysTrrValProTyrArgValProAsnAsnAsnLeuProIleProGluArg 732

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 DB 1022 AAAATCCCTTTGT 1081
 QY 773 TyrAspMetAlaArgThrProThrGlnGluGlnLeuLeuAlaIleAlaIleAla 792
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 DB 1718 -----AGCTGCCAGCCAGGCGGCTGAAGCTGCGGGGGCGGAGAGACAGAG 1765
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 LOCUS Pan troglodytes HCl9233 gene, VIRUAL TRANSCRIPT, partial sequence,
 DEFINITION genomic survey sequence.
 DQ051197
 ACCESSION DQ051197.1 GI:66904396

KEYWORDS	GSS.
SOURCE	Pan troglodytes (chimpanzee)
ORGANISM	Pan troglodytes
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
	Hominidae; Pan.
REFERENCE	1 (bases 1 to 2189)
AUTHORS	Nielsen,R., Bustamante,C., Clark,A.G., Gianowski,S., Sackton,T.B., Hubisz,M.J., Pedel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. A scan for positively selected genes in the genomes of humans and Chimpanzees (et) PLoS Biol. 3 (6), E170 (2005) 15869325
JOURNAL	2 (bases 1 to 2189)
PUBMED	Nielsen,R., Bustamante,C., Clark,A.G., Gianowski,S., Sackton,T.B., Hubisz,M.J., Pedel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. Direct Submission Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
TITLE	This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.
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Best Local Similarity:	45.9% Mismatches: 228
Query Match:	28.5% Indels: 95
DB:	14 Gaps: 9
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Db	167 AGCGCGCCCAAGAAGGCCACACAAGCCCAAG-----AAAGCTCCAAGAGCGAGAG 217
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Oy	367 Pro----- 367
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Oy	507	ValLeuSerGluLeuProGluProValaAlaArgPheIleArgIleTyrProLeuThr	526
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Oy	584	IleThrArgThrTyrSerLeuGlyLysSerSerArgGlyLeuLysIleTyrIleValaMetGlu	603
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Oy	604	IleSerAspAsnProGlyGluHisGluLeuGlyGluProGluPheArgTyrThrAlaGly	623
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Db	1250	GGAGGCTGCTCCCTGGGAGCGCTGAGCCCAAGATGATGACATTCATCAACAACCTTTCCT	130
Oy	704	AspLeuAsnSerValLeuTrpGlyAlaGluGluArgLysTrpValProTyrArgValaPro	723
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Oy	724	AsnAsnAsnLeuProIleProGluArgTyrLeuSerProAspAlaThrValSerThrGlu	743
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[illegible]

TITLE	Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.			
JOURNAL	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios			
PUBMED	Science 302 (5652), 1960-1963 (2003)			
REFERENCE	14671302			
AUTHORS	2 (bases 1 to 2169)			
TITLE	Clark,A.G., Glanowski,S., Nelson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Ciochello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.			
JOURNAL	Direct Submissions			
COMMENT	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA			
FEATURES	These sequences were made by sequencing genomic exons and ordering them based on alignment.			
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Alignment Scores:				
Prod. No.:	2.48e-121	Length:	2169	
Score:	1751.00	Matches:	352	
Percent Similarity:	63.4%	Conservative:	109	
Best Local Similarity:	48.4%	Mismatches:	198	
Query Match:	27.9%	Indels:	68	
DB:	14	Gaps:	12	
US-10-642-946-3 (1-1158) x AY418886 (1-2169)				
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DB	127	CAACCGTCACAAAGGCAAGACCTCAGAACGGCATGTCCGGCTTCAGATCATCAAAA	186	
QY	345	GLUASPSERPEROLYSGULUNHRAEPLVSTRAIValGULYGLYLYASPHIS	364	
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QY	365	LYS-----GIUPROAGLYGELY	370	
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DB	280	CTCACTCTCCCTGAGAAACAGAACCA-----GGATGTCCCTCTAGGCTTG	327	
QY	391	GLUSERHIAEGLLEGLUASPAHGLINTLEAHLASERSEMETLEAAGHISGLYLU	410	
DB	328	GAGTCTTGAGGGTTTCAGATGACCAAGCTTGAGGCTTCACAGCCAGCTCTTGCTTG	387	
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DB	388	GGAGCACACCGAGAGCGCTCAATTCACAGTCAGAGTCGAGAGACGGTGAACCTGTATGAT	447	
QY	431	GLYALITPCYALAGLUASPAHPLAATRGTHRLINTRILLEGILUALAEPHTRAGAG	450	
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QY	471	VALTTHTRPhePhEValGlyPheSEYASPAERSEGLINTHRTPYALMETVLYTAAH	490	
DB	568	GTCACATCATTCAGAGTCCAGTTCAGCAATACAGCCAGACCTGTGTGAAGATAGGAAC	627	
QY	491	GLYLYR--GLUGLUMETThRPhEISGLYASVALASPLYSAPHTRPROVALLEUSER	509	

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 30, 2006, 23:22:06 / Search time 1439 Seconds
(without alignments)
8416.119 Million cell updates/sec

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Perfect score: 6272
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Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 5244920 seqs, 3486124231 residues
Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=abs/ABSSMB.spool/US10642946/rnat.29092006.125306.12469/app.query.fasta.1
-DB=N.Geneseq -GMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs03p
-USER=US10642946 -CGN_1_1177@rnat.29092006.125306.12469 -NCPU=6 -ICPU=3
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-NARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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15: geneseqn2006a.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	6272	100.0	3935	10 ADF90653	Adf90653 Human hep

4	6272	100.0	3935	14 ADZ26196	Adz26196 Human gen
5	6254	99.9	3914	12 AD086121	Ad086121 Human tum
6	6284	99.9	3914	13 ACN38620	ACN38620 Tumour-as
7	6264	99.9	4125	13 ADRA44022	Adra44022 Human col
8	6256	99.7	3922	9 ACH03928	ACH03928 Human CDN
9	6227	99.3	3854	2 AAT97610	Aat97610 Human E2A
10	6206	98.9	4025	10 ADE79067	Ad79067 Human pro
11	6129	97.7	3872	10 ADE79063	Ad79063 Human pro
12	5725	91.3	3523	6 AB054610	Ab054610 Human ova
13	5077	80.9	3633	2 AAT97611	Aat97611 Mouse E2A
14	5049	80.5	3728	2 AAQ58708	Aaq58708 Mouse OSF
15	4925.5	78.5	3170	6 ABZ35234	Abz35234 Human gen
16	4882.5	77.8	3373	10 ADE79065	Ad79065 Human pro
17	4791	76.4	16161	6 AAD36071	Aad36071 Human adi
18	4213	67.2	2795	2 AAT97609	Aat97609 Human E2A
19	3598	57.4	2571	13 ADRO7375	Adro7375 Full leng
20	3488.5	55.6	2168	8 ABZ34695	Abz34695 Coding se
21	2904	46.3	2555	12 AD023365	Ad023365 Lung canc
22	2508	40.0	1853	3 AAT18001	Aat18001 Lung canc
23	2171.5	34.6	3772	3 AAZ64961	Aaz64961 Membrane-
24	2171.5	34.6	3772	4 AAS21439	Aas21439 Human CDN
25	2171.5	34.6	3772	5 AAF44107	Aaf44107 Human PRO
26	2171.5	34.6	3772	8 ACA64197	Ac64197 Novel hum
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28	2171.5	34.6	3772	8 ABX89336	Abx89336 DNA enco
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ALIGNMENTS

RESULT 1
ID ABZ34770 standard; cDNA; 3935 BP.
XX ABZ34770;
AC ABZ34770;
XX
DT 04-FEB-2003 (first entry)
XX
DE Coding sequence SEQ ID 128, upregulated in osteogenesis.
XX
KW Osteopathic; osteogenesis modulator; gene therapy; osteogenesis;
XX osteoporosis; bone disease; downregulator; human; enzyme; ss.
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OS Homo sapiens.
XX
PN WO200281745-A2.
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PD 17-OCT-2002.
XX
PP 05-APR-2002; 2002WO-1B002211.
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PR 05-APR-2001; 2001US-0281400P.
XX
PA (AVENTIS PHARMA SA.
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PI Garcia T, Roman Roman S, Baron R, Call K, Theilhaber J;
Connolly T, Jackson A, Bushnell SE, Rawadi G;

XX WPI; 2003-058567/05.
PT Novel isolated nucleic acid upregulated/downregulated in osteogenesis,
PT useful for bone disease therapy in subject.
XX
XX
PS Claim 26; Page 146-147; 237pp; English.

CC The present invention relates to novel nucleotide sequences, which are
CC differentially expressed in models of osteogenesis upon being put in
CC contact with a stimulator of osteogenesis. The present sequence is one
CC such sequence. This sequence can be used for diagnosing osteoporosis/bone
CC disease in a patient, promoting osteogenesis and/or preventing
CC osteoporosis/bone disease. The present sequence encodes an intracellular
CC enzyme

SQ Sequence 3935 BP; 923 A; 1243 C; 1185 G; 584 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1, 77e-290 Length: 3935
Score: 6272.00 Matches: 1158
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 8 Gaps: 0

US-10-642-946-3 (1-1158) x AB234770 (1-3935)

QY 1 MetAlaAlaValArgGlyAlaProLeuLeuSerCysLeuLeuAlaLeuLeuAlaLeuCys 20
Db 140 ATGGCGGCGGTGGCGGGGCGCCCTGCTCAGCTGCTCTCGCTGCTGCTGCTGCTGCTGCT 199
QY 21 ProGlyValArgProGlnThrValLeuThrAspArgGluIleGlnGlnPheLeuGlnGly 40
Db 200 CCGAGAGGCGCGCGGAGAGCGTGTGACCGAGACGAGTCCAGAGATTCCTCGAGGAGC 259
QY 41 PheLeuSerGlnLeuGlnProGluProArgGluAspValGlnAlaProProProPro 60
Db 260 TTCCTTCAGAGGTAAACCTGAGCCCGGAGAGACGACGTGAGGCCCGCGCGCTCC 319
QY 61 GluProThrProArgValArgIleValAlaGlnIleGlyIleValProGlyIleValArgProGly 80
Db 320 GAGCCCAACCCCGCGGTCCGAAAGCCCGCGGCGGCAAGCCAGGAAAGCGCGCAAGG 379
QY 81 ThrAlaAlaGlnValaProProGluValSerThrIleAspIleGlyIleValSerGlyValAsp 100
Db 380 ACGGCGCAGAAAGTGCCTCCGAAAGAACCAAGAGCAAGAGAGAAAGCAAGAAAGAC 439
QY 101 LysGlyProIleValProIleGlnSerLeuGlnGlySerProArgProProIleValGly 120
Db 440 AAAGGCCCAAGGTGCGCAAGAGAGTCTTGAGAGGGTCCCGCAGCGCGCCAAAGAGGG 499
QY 121 LysGlnLysProProIleValaThrIleValProIleGlnLysProProIleValaThrIleVal 140
Db 500 AAGGAGAAAGCACCAGGCAAGCAAGAGCCCAAGAGAGCAAGCAAGCAAGCAAGCAAG 559
QY 141 LysProIleGlnGlnProProIleValaThrIleValProIleGlnLysProProIleVala 160
Db 560 AAGCCCAAGAGAGAGCCCAAGGCAAGCAAGAGCCCAAGAGAGAGCCCAAGAGAGCC 619
QY 161 ThrIleLysProProSerGlyLysArgProProIleValaProSerGlnThrLeuGln 180
Db 620 ACCAAGAGCCCGCTCAGAGAGAGGGCCCGCCATTCGTGCTCCCTCAAGAAACCTGGAG 679
QY 181 TrpProLeuProProProProSerProGlyProGlnGlnLeuProGlnGlnGlyVala 200
Db 680 TGGCCACTGCCCCCAGCCCGCCAGCTGCGCCCGAGAGAGTACCCAGAGAGAGAGGGG 739
QY 201 ProLeuSerAspAsnTrpGlnAsnProGlnGlnGlnThrIleValaGlnIleGlnIle 220
Db 740 CCCCTCTCAATAATCTGGCAAGATCCAGAGAGAGCCCATGTGAGAGGACAGAGAGC 799
QY 221 GlnProGlnProGlnGlnGlnGlnGlnProThrLeuAspTyrAsnAspGlnIleGln 240

Db 800 CAGCTGAGCCGGAGAGAGAGACGAGCAACCACTGAGCTAACAATGACAGATTCAG 859
QY 241 ArgGluAspTyrGluAspPheGlnIleThrArgGlnIleGlnProArgProProPro 260
Db 860 AGGAGAGACTATGAGAGCTTTGAGTACATTCGGCGCCAGAAAGCAACCAAGGACACCCCA 919
QY 261 SerArgArgArgArgProGlnLysArgValaTrpProGluProProGlnGlnLysAlaProAla 280
Db 920 AGCAAGAGAGAGAGCCCGAGCGGCTTGGCCAGAGCCCTTGAGAGAGAGAGAGAGAGCC 979
QY 281 ProAlaProGlnGlnArgIleGlnProProValLysProLeuLeuProProLeuProPro 300
Db 980 CCAGCCCGGAGAGAGAGATTCAGCTCTGCTGAGAGCTCTGCTGCTGCTGCTGCTGCT 1039
QY 301 AspTyrGlyAspGlyTyrValIleProAsnTyrAspAspMetAspTyrTyrPheGlyPro 320
Db 1040 GACTATGGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1099
QY 321 ProProProGlnLysProAspAlaGlnArgIleThrAspGlnGlnLysGlnLysLeuLys 340
Db 1100 CTTCCGCCCCAGAGAGCCCGATGCTGAGCGCCAGAGCGAGAGAGAGAGAGAGAGAG 1159
QY 341 LysProLysLysGluAspSerSerProLysGlnGlnIleThrAspLysTrpAlaValGlnLys 360
Db 1160 AAACCCAAAG 1219
QY 361 GlyLysAspHisLysGlnProArgGlyGlyGlnGlnLysGlnGlnLysGlnLysTrpThrPro 380
Db 1220 GGCAGAGAGACCAAAAG 1279
QY 381 GluLysValLysCysProProIleGlyMetGlnSerHisArgIleGluAspAsnGlnIle 400
Db 1280 GAGAAAGTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1339
QY 401 ArgAlaSerSerMetLeuArgHisGlyLeuGlnIleGlnArgGlyArgLeuAsnMetGln 420
Db 1340 CGAGCTCTCATGCTGCGCCACGCGCTGGGGGACAGCGCGCGCGCTCAACATGTCAG 1399
QY 421 ThrGlyAlaThrGluAspAspThrTyrTrpAspValaTrpCysAlaGluAspAspAlaArg 440
Db 1400 ACCGGTGCACAG 1459
QY 441 ThrGlnTrpIleGlnValaAspThrArgTrpThrTrpArgPheThrGlyValIleThrGln 460
Db 1460 ACCAGTGAATGAGAGTGAACACAGAGAGAGATACCCGTTCAAGGGGTATCACCCAG 1519
QY 461 GlyArgAspSerSerIleHisAspAspPheValThrThrPhePheValGlyPheSerAsn 480
Db 1520 GGCAGAGACTCCAGATCCATGACATTTTGTGACACACTTCTGCTGCTGCTGCTGCT 1579
QY 481 AspSerGlnThrTrpValMetTyrThrAsnGlyTyrGlnGlnMetThrPheHisGlyAsn 500
Db 1580 GACAGCAGACATGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1639
QY 501 ValaAspLysAspThrProValLeuSerGlnLeuProGlnProValaValaIleArgPheIle 520
Db 1640 GTGACAGAGAGACACCCGTGCTGAGTAGAGCTCCAGAGCGGTGGTCTGTTTCATC 1699
QY 521 ArgIleTyrProLeuThrTrpAsnGlySerLeuCysMetArgLeuGlnValaLeuGlyCys 540
Db 1700 CGCATCTACCCACTACCTGAGATGAGAGCTGTGATGATGATGATGATGATGATGATGAT 1759
QY 541 SerValAlaProValTyrSerTyrTyrTrpIleGlnAsnGlnValaIleThrAspAspLeu 560
Db 1760 TCTGTGGCCCTGTCTACAGCTTACGACAGAAATGAGGTGGTCCACCAATGACTGCTG 1819
QY 561 AspPheArgHisIleSerTyrLysAspMetArgGlnLeuMetLysValaValaAsnGlnGln 580
Db 1820 GATTTCCGAGACACAGCTACAGAGACATGGCCAGCTCATAGAGTGGTGAACAGAGAG 1879
QY 581 CysProThrIleThrArgThrTyrSerLeuGlyLysSerArgGlyLeuLysIleTyr 600

Db 1880 TGCCCCACCATCA CCGCCACTTACAGCCTGGGCAAGAGCTCAGAGGCGCTCAAGATCTAT 1939
 Qy 601 AlMeEGluIleSerAspAsnProGlyGluHieGluLeuGlyGluProGluPheArgTy 620
 Db 1940 GCCATGAGATCTCAGACCAACCTGGGGAGCATGAATGGGGAGCCCGATTCCGCTAC 1999
 Qy 621 ThAlGlyIleHieGlyAsnGluValLeuGlyValArgGluLeuLeuLeuLeuMetGln 640
 Db 2000 ACTGCTGGGATCCATGGCAAGAGTCTGGCCGGAAGCTGTGCTGCTGCTCATATGAC 2059
 Qy 641 TyrLeuCyAspArgGlyTyrArgAspGlyAsnProArgValArgSerLeuValGlnAspThr 660
 Db 2060 TACCTGGCCGAGAGTACCGCGATGGGACCAACGCTGTGGCAGCCCTGGTGCAGACACA 2119
 Qy 661 ArgIleHieValValProSerLeuAsnProAspGlyTyrGluValAlaAlaGlnMetGly 680
 Db 2120 CGCATCCACCTGGGCGCTCATGAACTCATGGCTACAGAGGTGGCAGCGCAGATGGCG 2179
 Qy 681 SerGluPheGlyAsnThrAlaLeuGlyLeuTyrThrGluGluGlyPheAspIlePheGlu 700
 Db 2180 TCAAGATTTGGGAATGGGGCGCTGGGACTGGACTGGAGAGGAGGCTTTGACATCTTTGAA 2239
 Qy 701 AspPheProAspPheAsnSerValLeuTyrGlyAlaGluGluValArgLysTyrValProTyr 720
 Db 2240 GATTTCCGGATCTCACTGTGTCTGTGGGAGCTGGAGAGGAAATGGGTCCCTTAC 2299
 Qy 721 ArgValProAsnAsnAsnLeuProIleProGluArgTyrLeuSerProAspAlaThrVal 740
 Db 2300 CGGGTCCCCAACAATAACTTGCCTCATCCGTAACGCTTACCTTGCAGATGCAAGCGTA 2359
 Qy 741 SerThrGluValArgAlaIleIleAlaTyrMetGluLysAsnProPheValLeuGlyAla 760
 Db 2360 TCCACGAGAGTCCGGGCGCATTTGCTGTGATGAGAAAGAACCTTCTGGCTGGAGCA 2419
 Qy 761 AsnLeuAsnGlyGlyGluArgLeuValSerTyrProTyrAspMetAlaArgThrProThr 780
 Db 2420 AATCTGAACGGCGGCGAGCGGCTAGTATCTTACCTTACGATATGGCCCGCAGCTTACC 2479
 Qy 781 GlnGluGlnLeuLeuAlaAlaAlaMetAlaAlaAlaArgGlyGluAspGluVal 800
 Db 2480 CAGAGCAGCTGCTGGCGCAGCCATGGCAGCAGCCGGGGAGGATGAGCAGAGTTC 2539
 Qy 801 SerGluAlaGlnGluThrProAspHieAlaIlePheArgTyrLeuAlaIleSerPheAla 820
 Db 2540 TCCGAGGCCCGAGAGACTCCAGACACGCCATCTTCCGGGCTTGGCATCTTCTTCCGCC 2599
 Qy 821 SerAlaHieLeuThrLeuThrGluProTyrArgGlyGlyCysGlnAlaGlnAspTyrThr 840
 Db 2600 TCCGACACACTTCACTTGAACGAGCCCTTACCGCGAGGCTGCCAAGCCGAGCTACACC 2659
 Qy 841 GlyGlyMetGlyIleValAsnGlyAlaLysTyrAsnProArgThrGlyThrIleAsnAsp 860
 Db 2660 GGGCGCATGGGCACTGTCACACGGGGCAAGTGAACCCCGGACCGGAGCTATCAATGAC 2719
 Qy 861 PheSerTyrLeuHieThrAsnCysLeuGluLeuSerPheTyrLeuGlyCysAspLysPhe 880
 Db 2720 TTCAATTACCTGATACCAACTGCTGAGCTCTCTTCACTGGGCTGTGACAAATTC 2779
 Qy 881 ProHieGluSerGluLeuProArgGluTyrGluAsnAsnLysGlnAlaLeuLeuThrPhe 900
 Db 2780 CCTCATGAGAGTGAAGTCCCGCCCGAGTGGGAGAACAAAGAGCGCTGCTCACCTTC 2839
 Qy 901 MetGluGlnValHieArgGlyIleLysGlyValValThrAspGluGlnGlyIleProIle 920
 Db 2840 ATGAGCAGAGTGCACCGCGCATTAAGGGGTGTGTCGAGCAGACAGGCATCCCAT 2899
 Qy 921 AlaAsnAlaThrIleSerValSerGlyIleAsnHieGlyValLysThrAlaSerGlyGly 940
 Db 2900 GCCAAGCCCACTCTGTGAGTGAATTAATCAAGCGCTGAAGACAGCACTGGTGGT 2959
 Qy 941 AspTyrTyrArgIleLeuAsnProGlyGluTyrArgValThrAlaHieAlaGluGlyTyr 960
 Db 2960 GATTACGCGGAATCTTGAACCGGGGTGAATACCGGCTGACACCCACGCGGAGGGCTAC 3019

Qy 961 ThrProSerAlaLysThrCysAsnValAspTyrAspIleGlyAlaThrGlnCysAsnPhe 980
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 Qy 981 IleLeuAlaArgSerAsnThrLysArgIleArgGluIleMetAlaMetAsnGlyAsnArg 1000
 Db 3080 ATCTGGCTCTGCTCCACTGAGAGCCATCCGGAGATATGAGCCCATGAACGGAGACCG 3139
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 Db 3140 CTTATCCACACATTAACCATCGGCGCTTATGAGCCCCCAAGAGAGCGCTGCAGCAG 3199
 Qy 1021 ArgArgLeuGlnHieArgLeuArgLeuArgAlaGlnMetArgLeuArgArgLeuAsnAla 1040
 Db 3200 CGAGCGCTTACACACCGCTGGCGCTTCCGGGACAGATCGGCTGGCGCGCTCAACGCG 3259
 Qy 1041 ThrThrThrLeuGluProHieThrValProProThrLeuProProAlaProAlaThrThr 1060
 Db 3260 ACCACCACTTGAAGCCCACTGTGCTCCACGCTGCCCTGCCCTGCCCTGCACACACC 3319
 Qy 1061 LeuSerThrThrIleGluProTyrGlyLeuIleProProThrThrAlaGlyTyrGluGln 1080
 Db 3320 CTGAGCATTACCATTAAGCGCTGGGCGCTCATACGCCCAACCGCTGGTGGAGAG 3379
 Qy 1081 SerGluThrGluThrTyrThrGluValValThrGluPheGlyThrGluValGluProGlu 1100
 Db 3380 TCGAGACTGAGACCTTACACAGAGGTGTGACAGAGTTGGGACCGAGGTGGAGCGCCGAG 3439
 Qy 1101 PheGluThrLysValGluProGluPheGluThrGlnLeuGluProGluPheGluThrGln 1120
 Db 3440 TTGGGACCAAGGTGAGCGCCGAGTTTGAACCCAGTTGAGCTGTGAGTTCCAGACCAAG 3499
 Qy 1121 LeuGluProGluPheGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 1140
 Db 3500 CTGGAAACCGAGATTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATGACACTGGC 3559
 Qy 1141 GlnAlaPheProPheThrThrValGluThrTyrThrValAsnPheGlyAspPhe 1158
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RESULT 2
 ID ACC50076 strand: cDNA; 3935 BP.
 AC ACC50076;
 XX
 AC 12-JUN-2003 (first entry)
 XX
 DT
 XX
 DE Breast cancer associated cDNA sequence SEQ ID NO:1.
 XX
 KW Human; breast cancer; cytostatic; gene therapy; gene; ss.
 XX
 OS Homo sapiens.
 XX
 EN W02003004989-A2.
 XX
 PD 16-JAN-2003.
 XX
 PF 21-JUN-2002; 2002WO-US019669.
 XX
 PR 21-JUN-2001; 2001US-0299887P.
 XX
 PR 27-JUN-2001; 2001US-0301572P.
 XX
 PR 18-JUL-2001; 2001US-0306501P.
 XX
 PR 25-SEP-2001; 2001US-0325002P.
 XX
 PR 05-MAR-2002; 2002US-0362585P.
 XX
 PR 14-MAY-2002; 2002US-0380391P.
 XX
 PA (MILL-) MILLENIUM PHARM INC.
 XX
 PI Lillie J, Gannavarapu M, Glact K, Hoersh S, Kamatkar S;
 PI Mertens M, Monahan JE, Myer V, Wang Y, Xu Y, Zhao X, Meyers RE;
 PI Bast RC, Hortobagyi GN, Pusztai L, Meric F, Sahin A, Mills GB;

Db 1760 TCTGTGACCCCTGCTCAAGCTACTACGACAGAAATGAGGTGGTGGCCACGATGACCTG 1819
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 Db 1820 GAATTTCCGGACACACAGCTCAAGAGACATGCGCAGCTCATGAAGGTGTGAACGAGAG 1879
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 QY 601 AlMeGluIuIeserAapAnProGlylyuHIsGluLeuGlyGluProGluPheArGTYr 620
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 QY 701 AAspPheProAspLeuAsnSerValLeuTrpGlyAlaGluGluValAsnTrpValProTYr 720
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 Db 2540 TTCGAGGCCCGAGAGACTCCAGACCAAGCATCTTCGCGTGGCTTCCTCTCCCTCGCC 2599
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 Db 2600 TCCGCAACCTCACTTGAACGAGCCTTACCGGAGGCTGCGCAAGCCCGAGCTACACC 2659
 QY 841 GlyGlyMeGlylyleValaAnglyAlaAlaYrTrpAsnProArGThrGlyThrIleAsnAr 860
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 QY 861 PheSerTYrleuHIsThrAsnCyAsnGluLeuLeuSerPheTYrleuGlyCyAsnAllysphe 880
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 Db 2840 ATGAGACAGGTGACCGCGCATTTAAGGGGTGTGTACGAGACAGCAAGCAATCCCATTT 2899

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 Db 2960 GAATTCGGCGAATCTTGAACCCGGGTGAGTACCGGCTGACACCCACGAGGGGCTAC 3019
 QY 961 ThrProSerAlaIlybThrCYsAsnValaAspTYrAspIleGlyAlaThrGlnCYsAsn 980
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 QY 981 IleuValArGSerAsnTrpLybArgIleHIsGlyIleMeAlaMeAsnGlyAsnArG 1000
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 Db 3140 CCTATCCACACATTAAGCCATGCGCCTTATGACCCCCCAACAGCGAGCTTGACAG 3199
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 Db 3200 CGAGCCTCAACACACCGCTGGGGCTTGGGCAAGATCGGGCTGGCGCTCAACGCGC 3259
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 QY 1061 LeuSerThrThrIleGluProTrpGlyLeuIleProProThrThrAlaGlyTrpGluGlu 1080
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 QY 1121 LeuGluProGluPheGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 1140
 Db 3500 CTGGAACCCGAGTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGATGACCTGAC 3559
 QY 1141 GlnAlaPheProPheThrThrValGluThrTYrThrValaAsnPheGlyAspPhe 1158
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 RESULT 3
 ID ADF90653
 ID ADF90653 standard; DNA; 3935 BP.
 AC ADF90653;
 DT 26-FEB-2004 (first entry)
 XX
 DE Human hepatic-fibrosis disease marker SEQ ID 115.
 KW Hepatic fibrosis; marker; chronic hepatitis; liver cirrhosis;
 KW hepatic carcinoma; human; de.
 XX
 OS Homo sapiens.
 OS
 PN JP2003259877-A.
 PD 16-SEP-2003.
 XX
 PF 11-MAR-2002; 2002JP-00065013.
 XX
 PR 11-MAR-2002; 2002JP-00065013.
 XX
 PA (SUNU) SUMITOMO SEIRAKU KK.

Db 1880 TGGCCCACTCATCCGCCACTTACAGCTGGGCAAGAGCTCAGAGGCTCAAGATCTAT 1339
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 Qy 701 AaPheProAbaPnAbaPnSerValIleuTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 720
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 Qy 761 AaNIleuAbaPnGlyGlyGluArgIleuValSerTyTyTyTyTyTyTyTyTyTyTyTyTyTy 780
 Db 2420 AATCTGAACGGCGGCGAGCGGCTAGTATCTTACCTCAGATATGGCCCGCAGCCTTACC 2479
 Qy 781 GlnGluGluIleuValAlaAlaIleMetAlaAlaAlaArgGlyGluAbaPnProGluVal 800
 Db 2480 CAGGACAGCTGCTGGCGGCGAGCCATGGCAGAGCCCGGGGAGGATGAGAGCGAGTCC 2539
 Qy 801 SerGluAlaGlnIleuThyProAbaPnAlaAlaIlePheArgTyTyTyTyTyTyTyTyTyTyTy 820
 Db 2540 TCCAGAGCCAGGAGACTCCAGACAGCCATCTCCGGGCTGCTGCTGCTGCTGCTGCTGCT 2599
 Qy 821 SerAlaNIleuThyThyThyThyThyThyThyThyThyThyThyThyThyThyThyThy 840
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 Qy 841 GlyGlyMetGlyTy 860
 Db 2660 GGGGCGATGGGCTGCTGCAACGGGGCCAAAGTGAAACCCCGGAGCCGAGCTATCATGAC 2719
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 Db 2720 TTCTAGTTACTGATCAACAGCTGAGCTGAGCTCTCTTCACTGGGCTGTGACAGGTTCC 2779
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 Qy 941 AaPtyTy 960

Db 2960 GATTACTGGGAACTTGAACCCGGGTGAGTACCGGGTGAACGCCAGCGGAGGGCTAC 3019
 Qy 961 ThrProSerAlaIleThyThyThyThyThyThyThyThyThyThyThyThyThyThyThyThy 980
 Db 3020 ACCCCAGGCGCCAAAGACTGCAATGTGACTATGACATGGGGCCACTGAGCACTTC 3079
 Qy 981 IleuValAArgSerAbaPnTy 1000
 Db 3080 ATCTTGCTGCTTCAACTGGAAGCCATCCGGAGATCATGGCCATGAAAGGGAACCGG 3139
 Qy 1001 ProIleProIleAbaPnProSerArgProMetThyProGlnGlnArgIleuGlnGln 1020
 Db 3140 CTTATCCACATTAACCATCGGCTTATGACCCCAACAGAGCGCTGAGCAG 3199
 Qy 1021 ArgArgIleuGlnNIleArgIleuArgIleuArgIleuMetArgIleuArgIleuAbaPn 1040
 Db 3200 CGAGCCTTCAACACCGCTGCGGCTCGGGCAGAGATCGGCTGCGGCGCTCAACGCGC 3259
 Qy 1041 ThrThyThyThyThyThyThyThyThyThyThyThyThyThyThyThyThyThyThy 1060
 Db 3260 ACCACCACTTGAAGCCCACTGCTGCTCCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3319
 Qy 1061 LeuSerThyThyThyThyThyThyThyThyThyThyThyThyThyThyThyThyThyThy 1080
 Db 3320 CTGAGCACTACCATTAAGCTTGGGCTCATACCGCCCAACCGCTGCTGAGAG 3379
 Qy 1081 SerGluThyGluThyTy 1100
 Db 3380 TCGAGACTGAGACTTACAGAGGTGTGACAGATTTGGGACCGAGGTGAGCGCCGAG 3439
 Qy 1101 PheGluThyTy 1120
 Db 3440 TTGGGACCAAGGTGAGCCCGAGTTTGAAGCCAGTGTGAGCTGAGTTCGAGACCAG 3499
 Qy 1121 LeuGluProGluPheGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 1140
 Db 3500 CTGGAACCGGAGTTTGAAG 3559
 Qy 1141 GlnAlaPheProPheThyThyValGluThyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 1158
 Db 3560 CAGGCACTTCCCTTCAACAGTAGAGACTTACAGTAGAGACTTGGGAGCTTC 3613
 RESULT 4
 ADZ26196
 ID ADZ26196 standard; DNA; 3935 BP.
 AC ADZ26196;
 DT 16-JUN-2005 (first entry)
 XX
 DE Human gene Nb1a21871 nucleotide sequence SEQ ID NO:162.
 XX
 KW microarray; nervous system tumor; cytostatic; neoplasm;
 KM neurological disease; gene; ds; chromosome-7.
 XX
 OS Homo sapiens.
 XX
 PN WO2005030959-A1.
 XX
 PD 07-APR-2005.
 XX
 PF 24-SEP-2004; 2004WO-JP014441.
 XX
 PR 25-SEP-2003; 2003US-0505614P.
 XX
 PA (CHIB-) CHIBA PREPECTURE.
 PA (HISM) HISAMITSU PHARM CO LTD.
 PA (NIGA) NGK INSULATORS LTD.
 XX
 PI Nakagawara A, Ohira M, Ishii S, Goto T, Kubo H, Hirata T,
 PI Yoshida Y, Yamada S,
 XX
 WP1; 2005-273381/28.

QY 501 ValAspLysAspThrProValLeuSerGluLeuProGluProValAlaArgPheIle 520
 DB 1640 GTGGACAAAGGACACACCGGTGAGTGAAGCTCCAGAGCCGGGTGGTCTCTTCATC 1699
 QY 521 ArgIleTyrProLeuThrTrpAengIYSerLeuCYmeArGleuGluValIleuGlyCYs 540
 DB 1700 CGCATCTACCACTCACTGGAATGGACGCTGTGCATGGCTGGAGAGTGGCTGGGGTGC 1759
 QY 541 SerValAlaProValTyrSerTyrTyrAlaGlnAengIValAlaThrAspAspLeu 560
 DB 1760 TCTGTGGCCCTCTCTCAAGCTACTACGCAAGAAATGAGTGTGGCCAGTGTGACTG 1819
 QY 561 AspPheArgHisIleSerTyrLysAspMetArgIleLeuMetLysValValAengIuGlu 580
 DB 1820 GATTTCGGACACACAGCTACAGAGACATGCGCAGCTCATGAAGGTGGTGAACGAGAG 1879
 QY 581 CysProThrIleThrArgThrTyrSerLeuGlyLysSerSerArgGlyLeuLysIleTyr 600
 DB 1880 TGGCCCACTACACCGGCACTTACAGCTGGGCAAGAGCTCAGAGGGCTCAAGATCTAT 1939
 QY 601 AlaMetGluIleSerAspAsnProGlyGluHisGluLeuGlyGluProGluPheArgTyr 620
 DB 1940 GCCATGAGATCTCAAGCAACCTGGGGAGCATGAATGGGGAGCCCGAGTTCCGCTAC 1999
 QY 621 ThrAlaGlyIleHisGlyAengIValIleuGlyArgGluLeuLeuLeuLeuMetGln 640
 DB 2000 ACTGCTGGAGTCCATGAGCAAGAGTGTGGCCGAGAGCTGTGCTGCTGCATGACGAG 2059
 QY 641 TyrLeuCYsArgGlyTyrArgAspGlyAsnProArgValArgSerLeuValGlnAspThr 660
 DB 2060 TACCTTGGCGAGAGTACCGCGATGGGAAACCCAGTGTGGCAGCTGTGGCGAGGACAC 2119
 QY 661 ArgIleHisLeuValProSerLeuAsnProAspGlyTyrGlyValAlaAengIuMetGly 680
 DB 2120 CGCATCCACTGGTGGCTCCTACATGAACCTCATGAGCTGACAGGTGGCAGCGCAGATGG 2179
 QY 681 SerGluPheGlyAsnThrAlaLeuGlyLeuThrThrGluGluGlyPheAspIlePheGlu 700
 DB 2180 TCAGATTTGGGAATCGGGGCTGGGACTGTGAGCTGAGAGGGCTTTGACATCTTTGAA 2239
 QY 701 AspPheProAspLeuAsnSerValLeuTyrGlyAlaGluGlyValArgTyrProTyr 720
 DB 2240 GATTTCCCGGATTTCACTCTGTGCTGTGGGAGCTGAGAGAGGAAATGGGTCCCTTAC 2299
 QY 721 ArgValProAspAsnAsnLeuProIleProGluArgTyrLeuSerProAspAlaThrVal 740
 DB 2300 CCGGTCTCCCAACAATACTTGCCCATCCCTGAACGCTTACCTTTCGCAATGCCAGTGA 2359
 QY 741 SerThrGluValArgAlaIleIleAlaIleThrMetGluLysAsnProPheValLeuGlyAla 760
 DB 2360 TCCACGAGAGTCCGGGCACTCATCTGCTGATGGAAGAAACCTTTCGTGTGGAGAGA 2419
 QY 761 AsnLeuAsnGlyGlyValArgLeuValSerTyrProTyrAspMetAlaArgThrProThr 780
 DB 2420 AATCTGAAGCGGCGGAGGCTAGTATCTTACCTTACGATATGAGCCCGCAGCTTAC 2479
 QY 781 GlnGluGlnLeuLeuAlaAlaMetAlaAlaAlaArgGlyGlyLeuAspGluAspGluVal 800
 DB 2480 CAGGAGCACTGCTGGCCGACGATGGCAGAGCCGGGGAGGATGAGGACGAGGTGC 2539
 QY 801 SerGluAlaGlnGluThrProAspHisAlaIlePheArgThrLeuAlaIleSerPheAla 820
 DB 2540 TCCGAGGCCAGAGACTCCAGACACGCGCATCTTCGGGTGGCTTGCATCTCTTCGCGC 2599
 QY 821 SerAlaHisLeuThrLeuThrGluProTyrArgGlyGlyCYsGlnAlaGlnAspTyrThr 840
 DB 2600 TCCGACACACTCACTTGAACGAGCTTACCGCGAGGCTGCCAAGCCAGAGACTACAC 2659
 QY 841 GlyGlyMetGlyTyrValAengIValAlaTyrTrpAsnProArgThrGlyThrIleAsnAsp 860
 DB 2660 GGGCGCATGGGCTCTCAACGCGGCAAGTGGAAACCCCGGAGCTGATCATATGAC 2719
 QY 861 PheSerTyrLeuHisIleThrAsnCYsValuGluLeuSerPheTyrIleuGlyCYsAspLysPhe 880

DB 2720 TTCAGTTACCTGCATACCACTGCTCGAGCTCTCTTACTTGGGCTGTACAAGTTC 2779
 QY 881 ProHisGluSerGluLeuProArgGluTyrGluAsnAsnLysGluAlaLeuLeuThrPhe 900
 DB 2780 CCTCATGAGATGAGCTGCGCCCGAGTGGAGAAACAAGAGAGCGCTGCTCACTTC 2839
 QY 901 MetGluGlnValHisArgGlyTyrLeuGlyValValThrAspGluGlnGlyIleProIle 920
 DB 2840 ATGAGCAGGTGCACCGCGCATTTAAGGGGTGTGTACGAGCAGACAGCATCCCAATT 2899
 QY 921 AlaAsnAlaThrIleSerValSerGlyTyrIleAsnHisGlyValIleThrThrIleSerGly 940
 DB 2900 GCCAACGCCACATCTCTGTGATGGCATTAATCACGGGTGAAGACAGCAGTGGTGG 2959
 QY 941 AspTyrTrpArgIleLeuAsnProGlyGluTyrArgValThrAlaHisAlaGluGlyTyr 960
 DB 2960 GATTACTGGCGAATCTTGAACCCGGGTGATACCGGTGACAGCCACCGGAGGGCTTAC 3019
 QY 961 ThrProSerAlaLysThrCYsAsnValAspTyrAspIleGlyValThrGlnCYsAsnPhe 980
 DB 3020 ACCCCGAGCGCAAGACTTGCATATGTTGACTATGACATCGGGGCCACTCAGTGCAACTTC 3079
 QY 981 IleLeuAlaArgSerAsnThrLysArgIleArgGluIleMetAlaMetAsnGlyAsnArg 1000
 DB 3080 ATCTGGCTCGCTCCAACTGAAAGGCATCCGGAGATATGACCATGAACGAGAACCGG 3139
 QY 1001 ProIleProHisIleAspProSerArgPromeThrProGlnGlnArgLeuGlnGln 1020
 DB 3140 CCTATCCACACATATGACCCATTCGGCCCTTATGACCCCCCAACAGAGAGCGCTCGAGCG 3199
 QY 1021 ArgArgLeuGlnHisArgLeuArgLeuArgAlaGlnMetArgLeuArgLeuAsnAla 1040
 DB 3200 CGACGCTCAACACCGCTCGGCTTCGGGACAGATCGGCTGGCGGCTCAACGCGC 3259
 QY 1041 ThrThrThrLeuGlyProHisThrValProPheThrLeuProAlaProAlaThrThr 1060
 DB 3260 ACCACACCTTAGGCCCCCACTGCTCTCCAGCTGCCCCCTGCTGCAACACC 3319
 QY 1061 LeuSerThrThrIleGluProTyrGlyLeuIleProProThrThrAlaGlyTyrGluGln 1080
 DB 3320 CTGAGACATACATAGAGCTTGGGGCCCTCATACCGCAACACCGCTGGTGGAGGAG 3379
 QY 1081 SerGluThrGluThrTyrThrGluValValThrGluPheGlyThrGluValGluProGlu 1100
 DB 3380 TCGGAGACTGAGACCTACACAGAGGTGTGACAGAGTTTGGGACCGAGGTGAGCCCGAG 3439
 QY 1101 PheGlyThrLysValGluProGluPheGluThrGlnLeuGluProGluPheGluThrGln 1120
 DB 3440 TTTGGACCAAGTGAAGCCGAGTTTGAGACCCAGTTGAGCCTGAGTTGAGACCCAG 3499
 QY 1121 LeuGluProGluPheGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 1140
 DB 3500 CTGGAACCGGATTTGAGGAAGAAGAGAGAGAGAGAGAGAGATACCACTGGC 3559
 QY 1141 GlnAlaPheProPheThrThrValGluThrTyrThrValAsnPheGlyAspPhe 1158
 DB 3560 CAGGATTCCTCCCTTCAACAGATGAGACTTACAGATGAACTTTGGGGACTTC 3613
 DB
 RESULT 5
 ID AD086121
 ID AD086121 standard; cDNA; 3914 BP.
 AC AD086121;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Human tumour-associated antigenic target (TAT) cDNA sequence #2993.
 XX
 KW human; tumour-associated antigenic target; TAT; cytosstatic; gene therapy;
 KW cancer; cell proliferative disorder; gene; ss.
 XX
 OS Homo sapiens.

PN	XX	WO2004060270-A2.
PN	XX	
PD	XX	22-JUL-2004.
PF	XX	15-OCT-2003; 2003WO-US029126.
PF	XX	18-OCT-2002; 2002US-0418988P.
PR	XX	(GENTH) GENENTECH INC.
PA	XX	(WOTD/) WU T D.
PA	XX	(ZHOU/) ZHOU Y.
PI	XX	Wu TD, Zhou Y;
DR	XX	WPI, 2004-534300/51.
PT	XX	New nucleic acid molecule and encoded polypeptide, for diagnosing, preventing or treating cell proliferative disorders such as cancer.
XX	XX	Claim 1; SEQ ID NO 2993; 5504bp; English.
XX	XX	
XX	XX	The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that hybridises to (a) - sequence identity to (a) - (c); or (e) a sequence that hybridises to (a) - (c). Also described: (1) an expression vector comprising the above nucleic acid; (2) a host cell comprising the above expression vector; (3) a process for producing a polypeptide; (4) an isolated polypeptide comprising: (a) an amino acid sequence encoded by any of the above nucleotide sequences; (b) an amino acid sequence encoded by the full-length coding region of the above nucleotide sequences; or (c) a sequence having at least 80% identical to (a) or (b); (5) a chimeric polypeptide comprising the above polypeptide fused to a heterologous polypeptide; (6) an isolated antibody that binds to the above polypeptide; (7) a process for producing the antibody; (8) an isolated oligopeptide that binds to the above polypeptide; (9) a tumour-associated antigenic target (TAT) binding organic molecule that binds to the above polypeptide; (10) a composition of matter comprising the above (chimeric) polypeptide, antibody, oligopeptide or TAT binding organic molecule, in combination with a carrier; (11) an article of manufacture comprising a container and the composition of matter contained within the container; (12) methods of inhibiting the growth of a cell that expresses the above protein, where the growth of the cell is at least in part dependent upon a growth potentiating effect of the above protein; (13) a method of potentiating effect of the above protein; (14) a method of determining the presence of a protein in a sample suspected of containing the protein described above; (15) methods of diagnosing the presence of a tumour in a mammal; (16) a method for treating or preventing a cell proliferative disorder associated with increased expression or activity of the above protein; and (17) a method of binding an antibody, oligopeptide or organic molecule to a cell that expresses the protein described above. The TAT sequences have cytostatic activities, and can be used in gene therapy. The composition and methods are useful for diagnosing, preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative disorder or cancer. The present sequence represents a human TAT cDNA sequence from the present invention.
XX	XX	
XX	XX	Sequence 3914 BP; 903 A; 1242 C; 1184 G; 585 T; 0 U; 0 Other;
XX	XX	
XX	XX	Alignment Scores:
XX	XX	
XX	XX	Pred. No.: 4,25e-290 Length: 3914
XX	XX	Score: 6264.00 Matches: 1156
XX	XX	Percent Similarity: 100.0% Conservative: 2
XX	XX	Best Local Similarity: 99.8% Mismatches: 0
XX	XX	Query Match: 99.9% Indels: 0
XX	XX	DB: 12 Gaps: 0
XX	XX	
XX	XX	US-10-642-946-3 (1-1158) x ADQ86121 (1-3914)

QY 301 AspTyrGlyAspGlyTyrValIleProAsnTyrAspMetAspTyrTyrPheGlyPro 320
DB 1040 GACATATGTATGTTACGTATGATCCCAACTACATACATGACATTAATCTTGGGCT 1099
QY 321 ProProGlnGlyProAspAlaGluArgGlnThrAspGluGluGluGluLeuLys 340
DB 1100 CTCTCCGCCCAAGAACCCGATGCTGAGCGCCAGACACAGAGAGAGAGAGAGAGAG 1159
QY 341 LysProLysLysGluAspSerSerProLysGluGluGluGluGluGluGluGluLys 360
DB 1160 AAACCCCAAAAGAGAGACACAGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1219
QY 361 GlyLysAspHisLysGluProArgLysGluGluGluGluGluGluGluGluGluGlu 380
DB 1220 GGCAGAGACCAAAAG 1279
QY 381 GlyLysValLysCysProProIleGlyMetGlySerHisArgIleGluAspAsnGlnIle 400
DB 1280 GAGAAAGTCAAGTGTCCCCCATTTGGATGAGTCAACCGTATTGAGAGACACAGATC 1339
QY 401 ArgAlaSerSerMetLeuArgHisGlyLeuGlyAlaGlnArgGlyArgLeuAsnMetGln 420
DB 1340 CGAGCCCTCCATGCTGCGCCACAGCGCTGGGGGACAGCGCGGCTCAACATCAG 1399
QY 421 ThrGlyAlaThrGluAspAspTyrTyrAspGlyAlaTyrCysAlaGluAspAspAlaArg 440
DB 1400 ACCGGTCCCACTAG 1459
QY 441 ThrGlnTyrIleGluValAspThrArgArgThrThrArgPheThrGlyValIleThrGln 460
DB 1460 ACCCATGATTAAGGTGGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1519
QY 461 GlyArgAspSerSerIleHisAspAspPheValThrThrPhePheValGlyPheSerAsn 480
DB 1520 GGCAG 1579
QY 481 AspSerGlnThrThrValMetTyrThrArgGlyTyrGluGluMetThrPheHisGlyAsn 500
DB 1580 GACAGCAGACATGGGTGATGTACACAGCGCTATAGAGAAATGACCTTTCATGGGAC 1639
QY 501 ValAspLysAspThrProValLeuSerGluLeuProGluProValValAlaArgPheIle 520
DB 1640 GTGGACAGAGAGACACCCGCTGCTGAGTGAAGCTCCAGAGCGGTGGTGGCTTTCATC 1699
QY 521 ArgIleTyrProLeuThrTyrAsnGlySerLeuCysMetArgLeuGluValLeuGlyCys 540
DB 1700 CGCATCAACCACTCACTGGAATGGCAGCTGTGACGCTGGAGGTGGTGGGTGC 1759
QY 541 SerValAlaProValTyrSerTyrTyrAlaGlnAsnGluValAlaAlaThrAspAspLeu 560
DB 1760 TCTGTGGCCCTCTCTACAGCTACTACAGACAGAGATGAGGTGGTGGTGGTGGTGG 1819
QY 561 AspPheArgHisHisSerTyrLysAspMetArgGlnLeuMetLysValValAlaGlnGlu 580
DB 1820 GATTTCCGAGACACAGAGCTCAAGAGACATGCCAGCTTCATGAAGGTGGTGGTGGTGG 1879
QY 581 CysProThrIleThrArgThrTyrSerLeuGlyLysSerSerArgGlyLeuLysIleTyr 600
DB 1880 TGGCCACACATCACCCGCACTTACAGCTGGGCAAGAGCTCACAGAGCTCAAGATCTAT 1939
QY 601 AlaMetGluLysSerAspAsnProGlyGluHisGluLeuGlyGluProGluPheArgTyr 620
DB 1940 GCCATGAGATCTTCAGACCACTGGGAGACATGAACTGGGAGAGCCCGATTCCTGCTAC 1999
QY 621 ThrAlaGlyIleHisGluAsnGluValLeuGlyArgGluLeuLeuLeuLeuMetGln 640
DB 2000 ACTGCTGGATCCATGAGCAAGAGTCTGGGCGAGAGCTGTGCTGCTGCTGCTGCTGAG 2059
QY 641 TyrLeuCysArgGluTyrArgAspGlyAsnProArgValArgSerLeuValGlnAspThr 660
DB 2060 TACCTGTGCGAGAGATCCCGATGGAGACCCAGCTGTGCGAGCTGTGCGAGGACACA 2119

QY 661 ArgIleHisLeuValProSerLeuAsnProAspGlyTyrGluValAlaAlaGlnMetGly 680
DB 2120 CGCATCCACTGGTGGCTTCTACATGAACCTGATGGCTACAGAGTGGCAGAGAGAGG 2179
QY 681 SerGluPheGlyAsnThrAlaLeuGlyLeuTyrThrGluGluGlyPheAspIlePheGlu 700
DB 2180 TCAGAGTTGGGAAGTGGGGCTGGGAGCTGTGAGATGAGAGAGGCTTTGACATCTTGA 2239
QY 701 AspPheProAspLeuAsnSerValLeuTyrGlyAlaGluGluArgLysTyrValProTyr 720
DB 2240 GATTTCCCGGATCTCACTCTGTGCTGGGGAGCTGAGGAGAGAGAAATGGGCTCCCTAC 2299
QY 721 ArgValProAsnAsnLeuProIleProGluArgTyrLeuSerProAspAlaThrVal 740
DB 2300 CGGGTCCCAAAATTAATTTGCCATCCCTGAAGCGTACTTTCGCAATGCGCAGAGTA 2359
QY 741 SerThrGluValArgAlaIleIleAlaTyrMetGluLysAsnProPheValLeuGlyAla 760
DB 2360 TCCACGAGAGTCCGGGCCATCATTTGCTGATGAGAGAGAGAGAGAGAGAGAGAGAG 2419
QY 761 AsnLeuAsnGlyGlyGluArgLeuValSerTyrProTyrAspMetAlaArgThrProThr 780
DB 2420 AATCTGACCGCGGAGCGGCTAGTATCTTACCTCTACGATATGGCCCGCAGCGCTAC 2479
QY 781 GlnGluGluLeuLeuValAlaAlaMetAlaAlaAlaArgGlyGluAspGluAspGluVal 800
DB 2480 CAGAGCAGCTGTGGCCCGGACATAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2539
QY 801 SerGluAlaGlnGluThrProAspHisAlaIlePheArgTyrLeuAlaIleSerPheAla 820
DB 2540 TCCGAGAGCCAGAGAGATCCAGACAGCCATTTCCGGTGGCTTCCATCTCTCCGCC 2599
QY 821 SerAlaHisLeuThrLeuThrGluProTyrArgGlyGlyCysGlnAlaGlnAspTyrThr 840
DB 2600 TCCGACACCTCACTTGAACCGAGCCCTACCGGGAGAGCTGCCAAAGCCAGACTACAC 2659
QY 841 GlyGlyMetGlyIleValAsnGlyAlaLysTyrAspProArgThrGlyThrIleAsnAsp 860
DB 2660 GCGGAGTGGGCTGTCTCAACGGGGCCAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 2719
QY 861 PheSerTyrLeuHisThrAsnCysLeuGluLeuSerPheTyrLeuGlyCysAspLysPhe 880
DB 2720 TTCAGTTACCTGATACCAAGTCCCTGAGCTCTCTTCTACCTGGGCTGTGACAGATTC 2779
QY 881 ProHisGluSerGluLeuProArgGluTyrGluAsnAsnLysGluAlaLeuLeuThrPhe 900
DB 2780 CCTCATAGAGTGAAGCTGCCCGCGAGTGGAGAAACAAAGAGAGCGCTGCTCACCTTC 2839
QY 901 MetGluGluValHisArgGlyIleLysGlyValValThrAspGluGlnGlyIleProIle 920
DB 2840 ATGAGCAGAGTGCACCGCGCATTAAGGGGTGTGACGAGACAGAGAGAGAGAGAGAGAG 2899
QY 921 AlaAsnAlaThrIleSerValSerGlyIleAsnHisGlyValLysThrAlaSerGlyGly 940
DB 2900 GCCAGGCCACATCTCTGATGAGTGCATTAATCAGCGCTGAAGACAGCAGTGGTGGT 2959
QY 941 AspTyrTyrArgGluLeuAsnProGlyGluTyrArgValThrAlaHisAlaGluGlyTyr 960
DB 2960 GATTAATCGGAGATCTTGAACCGGGGTGAGTACCGGTGACAGCCACCGAGGGCTAC 3019
QY 961 ThrProSerAlaLysThrCysAsnValAspTyrArgIleGlyValaThrGlnCysAsnPhe 980
DB 3020 ACCCGAGAGCCAAAGCTGGCAATGTGACTATGATATGGGGGCCACTGATGCAATCTC 3079
QY 981 IleLeuAlaArgSerAsnTyrLysArgIleArgGluIleMetAlaMetAsnGlyAsnArg 1000
DB 3080 ATCTGCTGCTGCTCCAACTGGAAGCCATCCGGAGATGATAGGCCATGAACGGAGACCG 3139
QY 1001 ProIleProHisIleAspProSerArgProMetThrProGlnGlnArgArgLeuGlnGln 1020
DB 3140 CCTATCCACACATTAACCATTCGCGCTATGAGACCCCAACAGAGAGAGCGCTGAGAGAG 3199
QY 1021 ArgArgLeuGlnHisArgLeuArgLeuArgAlaGlnMetArgLeuArgArgLeuAsnAla 1040

DB 3200 CGAAGCCCTCAACACCGGCTTGGGGCTTGGGGCAAGATCGGCTGGGGCTTCAAGCC 3259
QY 1041 ThrThrThrLeuGlyProHisThrValProProThrLeuProAlaProAlaThrThr 1060
DB 3260 ACCACCAACCTGAGCCCGCCACACTGCTCCCAAGCTGCCCCCTGCCCCCAACCC 3319
QY 1061 LeuSerThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 1080
DB 3320 CTGAGACATCAATAGAGCCCTGGGGCTTCAATACCGCAACACCGCTGGGAGAG 3379
QY 1081 SerGluThrGluThrThrThrGluValThrThrGluThrGluValGluProGlu 1100
DB 3380 TCGAGACACGAGACCTACACAGAGGTGTGACAGACTTTGGACCGAGGTGAGCCGAG 3439
QY 1101 PheGlyThrLysValGluProGluPheGluThrGluLeuGluProGluPheGluThrGlu 1120
DB 3440 TTTGGGACCAAGGTGAGCCCGAGTTTGAAGCCAGTTGAGCCTGAGTTTGAAGCCAG 3499
QY 1121 LeuGluProGluPheGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 1140
DB 3500 CTGGAACCCGAGTTGAG 3559
QY 1141 GlnAlaPheProPheThrThrValGluThrThrValAsnPheGlyAspPhe 1158
DB 3560 CAGGCTTCCCTTCAACAGTAGAGACTTACACAGTGAACCTTTGGGACTTC 3613
RESULT 7
ADR44022
ID ADR44022 standard; DNA; 4125 BP.
AC ADR44022;
XX 18-NOV-2004 (first entry)
DT
DE Human colon tumour associated gene clone-33 SEQ ID NO:32.
XX
XX cancer; tumour; breast cancer; lung cancer; colon cancer; kidney cancer;
KM antibody; cytostatic; gene therapy; human; colon tumour tissue;
KM colon tissue; gene; db.
OS Homo sapiens.
XX
XX MO2004074506-A2.
PN
PD 02-SEP-2004.
XX
XX 30-JAN-2004; 2004WO-US003030.
XX
XX 13-FEB-2003; 2003US-044790P.
XX
XX (MERC-) MERGEN LTD.
XX
XX Hu Q, Peng A, Liu B, Love JR, Hao X, Ren W, Sheng Z;
XX
XX WPI; 2004-635589/61.
PT
PT Diagnosing and treating a cancer, e.g. breast, lung, colon, or kidney
XX cancer, comprises detecting and blocking the over expression of a gene of
XX a protein found in breast, lung, colon, or kidney tissue.
XX
XX Claim 22; SEQ ID NO 32; 220pp; English.
XX
XX The present invention describes a method for diagnosing and treating a
XX cancer, e.g. breast, lung, colon, or kidney cancer. The method comprises
XX detecting and blocking the over expression of a gene of a protein found
XX in breast, lung, colon, or kidney tissue. Also described is an antibody
XX or binding portion of an antibody that specifically binds a protein found
XX in breast tissue, lung tissue, colon tissue, or kidney tissue. The
XX antibody has cytostatic activity, and can be used in gene therapy. The
XX methods, antibodies, polynucleotides and polypeptides from the present
XX invention are useful for detecting, diagnosing, preventing and treating
XX cancer, e.g. breast, lung, colon, or kidney cancer. The present sequence

CC represents a nucleotide sequence given in the present invention, which is
CC over expressed in human colon tumour tissue. N.B. All 385 sequences
CC referenced in this patent are detailed in the US provisional application
CC SN 60/447,900, filed 02/13/2003. In this application only one sequence,
CC representing the longest sequence of each of the 65 clones is listed in
CC Appendix A (and given as SEQ ID NO:1 to 65 in the Sequence listing).
XX

SQ Sequence 4125 BP; 967 A; 1321 C; 1227 G; 610 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4,476-290	Length:	4125
Score:	6264.00	Matches:	1156
Percent Similarity:	100.0%	Conservative:	2
Best Local Similarity:	99.84	Mismatches:	0
Query Match:	99.84	Indels:	0
DB:	13	Gaps:	0

US-10-642-946-3 (1-1158) x ADR44022 (1-4125)

QY 1 MetAlaIaValArgGlyAlaProLeuLeuSerCysLeuLeuAlaLeuLeuAlaLeuCys 20
DB 306 ATGGCGGCGGTGCGGGGCGCCCTGCTCACTGCTCTGCGCTTGTGCTGCTGCTGCTGCT 365
QY 21 ProGlyGlyAspProGluThrValLeuThrAspAspGluLeuGluPheLeuGluGly 40
DB 366 CCGGAGGGGCGCGCGAGCGGTGCTGACCGAGCGAGATGAGAGAGATTCTGAGGGGC 425
QY 41 PheLeuSerGluLeuGluProGluProAlaAspAspValGluAlaProProProPro 60
DB 426 TTCTGTGAGAGCTGAGACCTGAGCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 485
QY 61 GluProThrProArgValArgGlyAlaGlnAlaGlyGlyLysProGlyLysAspProGly 80
DB 486 GAGGCCACCCCGGGGTCCGAAAAGCCAGCGGGGGGCGAAGCCAGGAGAGGCGCAAGG 545
QY 81 ThrAlaAlaGluValProProGluLysThrLysAspLysGlyLysGlyLysLysAsp 100
DB 546 ACGGCGCGAGAGTGTCTCCGGAAGAAGCAAGAGCAAGAGAGAGAGAGAGAGAGAGAGAG 605
QY 101 LysGlyProLysValProLysGluSerLeuGluGlySerProArgProProLysGly 120
DB 606 AAAGGCCCCAAGGTCCCAAGAGGTCTTGGAGGGGTCTCCCGAGGCGCGCCCAAGAGGGG 665
QY 121 LysGluLysProProLysAlaThrLysLysProLysGluLysProProLysAlaThrLys 140
DB 666 AAGGAGAGAGCCCAAGGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 725
QY 141 LysProLysGluGluProProLysAlaThrLysLysProLysGluLysProProLysAla 160
DB 726 AAGCCCAAG 785
QY 161 ThrLysLysProProSerGlyLysAspProProLysAlaProSerGluThrLeuGlu 180
DB 786 ACCAAG 845
QY 181 TrpProLeuProProProProSerProGlyProGluGluLeuProGluGluGlyAla 200
DB 846 TGGCCACTGCCCCCAAGCCCTGCGGCGCGAGAGCTACCCAGAGAGAGAGAGAGAGAGAG 905
QY 201 ProLeuSerAsnAsnTrpGlnAsnProGlyGluGluThrHisValGlnAlaGluGluHis 220
DB 906 CCCCTCTCAATTAATCTGAGCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 965
QY 221 GlnProGluProGluGluGluThrGluGlnProThrLysAspTrpAsnAspGlnLeu 240
DB 966 CAGCTGAG 1025
QY 241 ArgGluAspTrpGluAspPheGluThrLysArgGlnLysGlnProArgProProPro 260
DB 1026 AAGGAG 1085
QY 261 SerArgArgArgArgProGluArgValTrpProGluProProGluGluLysAlaProAla 280

Dh	1086	AGCAAGAGGAGGAGCCCGGAGCGGGTCTGGCCAGAGCCCTTGAGGAGAGAGCCCGGCGC	1145
Oy	281	ProAlaProGluGluArgIleGluProProValIlybProLeuLeuProProLeuProPro	300
Dh	1146	CCAGCCCCGGAGAGAGGATTGAGGCTCTGTGAAGCCTCTGTGCTCCCGCTGCCCCCT	1205
Oy	301	AsPtyrGlyAspGlyTyrValIleProAlenTyraAspMetAsPtyrTyrPheGlyPro	320
Dh	1206	GACTATGGTGTATGGTTAGCTGATCCCAACTCAGATGACATAGGACTATTACTTTGGGCGCT	1265
Oy	321	ProPProProGluIlybProAspAlaGluIlyrGlnIlybPheGluGluIlybGluIlybGlu	340
Dh	1266	CCTCCGCCCCAGAAACCCGATGCTGAGGCCAGAGGACGAAAGAAAGAGAGAGCTGAG	1325
Oy	341	LybPProLybLybGluAspSerSerProIlybGluGluIlybPheAsPtyrAlaValIlyb	360
Dh	1326	AAACCCAAAAGAGAGAGACGACGCCCCAGAGAGAGACGACMACTGGGCACTGGAGAG	1385
Oy	361	GlyIlybAspPheIlybGluProArgIlybGlyGluIlybGluIlybGluIlybTyrProThr	380
Dh	1386	GGCAAGGAGCCACAAAGAGCCCGAAAGGGCGAGGATTGGAGAGAGATGGACGCGTACG	1445
Oy	381	GluIlybValIlybCybProProProIleGlyMetGlySerHisArgIleGluAspAsnGlnIle	400
Dh	1446	GAGAAAGTCAAGTGTCCCCCAATGGATGAGTCAACCGATTATGAGAGACAAACAGATC	1505
Oy	401	ArgAlaSerSerMetLeuArgHisGlyLeuGlyAlaGlnArgGlyArgIlybAspMetCln	420
Dh	1506	CGAGCTCTCTCACTGCTGCGCCACGGCTGGGGGCGACGGCGGGCTCAACATGCAG	1565
Oy	421	ThrGlyAlaThrGluAspAspTyrTyrAspGlyAlaTyrCybAlaGluAspAspAlaArg	440
Dh	1566	ACGGGTGCACACTGAGAGCGACTATGATGGTGGTGTGGTGGCCAGAGAGATGCCAGG	1625
Oy	441	ThrGlnTyrPileGluValAspThrArgArgThrThrArgPheThrGlyValIleThrGln	460
Dh	1626	ACCCAGTGAATAGAGGTGAGACCCAGGAGACTACCCGATTCAACAGGGGTATCAACCCAG	1685
Oy	461	GlyIlybArgAspSerSerIleHisAspAspPheValThrThrPhePheValGlyPheSerAsn	480
Dh	1686	GGCAGAGACTCCAGATCAATGACGATTTGTGACCACTTCTGTGGGCTTCACGCAAT	1745
Oy	481	AspSerGlnThrTyrValMetTyrThrAsnGlyTyrGluGluMetThrPheHisGlyAsn	500
Dh	1746	GACAGCCAGCATGGGTATGTAACCAACGGCTATGAGAAATGACTTTCAATGGGAGAC	1805
Oy	501	ValAspIlybAspThrProValLeuSerGluLeuProGluProValValAlaArgPheIle	520
Dh	1806	GTGAGCAAGAGCACACCCGTGCTGATGAGCTCCAGAGCCGGTGGTGGCTGTTTCATC	1865
Oy	521	ArgIleTyrProLeuThrThrAsnGlySerLeuCybMetArgLeuGluValLeuGlyCys	540
Dh	1866	CGCATCTACCACTCACTCGAATGGACGCTGTGCAATGCCCTGGAGAGTCTGGGGTGC	1925
Oy	541	SerValAlaProValTyrSerTyrTyrAlaGlnAsnGluValAlaAlaThrAspAspLeu	560
Dh	1926	TCTGTGGGCCCTGTCTTACAGCTACACCAAGATAGAGTGTGTGGCCACCGAGATGACTG	1985
Oy	561	AspPheArgHisHisSerTyrIlybAspMetArgGluLeuMetIlybValIlybAsnGluGln	580
Dh	1986	GATTTCCCGGACCAACAGCTTACAGGACATGGCGGCACTCAGAAAGTGTGAACGAGAG	2045
Oy	581	CysPProThrIleThrArgThrTyrSerLeuGlyIlybSerSerArgGlyIlybLeuIlybIleTyr	600
Dh	2046	TGCCCCACCATCACCCGACTTACAGCTGTGGGCAAGACTCAGAGGCTTCMAATCATAT	2105
Oy	601	AlaMetGluIleSerAspAsnProGlyIlybGluGlnGlyGluProGluIlybArgTyr	620
Dh	2106	GCCATGGAGATCTCGACACACCTTGGGAGCATGAATCGGGGAGACCCGAGTTCCGCTAC	2165
Oy	621	ThrAlaGlyIleHisGlyAsnGluValLeuGlyArgGluLeuLeuLeuLeuMetGln	640
Dh	2166	ACTGTGTGGATTCATGAGCAAGAGGTGTGGGGCCAGAGCTGTGTCTCTCATCAAG	2225

QY	641	lyrlenCySaRggluTYrArqAbpQlyAaNPoArqyValaRSeRleuValGlNaSPthR	660
Db	2226	TACCTGTCCGAGAGTATACCGAGATGGAAACCACTGTGCCAGCTGTGTCAAGAACCA	2285
QY	661	ArgIleHsleuValProSeRleuAaNPProAaPgiTYrGluValAlaAGImecGly	680
Db	2286	CGCATCCACCTGTGTCCCTCACTGAACCTGATGGCTACGAAGTGGACGCCAGATGGGC	2345
QY	661	SerGluPheglYaenTPAlaLeuGlyLeuTPThrglugluglyPheAspIlePheGlu	700
Db	2346	TCAGAGTTTGGAAACTGGGCGCTGGGACTGTGCACTGAGAGGGCTTTGACATCTTTAA	2405
QY	701	AaPhePProAaPleuAaSeRValLeuTPGlylaGlugluAaGlyeTPyValProtyr	720
Db	2406	GATTTCCCGGAGTCTCACTGTGTCTGTGGGAGCTGAGAGAGAAATGGGTCCTCCATC	2465
QY	721	ArgValProAaAaAaAaNPProIleProGluARgTYrleuSeRProAspAlaThrVal	740
Db	2466	CGGGTCCCCAACATTAATTTGCCATTCCTGAAGCTACCTTTGGCCAGATGCCAGGTA	2525
QY	741	SerThrgluValaRgAlaIleIleAlaTPMeGluYbAaNPProPheValleuGlyAla	760
Db	2526	TCACGGAGGCTCCGGGCCATATTGCCGTGATGAGAGAAACCCCTTGTCTGGAGACA	2585
QY	761	AaNPleuAaNglyGlylaRgLeuValSeRtyrProtyrAaPMeAlaAaRThProthR	780
Db	2586	AATCTGAACGGCGGCGAGCGGCTAGATATCTTACCTTCAGATATGGCCGCAAGCTTACC	2645
QY	781	GlncgluInleuAlaAlaAlaMeAlaAlaAaRgGlyGluAaPgiuAaPgiuAl	800
Db	2646	CAGGAGCAGCTGTGGCCGAGCATATGGACACACCCGGGGAGAGATGAAGACAGAGTTC	2705
QY	801	SerGluAaGlngluTPThProAaHsAlaIlePheAaGTPleuAlaIleSeRPhela	820
Db	2706	TCCGAGGCCAGAGACTCCAGACCAAGCCCATCTTCGGTGGCTTGCATCTCTTGCC	2765
QY	821	SerAlaHsleuTPThLeuThrgluProtyrArgGlyGlyCysGlnAlaGlnAaSPtyrThr	840
Db	2766	TCCGAGACCTCACTTTGACCGAAGCCCTAACCGGAGGCTGCCAAGCCCAAGACTAACCC	2825
QY	841	GlYglYMeGlyIleValaSPGlyAlaIleSThPaNPoArqThrglyThIleAaNP	860
Db	2826	GGCGGCAAGGGCATCTGTCACAGGGGCGCAAGTGAAACCCCGGACCGGAGCTATCAATGAC	2885
QY	861	PheSeRtyrleuHsThThAaNPcyLeuGluLeuSeRPhetyrleuGlyCysAspLyAaPhe	880
Db	2886	TTCAATTAACCTGCATACCAACTGCCCTGGAGCTTCTCTTCTTACTCTGGGCTGTGACAACTTC	2945
QY	881	ProHsIuSeRgluLeuProArgGluTPGluAaNPuAaNPuGlyAlaLeuLeuThRPh	900
Db	2946	CCTCATGAGATGAGCTGCCCGCGAGTGGAGAAACAACAAGAGGCGCTCTCACTTC	3005
QY	901	MeGluGlnValHsAaRgGlyIleIleGlyAlaValThPaRpglugluglyIleProIle	920
Db	3006	ATGAGACGAGTGACCCGGGCAATTAAAGGGGTGTGACGAGCAGGACAAAGGATCCCCATT	3065
QY	921	AlaAaNPAlaThrIleSeRValSeRglyIleAaNPleGlyValIlySThPaSeRglyGly	940
Db	3066	GCCAAAGCCACATCTCTGTGATGGCATTAATCAAGCGCGTGAAGAACGCCAGTGTGTGT	3125
QY	941	AaPTyrtTPaRgIleleuAaNPProGlyGluTYrArqValThraAlaHsAlaGluglyTYr	960
Db	3126	GATTATCGGCCAATCTTGAACCCGGGTGATGATACCGCGTGAACGCCACCGCGAGGGCTTAC	3185
QY	961	ThProSeRAlaIlySThCyAaNPValaSPtyrAaPleGlyAlaIlySThPaSeRglyAaNPhe	980
Db	3186	ACCAGAGCCCAAGACCTGCAATGTTGACATATACATCCGGGAGCCACTCACTGACATCTTC	3245
QY	981	IleleuAlaAaRSeRSeRTPySaRgIleArgGluIleMeAlaMeAlaAaNPuAaNP	1000
Db	3246	ATCTGTGGTCTCACTGGAAACCGATCCGGAGAGTCAATCAATGAGCATGAACGGGAAACGGG	3305

QY 301 AaPTyGlyVaSPGlyTyValIleProAsnTyRAspAspMetAaPTyTyRPhGlyPro 320
DB 1019 GACTAAGTATGATGTTACGTGATCCCACTACAGATGACATGACATTAATCTTGAGGCT 1078
QY 321 ProProProGlnbYProAspAlaGluArgGlnThzAspGluGluysGluGluLeuys 340
DB 1079 CTTCCGCCCCAGAAAGCCGATGCTGAGCGCCAGCGAGACGAAAGAAAGAGAGCTGAA 1138
QY 341 LysProLysLysGluAspSerSerProLysGluGluThzAspLysTrpAlaValGluLys 360
DB 1139 AAACCCAAAAGAGAGACAGCAGCCCCCAGAGAGAGACCAAGTGGGAGCGAGAG 1198
QY 361 GlyLysAspHisLysGluProArgLysGluGluGluGluGluGluGluGluGluGluGlu 380
DB 1199 GCGAAGGACCAAAAGAGCCCCGAAAGGCGAGAGTGGAGAGAGAGAGAGCGCTACG 1258
QY 381 GluLysValLysCysProProIleGlyMetGluSerHisArgIleGluAspAsnGlnIle 400
DB 1259 GAGAAAGTCAAGTGTCCCCCAATTGGATGGAGTCACACCGTATTGAGAGCAACAGATC 1318
QY 401 ArgAlaSerSerMetLeuArgHisGlyLeuGlyAlaGlnArgGlyArgLeuAsnMetGln 420
DB 1319 CGAGCTCTCCATGCTGCGCCACGCGCTGGGGGACAGCGCGCGCTCAACATGCA 1378
QY 421 ThrGluValaThrGluAspAspTyTyTyRAspGlyAlaATrCysAlaGluAspAspAlaArg 440
DB 1379 ACCGGTGCCTAGTAGGACGACTACTATGATGTGCGTGTGTCGAGAGCGATGCGAG 1438
QY 441 ThrGlnTrpIleGluValaAspThrArgArgThzArgPheThrGlyValIleThrGln 460
DB 1439 ACCCATGGATTAAGGTGGACACACAGAGAGACTAACCGGTTCACAGCGCTCACCCAG 1498
QY 461 GlyArgAspSerSerIleHisAspAspPheValThzThrPhePheValGlyPheSerAsn 480
DB 1499 GGGAGAGACTCCGCAATCCATGACGATTTGTGACCACTTCTTCGGGGCTTCACCAAT 1558
QY 481 AspSerGlnThrTrpAlaMetTyTrpAsnGlyTyTrpGluGluMetThrPheHisGlyAsn 500
DB 1559 GACAGGACAGCATGGGAGTGAACCAACAGGCTATAGGAAATGACCTTTCATGGAGAC 1618
QY 501 ValAspLysAspThrProValLeuSerGluLeuProGluProValAlaArgPheIle 520
DB 1619 GTGGACAAGGACACCCCGTGTGAGTGAAGCTCCAGAGCGCGTGGTCTCTTCAATC 1678
QY 521 ArgGlyTyRProLeuThrTrpAsnGlySerLeuCysMetArgLeuGluValLeuGlyCys 540
DB 1679 CGCATCTACCACTCACTGGAAATGGCAGCTGTGATGCGCTGGAGGGTGTGGGGTGC 1738
QY 541 SerValAlaProValAlaTySerTyTyTyRAlaGlnAsnGluValAlaAlaThrAspAspLeu 560
DB 1739 TCTGTGGCCCCGTGTCAAGCTACTACGACAGAAATGAGTGTGGCCACCGATGACTG 1798
QY 561 AspPheArgHisIleSerTyTyLysAspMetArgGlnLeuMetLysValAlaAsnGluGln 580
DB 1799 GATTTCCGGCACACAGCTACAGACATGCGCACTCATGAAGTGGTGAACGAGAG 1858
QY 581 CysProThrIleThzArgThzTyRserLeuGlyLysSerSerArgGlyLeuLysIleTyR 600
DB 1859 TGGCCACACATCACCCGCACTTACAGCTGGGCAAGAGCTCACAGAGCCCTCAAGATCTAT 1918
QY 601 AlaMetGluLysLeuSerAspAsnProGluGluHisGluLeuGluGluProGluPheArgTyR 620
DB 1919 GCCATGAGATCTCAACAACCTTGGGAGCATGAATGGGGAGGCCAGATTCCCTC 1978
QY 621 ThrAlaGlyIleHisGluAsnGluValLeuGlyArgGluLeuLeuLeuLeuMetGln 640
DB 1979 ACTGCTGGGATCATGGACAAGAGTGTGGGCGGAGAGCTGTGTGCTGCTCAAGCGAG 2038
QY 641 TyRLeuCysArgGluTyTrpAspGlyAsnProArgValArgSerLeuValGlnAspThr 660
DB 2039 TACCTGTGCGAGATGACCGCATGGAAACCCAGTGTGCGAGCTGTGACGAGACACA 2098

QY 661 ArgIleHisLeuValProSerLeuAsnProAspGlyTyRGlulValAlaIleGlnMetGly 680
DB 2099 CGCATCCACTGTGTGCTTCACTGAACCTTGATGGCTAGAGGTGCAGCGAGATGGCG 2158
QY 681 SerGluPheGlyAsnTrpAlaLeuGlyLysTrpThzGluGluGlyPheAspIlePheGlu 700
DB 2159 TCAGATTTTGGGAAGCTGGCGCGCTGGGACTGTGAGCTGAGAGAGGGCTTTGACATCTTGA 2218
QY 701 AspPheProAspLeuAsnSerValLeuTrpGlyAlaGluGluArgLysTrpValProTyR 720
DB 2219 GATTTCCCGATCTCAACTGTGTCTGGGGAGCTGAGAGAGGAAAGGGTCCCTTAC 2278
QY 721 ArgValProAsnAsnAsnLeuProIleProGluArgTyRLeuSerProAspAlaThrVal 740
DB 2279 CGAGTCCCAACATACTTGCCTTGAACCTTGAACCTTACTTTCGCAATGCCAGGTA 2338
QY 741 SerThrGluValArgAlaIleIleAlaTrpMetGluLysAspProPheValLeuGlyAla 760
DB 2339 TTCACGGAAGTCCGGGCAATTCATTCCTGGATGGAGAAAGACCCCTTGTGCTGGAGCA 2398
QY 761 AsnLeuAsnGlyGlyGluArgLeuValSerTyRProTyRAspMetAlaArgThrProThr 780
DB 2399 AATGTGAAGCGGCGCAGCGGCTAGATCTTACCTTACGATATGCGCGCACGCTTACC 2458
QY 781 GlnGluGlnLeuLeuAlaAlaMetAlaAlaArgGlyGluAspGluAspGluVal 800
DB 2459 CAGAGACAGCTGTGCGCCAGCATGGCAGAGCCGGGGAGGATAGAGCGAGTGC 2518
QY 801 SerGluAlaGlnGluThrProAspHisAlaIlePheArgTrpLeuAlaIleSerPheAla 820
DB 2519 TCGAGAGCCCAAGAGACTCAGACACGCGCATTTCCGGTGGCTTCCATCTCTCGCC 2578
QY 821 SerAlaHisLeuThrLeuThrGluProTyRArgGlyCysGlnAlaGlnAspTyRThr 840
DB 2579 TCCGACACCTCACTTGAACCGAGCTCCGCGAGGCTGGCCAGAGCCAGACTACACC 2638
QY 841 GlyGlyMetGlyIleValAsnGlyAlaLysTrpAsnProArgThzGlyThrIleAsnAsp 860
DB 2639 GGGGAGTGGATCGTCAACGGGCGCAAGTGAACCCCGAGCGGAGCTATCAATGAC 2698
QY 861 PheSerTyRLeuHisThrAsnCysLeuGluLeuSerPheTyRLeuGlyCysAspLysPhe 880
DB 2699 TTCAGTTCCTGCATACCAAGTGCCTGAGAGCTCTCTTACTGGGCTGTGACAAATTC 2758
QY 881 ProHisGluSerGluLeuProArgLysTrpGluAsnAsnLysGluAlaLeuLeuThrPhe 900
DB 2759 CCTCATGAGAGTGAAGTGTGCGCGAGTGGAGAAACAAGAGAGCGCTGCTCACCTTC 2818
QY 901 MetGluGlnValHisArgGlyIleLysGlyValIleThrAspGluGlnGlyIleProIle 920
DB 2819 ATGAGACAGTGCACCGCGGCATTTAAGGGGTGTGACGAGAGAGCAAGGCAATCCCATTT 2878
QY 921 AlaAsnAlaThrIleSerValSerGlyIleAsnHisGlyValIleLysThzAlaSerGlyGly 940
DB 2879 GCCAAGCCACCATCTCTGTGATGGCAATTATCACGGCTGAAGAAGCAGCTGTGAT 2938
QY 941 AspTyRTrpArgIleLeuAsnProGluGlyTyRArgValThzAlaHisAlaGluGlyTyR 960
DB 2939 GATTAATGCGAATCTTGAACCCGGGTGAGTACCCTGTGACAGCCCAACCGAGGGCTAC 2998
QY 961 ThrProSerAlaLysThrCysAsnValAspTyRAspIleGlyAlaThrGlnCysAsnPhe 980
DB 2999 ACCCGAGGCGCAAGACTGCAATGTGACTATGACATCGGGGCCACTCAGTGCAACTTC 3058
QY 981 IleLeuAlaArgSerAsnTrpLysArgIleArgGluIleMetAlaMetAsnGlyAsnArg 1000
DB 3059 ATCTGGTGTGCTCCACTGAGAGGAGCATCCGGAGAGATATGCGCATGAACGGAAACGG 3118
QY 1001 ProIleProHisIleAspProSerArgProMetThrProGlnGlnArgLeuGlnGln 1020
DB 3119 CCTATCCACACATGAGACCATGCGCCCTATGAGACCCCAACAGAGAGCGCTGAGAGAG 3178
QY 1021 ArgArgLeuGlnHisArgLeuArgLeuArgIleGlnMetArgLeuArgArgLeuAsnAla 1040

DB 3179 GCACGCTTACACACCGCTGCGGCTTCGGGACAGATGCGGCTGCGGCTTCAACGCC 3238
 QY 1041 ThrThrThrLeuGlyProHisThrValProProThrLeuProProAlaProAlaThrThr 1060
 DB 3239 ACCACACCGCTTACACCGCTGCGGCTTCGGGACAGATGCGGCTGCGGCTTCAACGCC 3298
 QY 1061 LeuSerThrThrTlLeuGluProTlPglLysLeuLeuProProThrThrAlaGlyTlPglLys 1080
 DB 3299 CTGAGACATACCATATGAGGCTTGGGGCTTCATACCGCCCAACACCGCTTGGGAGAG 3358
 QY 1081 SerGluThrGluThrTlThrThrGluValValThrGluPheGlyThrGluValGluProGlu 1100
 DB 3359 TCGGAGACTGAGACCTTACACAGAGGTGTGACAGAGTTGGAGCCGAGGTGAGCCGAG 3418
 QY 1101 PheGlyThrLysValGluProGluPheGluThrGluLeuGluProGluPheGluThrGlu 1120
 DB 3419 TTTGGGACCAAGGTGAGCCGAGTTTGAACCCAGTTGAGGCTTGAAGTTCAGAGCCAG 3478
 QY 1121 LeuGluProGluPheGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 1140
 DB 3479 CTGGAACCCGAGTGTGAG 3538
 QY 1141 GlnAlaPheProPheThrThrValGluThrTlThrValAsnPheGlyAspPhe 1158
 DB 3539 CAGGCAATCCCTTCCACACAGTACAGACCTTACAGAGTAACTTTGGGACCTTC 3592

RESULT 9

AAT97610 standard; cDNA, 3854 BP.
 AAT97610:

27-MAR-1998 (first entry)

Human E2A-binding protein cDNA.

E2A-binding protein; E2A-BP; human; vascular smooth muscle cell;
 wound healing; angiogenesis; arteriosclerosis; gene therapy; ds.

Homo sapiens.

Key Location/Qualifiers
 CDS 1027..3564
 /tag= a

W09733900-A1.

18-SEP-1997.

14-MAR-1997; 97MO-US004117.

15-MAR-1996; 96US-0013439P.

(HARD) HARVARD COLLEGE.

Lee M, Haber E, Endege WO, Layne MD;

WPI; 1997-470808/43.

P-PSDB; AAW36816.

DNA encoding human and mouse E2A binding proteins - useful for inhibiting
 or stimulating growth of vascular smooth muscle cells, e.g. for wound
 healing or treatment of rheumatoid arthritis or retinopathic diabetes.

Claim 9; Page 55-60; 90pp; English.

This sequence represents a full-length nucleotide sequence that codes for
 human E2A binding protein (E2A-BP, see AAW36816). It was isolated from a
 human aortic RNA following 3 rounds of 5'RACE procedures. E2A-BP is
 expressed in vascular smooth muscle cells; mRNA is preferentially
 expressed in the aorta. E2A-BP interacts with E2A proteins in vivo, binds
 to both E12 and E47 and inhibits binding of E47 homodimer to an E-box

CC probe (see AAT97606). Mouse (see AAT97611) and rat (see AAT97612-13) E2A-
 CC BP sequences have also been isolated. E2A-BP nucleic acids may be used in
 CC gene therapy and antisense methods for treating vascular diseases such as
 CC arteriosclerosis, to produce transgenic or knock-out animals, as well as
 CC in methods of producing E2A-BP polypeptides that can be used
 CC therapeutically to promote vascular smooth muscle cell growth e.g. for
 CC wound healing, or to screen for modulator compounds useful e.g. for the
 CC treatment of arteriosclerosis and angiogenesis. The E2A-BP gene promoter
 CC can be used in gene therapy methods to direct vascular smooth muscle cell
 CC heterologous expression of the E2A-BP gene, antisense sequences or
 CC

Sequence 3854 BP; 899 A; 1214 C; 1161 G; 580 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,456-288 Length: 3854
 Score: 6227.00 Matches: 1149
 Percent Similarity: 99.8% Conservative: 1
 Best Local Similarity: 99.7% Mismatches: 2
 Query Match: 99.3% Indels: 0
 DB: Gaps: 0

US-10-642-946-3 (1-1158) x AAT97610 (1-3854)

QY 7 AlaProLeuSerCysLeuLeuAlaLeuLeuAlaLeuCySPProGlyArgProGlu 26
 DB 106 GGGCCCTGCTCAGCTGCTCTGCGCTTGGTGGCCCTGTGCGGCGGAGGGGCGCGAG 165
 QY 27 ThrValLeuThrAspAspGluLeuGluPheLeuGluGlyPheLeuSerGluLeuGlu 46
 DB 166 ACGGTGTGACCGACGAGATCCAGAGATCTTCGAGGGCTTCCTGTCAAGCTTAGA 225
 QY 47 ProGluProArgGluAspAspValGluAlaProProProProGluProThrProArgVal 66
 DB 226 CCTGAGCCCCGGGAG 285
 QY 67 ArgLysAlaGlnAlaGlyGlyLysProGlyLysArgProGlyThrAlaAlaGluValPro 86
 DB 286 CGAAGAGCCCGAGCGGGGGGCGAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 345
 QY 87 ProGluLysThrLysAspLysGlyLysLysGlyLysLysGlyLysLysGlyLysLysGly 106
 DB 346 CCGGAG 405
 QY 107 LysGluSerLeuGluGlySerProArgProProLysGlyLysGluLysProProLys 126
 DB 406 AAGAGTCTTGTGAGAGGTCCCGAGCGCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 465
 QY 127 AlaThrLysLysProLysGluLysProProLysAlaThrLysLysProLysGluLysPro 146
 DB 466 GCCACCAAGAGCCCAAG 525
 QY 147 ProLysAlaThrLysLysProLysGluLysProProLysAlaThrLysLysProProSer 166
 DB 526 CCAAGAGCCAG 585
 QY 167 GlyLysArgProProLysLeuAlaProSerGluThrLeuGluLysProLysProProPro 186
 DB 586 GGAAG 645
 QY 187 ProSerProGlyProGluLysLeuLeuProGluGluGlyAlaProLeuSerAsnAsnTyr 206
 DB 646 CCGAGCCCTGGGCGCGAG 705
 QY 207 GlnAsnProGlyGluGluThrHisValGluAlaGlnGluLysGlnProGluLysProGlu 226
 DB 706 CAGAAATCCAG 765
 QY 227 GlnThrGluGluProThrThrLeuAspTyrAsnAspGlnLeuArgGluAspTyrGluAsp 246
 DB 766 GAGACCGAG 825
 QY 247 PheGluTyrIleArgArgGluLysGluProArgProProProSerArgArgArgPro 266


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Db      826 TTTGAGTACATTGGCGCCAGAAAGCAACCGAGCCACCCCAAGCAGAAAGAGAGGCC 885
QY      267 GUAAGValATrProGluProProGluGluValAProAlaProGluGluA 286
Db      886 GAGCGGCTCTGGCGAGAGCCCCCTGAGAGAAAGGCCCGGCCCAAGCCCGGAGAGAG 945
QY      287 TlAGluProProVallyAsProleuLeuProProleuProProAspTyrGlyAspGlyTyr 306
Db      946 ATTGAGCTCTCTGGAAGCTCTGTGCTGCCCTGCTGCCCTGACTATGATGATGTTAC 1005
QY      307 ValIleProAntyAspAspMetAspTyrTyrPheGlyProProProGluLysPro 326
Db      1006 GTGATCCCCCAACTACGATGACATGACATGACTATTACTTTGGGCTCTCCGCCCAAGAGCC 1065
QY      327 AspAlaGluArgGlnThrAspGluGluValGluGluGluLysProLysGluAsp 346
Db      1066 GATGCTGAGCGCCAGACGAGCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1125
QY      347 SerSerProlyArgGluGluThrAspLysTrpAlaValGluLysGlyLysAspHisLysGlu 366
Db      1126 AGGAGCCCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1185
QY      367 ProArgLysGlyGluGluGluGluGluGluGluTyrThrProThrGluLysValLysCysPro 386
Db      1186 CCCCAGAAAGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1245
QY      387 ProIleGlyMetGluSerHisArgIleGluAspAsnGlnIleArgAlaSerSerMetLeu 406
Db      1246 CCATTTGGATGAGTACACCCGTTATGAGAGCAACAGATCCGAGGCTCTCTCATGCTG 1305
QY      407 ArgHisGlyLeuGlnIleValArgLysArgLysLeuAspMetGlnThrGlyValAThrGluAsp 426
Db      1306 CGGACAGGCTGTGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1365
QY      427 AspTyrTyrAspGlyAlaTyrCysAlaGluAspAspAlaArgThrGlnTyrIleGluVal 446
Db      1366 GACTACTATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1425
QY      447 AspThrArgArgThrThrArgPheThrGlyValIleThrGlnIleValArgAspSerSerIle 466
Db      1426 GACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1485
QY      467 HisAspAspPheValIleThrThrPhePheValGlyPheSerAspAspSerGlnThrTrpVal 486
Db      1486 CATGAGGATTTTGTGACACCTTCTGTGGGCTTACGACATGACAGCCAGAGATGGGTG 1545
QY      487 MetTyrThrAsnGlyTyrGluGluMetThrPheHisGlyAsnValAspLysAspThrPro 506
Db      1546 ATGTACACCAACGCGCTATGAGAAATGACCTTTCAATGGAACTGGAACAGACACACCC 1605
QY      507 ValLeuSerGluLeuProGluProValValAlaArgPheIleArgIleTyrProLeuThr 526
Db      1606 GTGCTGAGTGAAGCTCCAGAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1665
QY      527 TrpAsnGlySerLeuCysMetArgLeuGluValLeuGlyCysSerValAlaProValTyr 546
Db      1666 TGGAAATGGCAGCTGTGTCATGCTGTGAGGTCTGTGGGTGTGTGTGTGTGTGTGTGT 1725
QY      547 SerTyrTyrAlaGlnAsnGluValAlaIleThrAspAspLeuAspPheArgHisIleSer 566
Db      1726 AGCTACTACGACAGATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1785
QY      567 TyrLysAspMetArgGluLeuMetLysValValAsnGluGluCysProThrIleThrArg 586
Db      1786 TACAAAGACATGCGCAGCTCATGAAAGTGTGAAGAGAGAGAGAGAGAGAGAGAGAG 1845
QY      587 ThrTyrSerLeuGlyLysSerSerArgGlyLysLeuIleTyrAlaMetGluLysSerAsp 606
Db      1846 ACTTACAGCTGTGGCAAGAGACTCAAGAGGCTCAAGATCTATGCTATGAGACTCAGAC 1905
QY      607 AsnProGlyGluHisGluGluGluGluProGluPheArgTyrThrAlaGlyIleHisGly 626
Db      1906 AACCTTGGGAGAGTACACTGGGGAGAGCCGAGTTCCGCTACACTGTGGATTCATGCC 1965
QY      627 AsnGluValLeuGlyValArgGluLeuLeuLeuLeuMetGlnTyrLeuCysArgGluTyr 646
Db      1966 AACGAGGTGCTGGCGGAGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2025
QY      647 ArgAspGlyAsnProArgValArgSerLeuValAlaAspThrArgIleHisLeuValPro 666
Db      2026 CGGATGAGGAACCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2085
QY      667 SerLeuAsnProAspGlyTyrGluValAlaAlaGlnMetGlySerGluPheGlyAsnTrp 686
Db      2086 TCACATAACCTTGATGTGCTACGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2145
QY      687 AlaLeuGlyLeuTyrThrGluGluGlyPheAspIlePheGluAspPheProAspLeuAsn 706
Db      2146 GCGCTGGAGCTGTGACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2205
QY      707 SerValLeuTrpGlyValAlaGluGluArgLysTrpValProTyrArgValProAsnAspAsn 726
Db      2206 TCTGTCTCTGGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2265
QY      727 LeuProIleProGluArgTyrLeuSerProAspAlaThrValSerThrGluValArgAla 746
Db      2266 TTGCCATCCCTGTAAGCTTACCTTTGCGCAGATGCCAGTATCCAGAGAGTCCGGGCC 2325
QY      747 IleIleAlaTrpMetGluLysAsnProPheValLeuGlyAlaAsnLeuAsnGlyGlyGlu 766
Db      2326 ATCATTTGCTGATGAGAGAGAAACCCCTTGCTGTGAGAGAGAAATCTGAACCGCGCGAG 2385
QY      767 ArgLeuValSerTyrProTyrAspMetAlaArgThrProThrGlnGluGluLeuAla 786
Db      2386 CGGCTAGTATCTTACCTTACGATATGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 2445
QY      787 AlaAlaMetAlaAlaAlaArgGlyGluAspGluAspGluValSerGluAlaGlnGluThr 806
Db      2446 GCAGCATGTGGACAGACCCGGGGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 2505
QY      807 ProAspHisAlaIlePheArgTrpLeuAlaIleSerPheAlaSerAlaHisLeuThrLeu 826
Db      2506 CCAGACCAACGCACTTCCGTTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 2565
QY      827 ThrGluProTyrArgGlyGlyCysGlnAlaGlnAspTyrThrGlyGlyMetGlyIleVal 846
Db      2566 ACCGAGCCTTACCGCGAGAGCTGTCCAAAGCCAGAGATTAACCGAGCGCATGGCATCTGC 2625
QY      847 AsnGlyAlaLysTrpAsnProArgThrArgTyrThrIleAsnAspPheSerTyrLeuHisTrp 866
Db      2626 AACGGGGCCAAATGGAACCCCGGAGCGGAGACTATCAATGACTTCACTTCACTTCACT 2685
QY      867 AsnCysLeuGluLeuSerPheTyrLeuGlyCysAspLysPheProHisGluSerGluLeu 886
Db      2686 AACTGCTGAGACTCTCTTCACTGAGCTGTGACAAATTCCTCATGAGAGTGAGCTG 2745
QY      887 ProArgGluTrpGluAsnAsnLysGluAlaLeuLeuThrPheMetGluGlnValHisArg 906
Db      2746 CCCCAGAGTGGAGAAACAAGAGAGGCTGTCTCACTTATGAGAGAGAGAGAGAGAGAG 2805
QY      907 GlyIleLysGlyValValThrAspGluGlnGlyIleProIleAlaAsnAlaThrIleSer 926
Db      2806 GGCATTAAAGGGGTGTGTGACGAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2865
QY      927 ValSerGlyIleAsnHisGlyValLysThrAlaSerGlyIleAspTyrTrpArgIleLeu 946
Db      2866 GTGAGTGCATTAATCAACGCGTGAAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2925
QY      947 AsnProGlyGluTyrArgValThrAlaHisAlaGluGlyTyrThrProSerAlaLysThr 966
Db      2926 AACCCGGGTGATACCGGCTGTGACGCGCAGCGAGAGGCTTACACCCCGAGAGAGAG 2985
QY      967 CysAsnValAspTyrAspIleGlyAlaThrGlnCysAspPheIleLeuAlaArgSerAsn 986
Db      2986 TGCAATGTTGACTATGACATCGGGGCACTGAGTGAATTTCACTGTGCTGTGCTGCAAC 3045
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QY 987 TTPlybAryglleArygluileMeAlaMeAlaanglyAaAmAryProIleProhIstleAap 1006
 DB 3046 TGGAAAGCCGATCCGGAGATCATGGCCATGAACGGGAACCGGCGCTATCCACACATAGAC 3105
 QY 1007 ProSerAryProMetThrProglInglInAryArygluInglInAryArygluInglInAry 1026
 DB 3106 CCATGGCGGCTCTATGACCCGCCAACAGCGACCCCTGACAGCAGACGCTTACAAACCGCC 3165
 QY 1027 LeuArygluArygluArygluArygluArygluArygluArygluArygluArygluAryglu 1046
 DB 3166 CTGGCGGCTCTGAGGACAGATGGCGGCTGGCGGCTGAGGACGAGGACGAGGACGAGGAC 3225
 QY 1047 HstThrValProProThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 1066
 DB 3226 CACACTGCTCTCCACGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 3285
 QY 1067 ProTPGlyLeuIleProProThrThrThrThrThrThrThrThrThrThrThrThrThrThr 1086
 DB 3286 CCTGGGCGCTCATACCGGACCAACCGGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3345
 QY 1087 ThrGlValValThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 1106
 DB 3346 ACAGAGAGTGTGACAGATTTGGAGCGAGTGGAGCGGAGTTTGGAGCGGAGTGGAGGAG 3405
 QY 1107 ProGlThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 1126
 DB 3406 CCGGAGTTTGAACCCAGTTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCT 3465
 QY 1127 GluGlThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 1146
 DB 3466 GAAAG 3525
 QY 1147 ThrValThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 1158
 DB 3526 ACAGTGAAGACCTACACAGTGAAGCTTGGGAGCTTC 3561
 RESULT 10
 ADE79067
 ID ADE79067 standard; DNA; 4025 BP.
 AC ADE79067;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human protein modification and maintenance molecule (PMMW)-47 gene.
 XX
 KW protein modification and maintenance molecule; PMMW;
 KW protein modification; protein maintenance; protein function;
 KW protein conformation; protein stabilization; protein degradation; kinase;
 KW phosphatase; protease; protease inhibitor; isomerase; transferase;
 KW molecular chaperone; anti-HIV; anti-allergic; anti-inflammatory;
 KW anti-inflammatory; anti-parkinsonian; nootropic; anticonvulsant;
 KW anti-atherosclerotic; anti-asthmatic; immunosuppressive; anticholinergic;
 KW cytochrome; hepatotropic; dermatological; antidiabetic; nephrotoxic;
 KW antitumor; thymotropic; neuroprotective; osteoprotective; antihypertensive;
 KW antiparasitic; antihelminthic; antiparasitic; uropathic; ophthalmological;
 KW antineoplastic; haemostatic; antibacterial; virucide; protozoacide;
 KW fungicide; gene therapy; cell proliferative disorder; arteriosclerosis;
 KW hepatitis; polycythaemia vera; psoriasis; primary thrombocytopaenia;
 KW cancer; developmental disorder; anaemia; mental retardation;
 KW neurological disorder; Alzheimer's disease; Parkinson's disease;
 KW epilepsy; autoimmune disorder; inflammatory disorder; AIDS; allergies;
 KW asthma; autoimmune thyroiditis; Crohn's disease; diabetes mellitus;
 KW glomerulonephritis; Goodpasture's syndrome; multiple sclerosis;
 KW arthritis; osteoporosis; pancreatitis; Sjogren's syndrome;
 KW microbial infection; human; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO2003063688-A2.
 XX
 PD 07-AUG-2003.

XX
 PF 23-JAN-2003; 2003WO-US002500.
 XX
 PR 25-JAN-2002; 2002US-0351928P.
 PR 25-FEB-2002; 2002US-0359903P.
 PR 21-MAR-2002; 2002US-0366837P.
 XX
 PA (INCYTE) INCYTE GENOMICS INC.
 XX
 PI Hafelia AD, Li JX, Gorrard AB, Chawla NK, Sprague WM, Lee SY;
 PI Chang H, Elliott VS, Ramkumar J, Khare R, Emertling EM, Kabie AB;
 PI Tang YF, Yue H, Gietzen KJ, Lee S, Swarnakar A, Baughn MR;
 PI Wilson AD, Jin P, Chien D, Hawkins PR, Jiang X, Jackson AA;
 PI Bharia U, Burtill JD, Blake JJ, Ho A, Zheng X, Leon CH, Margolis JP;
 PI Tran UK, Lal PG, Warren BA, Xu Y, Honchell CD, Becha SD,
 PI Lehn-Mason PM;
 DR WPI; 2003-636761/60.
 DR P-Psdb; ADE79009.
 XX
 PT New human protein modification and maintenance molecules and
 PT polynucleotides, useful for diagnosing, treating or preventing autoimmune
 PT or inflammatory disorders (e.g. AIDS, allergy or anemia), multiple
 PT sclerosis or cancer.
 XX
 PS Claim 5; SEQ ID NO 105; 405dp; English.
 XX
 CC This invention relates to novel isolated human proteins, which are human
 CC protein modification and maintenance molecules (PMMW). The cellular
 CC processes regulating modification and maintenance of protein molecules
 CC coordinate their function, conformation, stabilization and degradation.
 CC Each of these processes is mediated by key enzymes or proteins such as
 CC kinases, phosphatases, proteases, protease inhibitors, isomerases,
 CC transferases and molecular chaperones. Compounds which modulate the
 CC proteins of the invention may have anti-HIV, anti-allergic,
 CC anti-inflammatory, anti-atherosclerotic, anti-asthmatic, immunosuppressive,
 CC anticonvulsant, anti-atherosclerotic, anti-asthmatic, immunosuppressive,
 CC anticholinergic, cytochrome, hepatotropic, dermatological, antidiabetic,
 CC nephrotoxic, antitumor, thymotropic, neuroprotective, osteoprotective,
 CC antiparasitic, antihelminthic, antiparasitic, uropathic,
 CC ophthalmological, antineoplastic, haemostatic, antibacterial, virucide,
 CC protozoacide or fungicide activities. The DNA sequence which encodes the
 CC proteins of the invention may be useful for gene therapy. The human
 CC protein modification and maintenance molecules (PMMWs), the DNA sequences
 CC which encode them and their modulating compounds are useful for
 CC diagnosing, treating or preventing disorders associated with aberrant
 CC expression of PMMW, particularly cell proliferative disorders (for
 CC example arteriosclerosis, hepatitis, polycythaemia vera, psoriasis,
 CC primary thrombocytopaenia or cancer), developmental disorders (for
 CC example anaemia or mental retardation), neurological disorders (for
 CC example Alzheimer's disease, Parkinson's disease or epilepsy),
 CC autoimmune/inflammatory disorders (for example AIDS, allergies, asthma,
 CC autoimmune thyroiditis, Crohn's disease, diabetes mellitus,
 CC glomerulonephritis, Goodpasture's syndrome, multiple sclerosis,
 CC arthritis, osteoporosis, pancreatitis, Sjogren's syndrome) or microbial
 CC infections. The present sequence is that of a DNA sequence which encodes
 CC a human PMMW of the invention.
 XX
 SQ Sequence 4025 BP; 929 A; 1265 C; 1227 G; 604 T; 0 U; 0 Other;
 XX
 Alignment Scores:
 Pred. No.: 2,576-287 Length: 4025
 Score: 6206.00 Matches: 1154
 Percent Similarity: 97.0% Conservative: 3
 Best Local Similarity: 96.7% Mismatches: 1
 Query Match: 98.9% Indels: 35
 DB: 10 Gaps: 1
 US-10-642-946-3 (1-1158) X ADE79067 (1-4025)
 QY 1 MetAlaAlaValArygluArygluArygluArygluArygluArygluArygluArygluAryglu 20
 DB 119 ATGGCGGCGGCTCTGAGGAG 178

OY	21	ProGlyVgIYargProGlnThrValLeuThrAspArgGluIleGluGluPheLeuGluGly	40
Db	179	CTGGAGGGCGCCCGCAGCGGTGTGCACCGACGAGATGTGAAGATTCTTCAGAGGGC	238
OY	41	PheLeuSerGlnLeuGluPProGluProArgGluAspAspValGluAlaProProProPro	60
Db	239	TTCCGTGTGAGACTGAACTTAGCCCGCGAGAGACAGCTGTGAAGCCCCCGCCCTCC	298
OY	61	GluProThrProArgValArgLysAlaGluAlaGlyGlyLysProGlyLysArgProGly	80
Db	299	GAGCCACACCCCGGGGTCCGAAAACCCCGCGGGGGCGAACCCAGGGAGACGGCCACGGG	358
OY	81	ThrAlaAlaGluValProProGluLysThrLysAspLysGluLysLysGlyLysLysAsp	100
Db	359	ACGGCCGCGAAGTGCTCTCCGAAAAGACCAAGAGCAAGAGGAGAAAGCAAGAAAGAC	418
OY	101	LysGlyProLysValProLysGluSerLeuGluGlySerProArgProProLysLysGly	120
Db	419	AAAGGCCCAAGGTGCCCAAGAGTCTTTGAGGGGTCCCGCAGGCCGCCCAAGAAAGGG	478
OY	121	LysGluLysProProLysAlaThrLysLysProLysGluLysProProLysAlaThrLys	140
Db	479	AAGGAGAAAGCCACCAAGGCCCAAGAAAGCCCAAGAGAAACCACTAAGGCCACCAAG	538
OY	141	LysProLysGluGluProProLysAlaThrLysLysProLysGluLysProProLysAla	160
Db	539	AAGCCCAAGAGAAACCAACCCAGGCCACCAAGAAACCCCAAGAGAAACCAACCCAGGC	598
OY	161	ThrLysLysProProSerGlyLysArgProProLysAlaProSerGluThrLeuGlu	180
Db	599	ACCAAGAAAGCCCCGTCAAGGAAAGGGCCCCCATCTGTGCTCCCTCAGAAACCTGGAG	658
OY	181	TrpProLeuProProProProSerProGlyProGluGluLeuProGluGluGlyVala	200
Db	659	TGGCCACTGCCCCCACCACCCCTGAGCCCTGAGCCCGAGAGACTACCCAGAGAGAGGGGG	718
OY	201	ProLeuSerAspAspThrGlnAspProGlyGluGluThrHisValGluAlaGlnLysHis	220
Db	719	CCCCCTCAAAATTAATGCGACAGATCCAGAGAGAGACCCATGTGAGGACCGGAGGAC	778
OY	221	GlnProGluProProGluGluGluThrGluGlnProThrLeuAspTyrAspAspGlnIleGlu	240
Db	779	CGGCTGTAGCCGAGAGAGAGACCCAGCAACCACTGACTTCAATGACCAAGTTCAG	838
OY	241	ArgGluAspTyrGluAspPheGluLysTyrIleArgArgGlnLysGlnProArgProProPro	260
Db	839	AGGAGAGACTTAGGACTTTGAGTACATTGCGCCGCCAAGAACCAACCCAGGCCACCCCA	898
OY	261	SerArgArgArgArgProGluArgValTrpProGluProProGluGluLysAlaProAla	280
Db	899	AGCAGAAAGAGAGAGCCGAGCGGGTCTGCGCAGAGACCCCTGAGAGAAAGGCCCGCGCC	958
OY	281	ProAlaProGluGluArgIleGluProProValLysProLeuLeuProProLeuProPro	300
Db	959	CCAGCCCCCGAGAGAGAGATTGAGCTCTCTGTGAAGCCTCTGTCTGCCCGCCGTGCCCT	1018
OY	301	AspTyrGlyAspGlyTyrValIleProAspAspTyrAspAspMetAspTyrTyrPheGlyPro	320
Db	1019	GACTATGTGTGTTGTTAGTGTGATCCCAACTACATGACATGACTATTACTTTGGGCT	1078
OY	321	ProProProGluLysProAspAlaGluLysGlnThrAspGluGluLysGluGluLeuLys	340
Db	1079	CCTCGGCCCGCAGAAAGCCGATGCTGAGCGCAGAGAGCAAGAAAGAAAGAGAGCTGAG	1138
OY	341	LysProLysLysGluAspSerSerProLysGluGluThrAspLysTrpAlaValGluLys	360
Db	1139	AAACCCAAAAGAGAGACAGCAGCCCCCAAGAGAGAGACCACTAGTGCGCACTGGAGAG	1198
OY	361	GlyLysAspHisLysGluProArgLysGlyGluGluLeuGluGluGluGluTrpThrProThr	380
Db	1199	GGCAAGAGCAACAAAGACCCCGAAAGGCGAGGTTTGAGAGAGAGTGAACGCTACAG	1258

QY	381	GIULYSVALIVS	QY	ProPro1	leg	met	G	use	H	is	Arg	I	leu	l	u	b	s	p	a	n	g	i	n	l	e	400		
Db	1259	GAGAA	GTC	TCA	GTG	TCT	CCC	CA	T	T	G	G	A	T	G	A	G	T	C	A	C	C	G	A	T	1311		
QY	401	Arg	Ala	Ser	Ser	Met	Leu	Arg	H	is	G	Leu	G	Val	Ala	G	Arg	G	I	Val	Arg	Leu	Ser	Met	Gln	420		
Db	1319	CGAG	CTC	TCT	CC	A	T	C	A	T	C	T	G	G	CC	A	C	G	G	C	T	G	G	G	C	137		
QY	421	Thr	G	I	Val	Ala	Thr	G	Leu	Asp	Tyr	Tyr	Asp	G	Val	Ala	T	Arg	Cys	Ala	Ala	G	Leu	Asp	Ala	Arg	440	
Db	1379	ACCG	GTG	CCA	CT	G	A	G	A	G	A	C	T	A	T	A	T	A	T	G	T	G	T	G	T	143		
QY	441	Thr	G	I	Val	Thr	P	I	leu	G	Val	Ala	Asp	Thr	Arg	Ala	G	Thr	Thr	Arg	Phe	Thr	G	Val	I	leu	Arg	460
Db	1439	ACCC	A	G	T	G	A	T	G	A	T	G	A	T	G	A	C	C	A	C	C	G	G	T	T	149		
QY	461	G	Leu	Arg	Asp	Ser	Ser	I	leu	His	Asp	Asp	Phe	Val	Thr	Thr	Phe	Phe	Val	G	I	leu	Phe	Ser	Arg	480		
Db	1499	GCG	A	G	A	G	A	C	T	C	A	T	C	A	T	C	A	T	C	A	T	T	T	T	T	155		
QY	481	Asp	Ser	G	I	Thr	Tyr	Val	Met	Tyr	Thr	Asn	G	I	Tyr	G	Leu	I	Met	-----	-----	-----	-----	-----	495			
Db	1559	GAC	A	C	C	A	C	A	G	A	C	A	T	G	G	T	G	A	G	A	A	T	G	T	161			
QY	495	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	495				
Db	1619	AGG	C	T	T	G	G	C	T	G	C	T	C	C	A	T	G	T	G	G	G	C	G	A	167			
QY	496	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	506				
Db	1679	TAC	T	G	C	T	G	A	G	C	T	G	C	T	C	C	C	A	G	C	T	T	T	C	173			
QY	506	O	Val	Leu	Ser	G	Leu	Leu	Pro	G	Leu	Pro	Val	Val	Ala	Arg	Phe	I	Leu	I	Leu	Tyr	Pro	Leu	526			
Db	1739	CGT	G	T	G	A	T	G	A	G	T	C	C	C	A	G	A	C	C	G	T	G	T	G	179			
QY	526	T	Trp	Asn	G	I	Ser	Leu	Cys	Met	Arg	Leu	G	Val	Leu	G	I	Cys	Ser	Val	Ala	Pro	Val	Tyr	546			
Db	1799	CTG	A	A	T	G	A	T	G	A	C	T	G	C	A	T	C	G	C	T	G	G	A	T	185			
QY	546	R	Ser	Tyr	Tyr	Ala	G	Leu	Asn	G	Val	Val	Ala	Thr	Arg	Asp	Leu	Asp	Phe	Arg	H	is	Ser	566				
Db	1859	CAG	C	T	A	C	T	A	C	C	A	G	A	T	G	A	G	T	G	T	G	C	C	A	191			
QY	566	T	Tyr	Leu	Asp	Met	Arg	G	Leu	Met	Leu	Val	Val	Asn	G	Leu	G	I	Cys	Pro	Thr	I	leu	Arg	586			
Db	1919	CTA	C	A	G	A	G	A	C	A	T	G	C	A	T	A	T	A	G	T	G	A	C	A	197			
QY	586	G	Thr	Tyr	Ser	Leu	G	I	Ser	Ser	Arg	G	I	Leu	Val	I	leu	Tyr	Ala	Met	G	Leu	I	Ser	606			
Db	1979	CAC	T	T	A	C	A	G	C	T	G	G	C	A	G	A	G											

Db	2339	CTGTGTCTTGGGAGCTGAGGAGGAAATGGGTCCTTACCGGGTCCCAACATTAA	2398
Qy	726	nLeuProIleProGluuArgTyrLeuSerProAspAlaThrValSerThrGluValArgAl	746
Db	2399	CTTGCCCATCCCTGAACGCTTACTTTGGCCAGATGCCACGGTATCCACGAGGCTCGGGC	2458
Qy	746	AlIleIleAlaIrrPmetGluYsaamProPheValLeuGlyValAsnLeuMetnIYglYgl	766
Db	2459	CATCATTTGGCTGGATGGAGAAACCCCTTGTCCTGAGCAATCTGAACGGGGCGGA	2518
Qy	766	uArgLeuValSerTyrProTyrAspMetAlaArgThrProThrGlnGluInuLeuAla	786
Db	2519	GGGGCTAGTATCTTACCCCTTACGATATGGCCCGCAGCGCTATCCACGAGGACGTGGC	2578
Qy	786	AlAlaAlaMetAlaAlaAlaArgGlyGluuBspGluuBspGluValSerGluValGlnGlu	806
Db	2579	CGCAGCCATGCGACAGAGCCCGGGGGAGAGAGAGAGAGAGGTCTCCAGAGCCACGAGGAC	2638
Qy	806	rProAspHisAlaIlePheArgTyrPLeuAlaIleSerPheAlaSerAlaHisLeuThrLe	826
Db	2639	TCCAGACCAACGCCCATCTTCGGGTGGCTTGCCATCTCTCGCCCTCCGCAACCTCACCTT	2698
Qy	826	uThrGluProTyrArgGlyGlyYcYglnAlaGlnuBspTyrThrGlyGlyMetGlyIleVa	846
Db	2699	GACCGAGCCCTAACCGCGAGGCTCCCAAGCCCAAGACTACACCGCGGCAATGGCGATCGT	2758
Qy	846	lAsnGlyAlaIleYrTPAsnProArgThrGlyThrIleAsnAspPheSerTyrLeuHisThr	866
Db	2759	CAACGGGGGCCAAGTGAACCCCCCGAGCCGGAGCTATCAATGATCTTCAAGTTACCTGCATAC	2818
Qy	866	rAsnCyLeuGluInuLeuSerPheTyrLeuGlyYcAspBspPheBspHisGluSerGluLe	886
Db	2819	CAACTGCGCTGGAGCTCTCTCTTACTGAGCTGGCTGTGACAAAGTTTCCCTCATGAGATGAGCT	2878
Qy	886	uProArgGluTrpGluuAsnLeuYsgluValaLeuLeuThrPheMetGluGlnValHisArg	906
Db	2879	GCCCGCCAGTGGGAGGAACAAACAGAGAGCGCTGCTCATCTTCATGGAGCGAGTGACCG	2938
Qy	906	gGlyIleLeuYsglyValaIleThrAspGluGlnGlyIleProIleAlaAsnAlaThrIleSe	926
Db	2939	CGGCTTAAAGGGGGGTGTGACGAGACGACGACGATCCCATTTGCAACGCGCACATCTC	2998
Qy	926	rValSerGlyIleAsnHisGlyValaYsThrAlaSerGlyGlyuBspTyrTrpArgIleLe	946
Db	2999	TGTGAGTGGCATTTATCAACGCGCTGTAACAGCCAGGTGTGTATTACTGGCCAAATCTT	3058
Qy	946	uAsnProGluYguTyrArgValaIleThrAlaHisAlaGlnGluYrThrProSerAlaIleThr	966
Db	3059	GAACCCGGGTGTGATCCCGCTGACAGCCACGCGGAGGCTTACACCCCGAGCGCCAGAC	3118
Qy	966	rCyAsnValuBspTyrAspIleGlyValaThrGlnCyAsnBspHeileuAlaArgSerAs	986
Db	3119	CTGCAATTTTGACTTATGACATCGGGGGCCACTCAGTGCAACTTCATCTCGCTCCCTCCAA	3178
Qy	986	nTrpLysArgIleLeaArgGluIleMetAlaMetAsnGlyAsnBspProIleProHisIleAs	1006
Db	3179	CTGGAGAGGCATCCGGAGATCATGGCCATGAACGGGAACGGGCTTATCCACACATTAGA	3238
Qy	1006	pProSerArgProMetThrProGlnGlnuArgYrGluGlnGlnuArgYrGluGlnHisArg	1026
Db	3239	CCCATCGGGCCCTATGACCCCCCAACAGAGAGCGCTGCAGAGAGGAGCGCTTAAACAACCG	3298
Qy	1026	gLeuArgLeuArgAlaGlnMetArgLeuArgYrGluuBspAlaThrThrThrLeuGlyPyr	1046
Db	3299	CCTGGGGCTTCCGGGACAGATGCGGCTCGGGGCTTCAACGCCACACACACCTTAAAGGCC	3358
Qy	1046	ohiSerThrValProProThrLeuProProAlaProAlaThrThrLeuSerThrThrIleGly	1066
Db	3359	CCACACTGTGCTCCCAAGCTGCCCCCTGCCCCCTGCACACACCTGAGACATTACATTAGA	3418
Qy	1066	uProTrpGlyLeuIleProProThrThrAlaGlyTrpGlnGluSerGluThrGluThrTyr	1086

Db	3419	GCCTGGGGGCTCATTACCGCAACACACCGCTGGCTGGAGAGTGGAGACTGAGACCTA	344
Oy	1086	rThGluValValThrGluPheGlyYThrGluValGluProGluPheGlyYThrValValG	1100
Db	3479	CACAGAGGTGTGTACAGAGTTTGGACCGAGAGTGAAGCCAGTTTGGACCAAGTTGA	353
Oy	1106	uProGluPheGluThrGlnLeuGluProGluPheGluThrGlnLeuGluProGluPheG	1122
Db	3539	GCCGAGTTTGAAGCCAGTTTGGAGCCCTGATTTGAGACCCAGCTGGAGAACCGAGTTTA	359
Oy	1126	uGluGluGluGluGluGluYSGluGluGluValLeaIaThrGlyGlnAlaPheProPheTh	114
Db	3599	GGAAGAGCAGGAGGAGGAGAAAGAGAGAGATACCCATGGCCAGGACTTCCCTTCAC	365
Oy	1146	rThValGluThrYrYrThrValAlaPheGlyYAspPhe	1158
Db	3659	AACAGTAGAGCCTTACACAGTGAACCTTTGGGAGCTTC	3695
RESULT 11			
ID	ADE79063	standard; DNA; 3872 BP.	
XX	ADE79063;		
DT	29-JAN-2004	(first entry)	
DE	Human protein modification and maintenance molecule (PMM)-43 gene.		
XX			
KM	protein modification; protein maintenance; protein function;		
KM	protein conformation; protein stabilisation; protein degradation; kinase;		
KM	phosphatase; protease; protease inhibitor; isomerase; transferase;		
KM	molecular chaperone; anti-HIV; antiallergic; antiinflammatory;		
KM	antianememic; antiparkinsonian; nocotropic; anticonvulsant;		
KM	antiartherosclerotic; antiaslathmic; immunosuppressive; antithyroid;		
KM	cytostatic; hepatotropic; dermatological; antidiabetic; nephrotropic;		
KM	antigout; chymotimetic; neuroprotective; osteopathic; antiarthritic;		
KM	antiparasitic; antihelminthic; antispasmodic; uterathic; ophthalmological;		
KM	antirheumatic; haemostatic; antibacterial; viruicide; protozoicide;		
KM	fungicide; gene therapy; cell proliferative disorder; arteriosclerosis;		
KM	hepatitis; polycythemia vera; psoriasis; primary thrombocytopaenia;		
KM	cancer; developmental disorder; anaemia; mental retardation;		
KM	neurological disorder; Alzheimer's disease; Parkinson's disease;		
KM	epilepsy; autoimmune disorder; inflammatory disorder; AIDS; allergies;		
KM	asthma; autoimmune thyroiditis; Crohn's disease; diabetes mellitus;		
KM	glomerulonephritis; Goodpasture's syndrome; multiple sclerosis;		
KM	arthritis; osteoporosis; pancreatitis; Sjogren's syndrome;		
XX	microbial infection; human; gene; ds.		
XX			
OS	Homo sapiens.		
PN	WO2003063688-A2.		
XX			
PD	07-AUG-2003.		
PF	23-JAN-2003; 2003WO-US002500.		
XX			
PR	25-JAN-2002; 2002US-0351928P.		
PR	25-FEB-2002; 2002US-035903P.		
PR	21-MAR-2002; 2002US-0366837P.		
XX			
PA	(INCYTE) INCYTE GENOMICS INC.		
XX			
PI	Hafelia ADZ, Li JX, Gorvad AE, Chawla NK, Sprague MW, Lee SY,		
PI	Chang H, Elliott VS, Rankumat J, Khare R, Emerling BM, Kable AE,		
PI	Tsang YF, Yue H, Gietzen KU, Lee S, Swarnakar A, Baughn MR,		
PI	Wilson AD, Jin P, Chien D, Hawkins PR, Jiang X, Jackson AA,		
PI	Bhatia U, Burrill JD, Blake JJ, Ho A, Zheng W, Iaconi CH, Margulis JP,		
PI	Tian UK, Lal PG, Warren BA, Xu Y, Honchell CD, Becha SD,		
PI	Lehr-Mason PM,		
XX			
XX	WPI, 2003-636761/60.		
DR	P-PSDB; ADE79005.		

QY 481 AASPserGlnThrTrrValMetTrrThraenglyTrrGluGluMetThrPheHISGlyasn 500
 DB 1458 GACAGCGACACATGGGTGATGTACACCAACGGCTAAGAGAAATGACCTTTATATGGGAAC 1517
 QY 501 ValAspLyAspThrProValLeuSerGluLeuProGluProValAlaIAspPheIle 520
 DB 1518 GTGGACAAAGACACCCGTGTGATGAGTCCCGAGACCCTGGTGGTGGCTGTTTCAAC 1577
 QY 521 ArgIleTrrProLeuThrTrrPheGlySerLeuCyMetArgLeuGluValLeuGlyCyv 540
 DB 1578 CGCATCTACCCACTCACCTGGAATGGCAGCTGTGATCGCTCGAGAGGTGGTGGGTGC 1637
 QY 541 SerValAlaProValTrrSerTrrTrrAlaGlnAsnGluValAlaIAspPheAspLeu 560
 DB 1638 TCTGTGGCCCTGTCTACAGCTACTACGACAGAAAGAGTGTGGCCACCGATGACCTG 1697
 QY 561 AASPpheArgHISerTrrLyAspMetArgGlnLeuMetLyAspValAlaAsnGluGlu 580
 DB 1698 GATTTCCGGACACACAGCTACAGAGACATGCCCACTCATAGAGGTGGTGAACAGAGAG 1757
 QY 581 CyvProThrIleThrArgThrTrrSerLeuGlyLySerSerArgGlyLeuLySileTrr 600
 DB 1758 TGGCCACCATCACCCGCACTTACAGCTGGGCAAGACTCACAGAGGCTCAAGATCTAT 1817
 QY 601 AlaMetGluIleSerAspAsnProGlyGluHISGluLeuGlyGluProGluPheArgTrr 620
 DB 1818 GCCATGAAGATCTCAACAACCTGGGAGCATGAATCGGGAGAGCCCAATGCCCTAC 1877
 QY 621 ThrAlaGlyIleHISGlyAsnGluValLeuGlyAlaArgGlyLeuLeuLeuLeuMetGln 640
 DB 1878 ACTGCTGGGATCATAGGCAAGAGTGTGGCCGAGAGCTGTGTGCTGCTCAGCGAG 1937
 QY 641 TrrLeuCyArgGlyTrrTrrArgAspGlyAsnProArgValArgSerLeuValGlnAspThr 660
 DB 1938 TACCTTGCCGAGAGTACCGCGATGGGAACCCACGTGTGGCAGCTGTGTGCGAGCA 1997
 QY 661 ArgIleHISLeuValProSerLeuAsnProAspGlyTrrGluValAlaIAsnMetGly 680
 DB 1998 CGCATCACTGGTGGCTTACTGAAACCTGATGGCTACAGGTGGCAGAGGAGATGGAG 2057
 QY 681 SerGluPheGlyAsnTrrAlaLeuGlyLeuTrrThrGluGluGlyPheAspIlePheGlu 700
 DB 2058 TCAGAGTTTGGGAACGTGGGGCTGGGACTGTGAGCTGAGAGGAGCTTTGACATCTTGA 2117
 QY 701 AASPpheProAspLeuAsnSerValLeuTrrGlyAlaGluGluArgLySrrValProTrr 720
 DB 2118 GATTTCCGGATCTCAACTGTGTCTGTGGGAGCTGAGGAGAGAAATGGGTCCCTAC 2177
 QY 721 ArgValProAsnAsnLeuProIleProGluArgTrrLeuSerProAspAlaThrVal 740
 DB 2178 CGGGTCCCAACAATACCTTGGCCATCCCTGAACGCTACTTTCGCCAGATGGCAGAGTA 2237
 QY 741 SerThrGluValArgAlaIleIleAlaTrrPheGlyLeuAsnProPheValLeuGlyAla 760
 DB 2238 TCACAGGAGGTCCGGGCACTTGGCTGTGATGAGAGAACCCCTTTCGTGGCTGGAGGA 2297
 QY 761 AsnLeuAsnGlyGlyGluArgLeuValSerTrrProTrrAspMetAlaArgTrrProThr 780
 DB 2298 AATCTGAACGGCGGCAAGCGGCTAGTATCTTACCCCTACGATATGGGCCCGCAGCTACC 2357
 QY 781 GlnGluGlnLeuLeuAlaAlaIAspMetAlaAlaAlaArgGlyGlyLeuAspGluAspGluVal 800
 DB 2358 CAGAGAGAGCTGTGGCGGAGCCATGGCAGAGCCCGGGGGAGAGTGGAGAGAGTGC 2417
 QY 801 SerGluAlaGlnGluTrrProAspHISAlaIlePheArgTrrPheAlaIleSerPheAla 820
 DB 2418 TCCGAGGCCACAGAGATCCAGACACGCGATCTTCCGAGGTGGCTTGGCACTCTTCGCC 2477
 QY 821 SerAlaHISLeuThrLeuThrGluProTrrArgGlyGlyCySglAlaIAsnAspTrrThr 840
 DB 2478 TCCGACACCTCACTTGAACGAGCCCTTACCGGAGAGGCTCCAGAGCCGAGACTACACC 2537

QY 841 GlyGlyMetGlyIleValAsnGlyValAlaSerTrrAsnProArgTrrGlyThrIleAsnAsp 860
 DB 2538 GCGGCACTGGGCACTGTACACGGGGCCAAAGTGAACCCCGGAGCGGACATCATATGAC 2597
 QY 861 PheSerTrrLeuHISThrAsnCySglLeuGlyLeuSerPheTrrLeuGlyCyAspLySrrPhe 880
 DB 2598 TTCAGTTACCTGCATACCAACTGCTGGAGCTCTCTTCACTCGGCTGTGACAAAGTTC 2657
 QY 881 ProHISGlySerGlyLeuProArgGlyTrrGluAsnAsnLySglValAlaLeuLeuThrPhe 900
 DB 2658 CCTCATGAGAGTGAAGTCCCGGAGTGGAGAAACAAAGAGAGCGCTGTCTACCTTC 2717
 QY 901 MetGluGlnValHISArgGlyIleLySglValValThrAspGluGlnGlyIleProIle 920
 DB 2718 ATGGAGCAGTGCACCGT-----GGCATTTAATCAGCGCGTGAAGACAGCCAGTGTGT 2735
 QY 921 AlaAsnAlaThrIleSerValSerGlyIleAsnHISGlyValLyThrAlaSerGlyGly 940
 DB 2736 -----GGCATTTAATCAGCGCGTGAAGACAGCCAGTGTGT 2771
 QY 941 AspTrrTrrArgIleLeuAsnProGlyGlyTrrArgValTrrAlaHISAlaGlyGlyTrr 960
 DB 2772 GATTACTGGCGAATCTTGAACCGGCTGAGTACCGGTGACAGCCACGCGGAGGACTAC 2831
 QY 961 ThrProSerAlaLyThrCyAsnValAspTrrAspIleGlyAlaThrGlnCyAsnPhe 980
 DB 2832 ACCCGAGCGCCAAACCTTGCAATGTGACTATGACATCGGGCCACTGAGTCAACTTC 2891
 QY 981 IleuAlaArgSerAsnTrrLyAspGlyIleArgGlyIleMetAlaMetAsnGlyAsnArg 1000
 DB 2892 ATCTGGCTCGCTCCAACTGGAAGCGCATCCGGGAGATCATGCGCATGAACCGGAACCG 2951
 QY 1001 ProIleProHISAlaAspProSerArgProMetTrrProGlnGlnArgArgLeuGlnGln 1020
 DB 2952 CCTATCCACATAGACCCATCGGCTATGACCCCAACAGACAGCGCTGACAGAG 3011
 QY 1021 ArgArgLeuGlnHISArgLeuArgLeuArgAlaGlnMetArgLeuArgArgLeuAla 1040
 DB 3012 CGAGCCCTTAAACAACACCGCTGGGCTGGGGCAGAGATGGCGCTGGGGCTCAACCGCC 3071
 QY 1041 ThrThrThrLeuGlyProHISThrValProProThrLeuProProAlaProAlaThrThr 1060
 DB 3072 ACCACACCTTGGGCGCCCACTGTGCTCCACAGCTGCCCGCTGCCCTGCCACACCC 3131
 QY 1061 LeuSerTrrThrIleGluProTrrGlyLeuIleProProThrThrAlaGlyTrrGluGlu 1080
 DB 3132 CTGAGCACTACCATAGAGCTTGGGCTCTCATACCGCAACAGCTGGCTGGAGAGAG 3191
 QY 1081 SerGluThrGluThrTrrThrGluValValThrGluPheGlyThrGluValGluProGlu 1100
 DB 3192 TCGAGACTGAGACTTACACAGAGGTGGTGAACAAGTTTGGAGCGAGGTGAGCCGAG 3251
 QY 1101 PheGlyThrLyAspValGluProGluPheGlyThrGlnLeuGluProGluPheGlyThrGln 1120
 DB 3252 TTTGGGACCAAGTGAAGCCCGAGTTTGAAGCCCAAGTTTGAAGCTTGAAGACCCAG 3311
 QY 1121 LeuGluProGluPheGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 1140
 DB 3312 CTGAAACCGGAGTTTGAAG 3371
 QY 1141 GlnAlaPheProPheThrThrValGluThrTrrTrrValAsnPheGlyAspPhe 1158
 DB 3372 CAGGACTTCCCTTCAACAACATTAAGACTTACAGAGTGAACCTTTGGGAGACTTC 3425

RESULT 12
 ABQ54610
 ID ABQ54610 standard; cDNA; 3523 BP.
 XX
 AC ABQ54610;
 XX
 DT 22-AUG-2002 (first entry)
 XX
 DE Human ovarian antigen HNTAK22 cDNA, SEQ ID NO:490.

XX Human: ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KM ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KM infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KM PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
 KM inflammatory condition; immune disorder; blood disorder;
 KM cardiovascular disorder; respiratory disorder; neurological disorder;
 KM gastrointestinal disorder; urinary system disorder; drug screening;
 KM gene therapy; chromosome mapping; forensic analysis;
 KM antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KM antiinflammatory; gynaecological; reproductive; chromosome 7; gene; ss.
 XX Homo sapiens.
 OS
 PN MO20020677-11.
 PD 03-JAN-2002.
 PF 07-JUN-2001; 2001MO-US018569.
 PR 07-JUN-2000; 2000US-0209467P.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Birse CE, Rosen CA;
 XX WPI, 2002-147878/19.
 DR P-PSDB; ABP41533.
 XX
 PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
 PT cancer), immune disorders, cardiovascular disorders and neurological
 PT diseases.
 PS Claim 1; SEQ ID NO 490; 2922pp; English.
 XX
 CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP42228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosing or preventing various ovary and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis), systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents a cDNA encoding a human ovarian antigen of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 3523 BP; 862 A; 1069 C; 1054 G; 535 T; 0 U; 3 Other;

Alignment Scores:

Pred. No.: 2,1e-264
 Score: 5725.00
 Percent Similarity: 99.8%
 Best Local Similarity: 99.6%

Length: 3523
 Matches: 1054
 Conservative: 2
 Mismatches: 2

Query Match:	91.3%	Indels:	0
DB:	6	Gaps:	0
US-10-642-946-3 (1-1158) x ABQ54610 (1-3523)			
QY 101	LYSG1ProlyVala1ProlyGluSerLeuGluGlySerProArgProProlyGlyGly	120	
DB 2	AAAGGCCCAAGGTGCGCAAGAGTCTTGAGAGGGTCCCCAGGCGGCCCAAGAGGGG	61	
QY 121	LYSG1LYSPProProLySa1aThrLYSPProLYSG1LYSPProProLySa1aThrLYS	140	
DB 62	AAAGRAAGGACCAAGCCCAAGGCGCAAGAAAGCCCAAGAGAGGCACTTAAGGCAACAAG	121	
QY 141	LYSPProLYSG1LYSPProProLYSa1aThrLYSPProLYSG1LYSPProProLYSa1a	160	
DB 122	AAAGCCCAAGGAGAGAGCCCAAGGCGCAAGAAAGCCCAAGAGAGAGCCCAAGAGGCG	181	
QY 161	ThrLYSPProSerGlyLYSPArgProPro1LeuVala1ProSerGlyThrLeuGlu	180	
DB 182	ACCAAGAGCCCGGTCAAGAGAGAGAGCCCGCATTCCTGCTCCCAAGAAACCTGAGAG	241	
QY 181	TrpProLeuProProProProSerProGlyProGluGluLeuProGluGlyGlyA1A	200	
DB 242	TGGCCACTGCCCCCAAGCCCGGCGCCGAGAGACTACCCAGAGAGGAGGCGG	301	
QY 201	ProLeuSerAsnAsnTrpGluAsnProGlyGluGluThrHisValGlu1aGlu1a	220	
DB 302	CCCTCTCAATTAATCGGAGAAATCCAGAGAGAGAACCATGTGAGGCAAGGAGAGAC	361	
QY 221	GlnProGlu1ProGluGluGlu1ThrGluGlu1nProThrLeuAspTrpAsnAsn1Glu	240	
DB 362	CAGCTGAGCGGAG	421	
QY 241	ArgGluAspTrpGlu1aAspPheGlu1aTrp1LeuArgGlu1aGlu1aProArgProPro	260	
DB 422	AGGAGAGAGATGAGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG	481	
QY 261	SerArgArgArgArgProGluArgVal1TrpProGluProProGluGluVala1a	280	
DB 482	AGGAG	541	
QY 281	ProAlaProGluGluArg1Leu1ProProVala1aProLeuProProLeuProPro	300	
DB 542	CAAGCCCCGAG	601	
QY 301	AspTrpGlyAspGlyTrpVal1aProAsnTrpAspAspMetAspTrpTrpPheGlyPro	320	
DB 602	GACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	661	
QY 321	ProProProGlu1aProProAsn1aGluArg1aThrAspGluGluGluGluLeuLYS	340	
DB 662	CTCCGCCCCCAAG	721	
QY 341	LYSPProLYSG1LYSPSerSerProLYSG1Glu1aThrAspLYSPTrp1aValGluLYS	360	
DB 722	AAACCCAAAG	781	
QY 361	GlyLYSPAsn1aLYSPGlu1aProArg1aGlyGluGluGluGluGluGlu1aTrpTrp	380	
DB 782	GGCAAGAGACCAAG	841	
QY 381	GluLYSPValaLYSPProPro1LeuGluGluGluGluGluGluGluGluGluGluGluGlu	400	
DB 842	GAGAAAGTCAAGTGTCCCAATGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	901	
QY 401	ArgAlaSerSerMetLeuArg1aGlyLeuGlyValaGluArg1aArgLeuAsnMetGln	420	
DB 902	CAAGCTCTCTCATGTGCGCAAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	961	
QY 421	ThrGlyVala1aThrGluAspAspTrpTrpAspGlyVala1aTrpCysAlaGlu1aAspAsp	440	
DB 962	ACCGGAGCAGTGAAG	1021	

ID AAT97611 standard; cDNA; 3633 BP.
 XX
 AC AAT97611;
 XX
 DT 27-MAR-1998 (first entry)
 XX
 DE Mouse E2A-binding protein cDNA.
 XX
 KM E2A-binding protein; E2A-BP; mouse; vascular smooth muscle cell;
 wound healing; angiogenesis; arteriosclerosis; gene therapy; ds.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT CDS 46..3432
 /tag= a
 XX
 PN MO9733900-A1.
 XX
 PD 18-SEP-1997.
 XX
 PF 14-MAR-1997; 97MO-US004117.
 XX
 PR 15-MAR-1996; 96US-0013439P.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Lee M, Haber E, Endege WO, Layne MD;
 XX
 DR MPI; 1997-470808/43.
 XX
 DR P-PSDB; AAW36817.
 XX
 PT DNA encoding human and mouse E2A binding proteins - useful for inhibiting
 PT or stimulating growth of rheumatoid arthritis or retinopathic diabetes.
 XX
 PS Claim 13; Page 62-68; 90pp; English.
 XX
 XX This sequence represents a full-length nucleotide sequence that codes for
 CC mouse E2A binding protein (E2A-BP, see AAW36817). It was isolated using
 CC 5'RACE with primers designed from mouse AEBP cDNA. E2A-BP is expressed in
 CC vascular smooth muscle cells; mRNA is preferentially expressed in the
 CC aorta. E2A-BP interacts with E2A proteins in vivo, binds to both E12 and
 CC E47 and inhibits binding of E47 homodimer to an E-box probe (see
 CC AAT97606). Human (see AAT97609-10) and rat (see AAT97612-13) E2A-BP
 CC sequences have also been isolated. E2A-BP nucleic acids may be used in
 CC gene therapy and antisense methods for treating vascular diseases such as
 CC arteriosclerosis, to produce transgenic or knock-out animals, as well as
 CC in methods of producing E2A-BP polypeptides that can be used
 CC therapeutically to promote vascular smooth muscle cell growth e.g. for
 CC wound healing, or to screen for modulator compounds useful e.g. for the
 CC treatment of arteriosclerosis and angiogenesis. The E2A-BP gene promoter
 CC can be used in gene therapy methods to direct vascular smooth muscle cell
 CC -specific expression of the E2A-BP gene, antisense sequences or
 CC heterologous genes
 XX
 SQ Sequence 3633 BP; 927 A; 1065 C; 1043 G; 598 T; 0 U; 0 Other;
 XX
 Alignment Scores:
 Pred. No.: 1,9e-233 Length: 3633
 Score: 5077.00 Matches: 960
 Percent Similarity: 87.3% Conservative: 54
 Best Local Similarity: 82.6% Mismatches: 110
 Query Match: 80.9% Indels: 38
 DB: 2 Gaps: 9
 US-10-642-946-3 (1-1158) x AAT97611 (1-3633)
 QY 1 MetAlaAlaValArgGlyAlaProLeuLeuSerCysLeuLeuAlaLeuLeuAlaLeuCys 20
 DB 46 ATGGCTCCAGTGGACCGGATCCCTGCGGCGCTCTGGACATCGCTGAGCGCTGTC 105
 QY 21 ProGlyGlyArgProGlnThrValLeuThrAspAspGluLeuGluGluPheLeuGluGly 40

DB 106 CTTGAGGGGAAACCAAGACGGTCTGACGACGACGAGATCGAGAGTTCTCTGAAAGC 165
 QY 41 PheLeuSerGluLeuGluProGlu-----ProArgGluAspAspValGluAlaProPro 58
 DB 166 TTCCTTCGGAGTTGAGACCCAGTCCCGCCCGGGGAGAGAGCACTGGAGATGCCAGCCG 225
 QY 59 ProProGluProThrProArgValArgValAlaGlnAlaGlyGlyLysProGlyLysArg 78
 DB 226 CTTCCCGAACCACCCAGCGTCCCGCAATCCAGGCGAGGGGCAAG----- 273
 QY 79 ProGlyThrAlaAlaGluValProProGluLysThrLysAspLysGlyLysLysGlyLys 98
 DB 274 CAGCGGCGAGATTTAGAGTCTCTCCAGAAAAAACAAGACAAAGAGAAAGAAAG 333
 QY 99 LysAspLysGlyProLysValProLysGluSerLeuGluGlySerProArgProLys 118
 DB 334 AAGGACAAAGGCCCAAGGACCAAAA-----CCCTGGAGGGGCTTACAGGCCCAACAG 390
 QY 119 LysGlyLysGlyLysProProLysValAlaThrLysLysProLysGlyLysProProLysAla 138
 DB 391 AAACCAAGAGAGAGCCACCCAGGACCAAGAGACCCAGAGAGAAACCAACCAAGGCC 450
 QY 139 ThrLysLysProLysGluGluProProLysValAlaThrLysLysProLysGlyLysProPro 158
 DB 451 ACCAGAGGCCCAAGAGAGAGCCACCAAGGCCCAAGAGAGCTTAAGAGAGAGCAACC 510
 QY 159 LysAlaThrLysLysProProSerGlyLysArgProProLysLeuAlaProSerGluThr 178
 DB 511 AAGGCCACTTAAGAGGCTCCGAGAGAAAGATTCACAGTGTCGCCCTTGGAAG 570
 QY 179 LeuGluTrpProLeuProProProProSerProGlyProGluGluLeuProGluGluGly 198
 DB 571 CTGGATCGGTACTCCCTCCACCTTCAACCCAGGCGCCAGAGCTACCGCGAGAGAGA 630
 QY 199 GlyAlaProLeuSerAsnAsnTrpGluAsnProGluGluGluThrIstValGluAlaGln 218
 DB 631 GACACACCTTCCCAATGCTGCGCAAGGTCAAGAGAGAGAGCCAGAGGAGGCCAAG 650
 QY 219 GluHisGlnProGluProGluGluGluThrGluGlnProThrLeuAspTyrAsnAspGln 238
 DB 691 GAGCCCGGCGAGAGCCAGAGAGAGAGATGAGATCCCACTGAGCTACATGACAG 750
 QY 239 IleGluArgGluAspTyrGluAspPheGluTyrIleArgArgGlnLysGlnProArgPro 258
 DB 751 ATGAGAAAGAGAGATTACAGAGATTGAGTGCATCCGTCGAGAGAGAGCCAGGCCA 810
 QY 259 ProProSerArgArgArgArgProGluArgValTrpProGluProGluGluLysAla 278
 DB 811 ACACCCAGAGAGG-----AGGCTCTGCGCAAGGCGCTTGAAGAGAGACT 858
 QY 279 ProAlaProAlaProGluGluArgGluGluProProValLysProLeuLeuProProLeu 298
 DB 859 GAAAGCCAGAGAAAGAAAGAGAGTGCAGGCCACTGTAAAGCCCTG-----CTG 909
 QY 299 ProProAspTyrGlyAspGlyTyrValIleProAsnTyrAspAspMetAspTyrTyrPhe 318
 DB 910 CTTCCGAGATAGGGATAGCTACGTGATCCCACTATGATGACTTTCATTTTC 969
 QY 319 GlyProProProGluProGluProAspAlaGluArgGlnThrAspGluGluLysGluGlu 338
 DB 970 CCCACCTTCCACCGCAAGAGCTGTGTTGGACAAAGAGGTGATGAGAAAGAGAGAG 1029
 QY 339 LeuLysLysProLysLysGluAspSerSerProLysGluGluThr---AspLysTrpAla 357
 DB 1030 ATGAGAGAGCCCAAGAGAGAGGTAGTACCCCAAGAGAGACACAGAGACAAGTGAGCC 1089
 QY 358 ValGluLysGlyLysAspHisLysGluProAlaGlyLysGluGluGluGluGluTrp 377
 DB 1090 GTGGAGAAAGAAAGAGACCAAGAGGCGCCGAGAGGGGTGAGAGGTGAGAGAGGTGG 1149
 QY 378 ThrProThrGluLysValLysCysProProIleGlyMetGluSerHisArgIleGluAsp 397

Db 1150 GGGCCAGTGGAGAAATCAAGTGGCCACCTATTGGATGGAGTCAACCCGACTGAGGAC 1209
QY AaenGlnIleArgAlaSerSerMetLeuAghIeGlyLeuGlyValAgIaArgGlyArgLeu 417
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[illegible]

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Best Local Similarity:	82.3%	Mismatches:	113
Query Match:	80.5%	Indels:	38
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QY	59 ProProGluProThrProArgValArgLysAlaGlnAlaGlyGlyLysProGlyLysArg	78	
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DB	474 ACCAAGAAAGCCCAAGAGAACCAACCAAGGCCACCAAGAGGCTTAAGAGAAAGCAACC	533	
QY	159 LysAlaThrLysLysProProSerGlyLysAlaGProProIleLeuAlaProSerGluThr	178	
DB	534 AAGGCACCTTAAGAGGCCCTCCGGCAGAGAAAGTTCTCACTGTGGCCCTCTTGAAGACG	593	
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QY 941 sPpTyrTrpArg11eLeuAsnProGlyGluTyrArgVal1ThraH1sAlaGluGlyTyrT 961
DB 2207 ATTTACTGGCGAATCTTGAACCCGGGTGAGTACCGGCTGACACCCACCGGAGGGCTTCA 2266
QY 961 hrProSerAlaLysThrCybAsnVal1AspTyrAsp11eGlyAlaThrGlnCybAsnPhe 981
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QY 981 lAeLeuAlaArgSerAsnTrpLysArg11eArgGlu11eMetAlaMetAsnGlyAsnaArgP 1001
DB 2327 TCCGTGCTGCTCCAACTGGAAAGCGCATCCGGGAATCATGGCCATGAACGGGAACCGG 2386
QY 1001 ro11eProH1s11eAspProSerArgProMetThrProGlnGlnArgArgLeuGlnGlnA 1021
DB 2387 CTATCCCAACATTAACCATGCGCCTTAATGACCCCAACAGGAGCGCTGGAGAC 2446
QY 1021 rGArgLeuGlnH1sArgLeuArgLeuArgAlaGlnMetArgLeuArgArgLeuAsnAlaT 1041
DB 2447 GACGCTACAAACACGCGCTGGGCTTGGGCAACAGTGGCGGCTGCCTCAACGCCA 2506
QY 1041 hrThrThrLeuGlyProH1sThrVal1ProProThrLeuProProAlaProAlaThrThL 1061
DB 2507 CCACCACTTAAGGCCCCCACTGTGCTCCACAGCTGCCCCCTGGCCACCAACCC 2566
QY 1061 eUsSerThrTr11eGluProTyrGlyLeu11eProProThrThra1AaGlyTyrGluGluS 1081
DB 2567 TGAACATTAACATTAAGCCCTGGGCTCATACCGCAACACCGCTGGCTGGAGAGAGT 2626
QY 1081 eArg1uThrGluThrTyrThrGluVal1Val1ThrGluPheGlyThrGluVal1GluProGluP 1101
DB 2627 CCGAGACTGAACCTAACACAGAGGTGTGACAGAGTTGGAGACCGAGGTGGAGCCGAGT 2686
QY 1101 hrg1LysThrLysVal1GluProGluPheGluThrGluLeuGluProGluPheGluThrGluL 1121
DB 2687 TTGGGACCAAGGTGAGCGCGAGTTTGAGAACCCAGTTGAAGCTTGATTGAGACCCAG 2746
QY 1121 eGluProGluPheGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 1141
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Db 2807 AGGCATTCCCTTCACAAGTAGAGACTTACACAGTGAATTGGGACTTC 2859

Search completed: September 30, 2006, 23:57:34
Job time : 1662 secs

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REFERENCE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
AUTHORS Hominiidae; Homo.
TITLE
JOURNAL
FEATURES
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Matches 26; Conservative 1; Mismatches 11; Indels 0; Gaps 0;
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AX517772/c 41 bp DNA linear PAT 05-OCT-2002
LOCUS AX517772
DEFINITION Sequence 3970 from Patent WO02052044.
ACCESSION AX517772
VERSION AX517772.1 GI:23566740
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
AUTHORS Nakamura, Y., Sekine, A., Iida, A. and Saito, S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 3970 04-JUL-2002;
Riken (JP)
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AX612102/c 45 bp DNA linear PAT 17-FEB-2003
LOCUS AX612102
DEFINITION Sequence 3127 from Patent WO02072882.
ACCESSION AX612102
VERSION AX612102.1 GI:28407531
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
AUTHORS Cullen, P. and Seedorf, U.
TITLE Coronary chip
JOURNAL Patent: WO 02072882-A 3127 19-SEP-2002;
OGHAM GmbH (DE)

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AX612103/c 45 bp DNA linear PAT 17-FEB-2003
LOCUS AX612103
DEFINITION Sequence 3128 from Patent WO02072882.
ACCESSION AX612103
VERSION AX612103.1 GI:28407532
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
AUTHORS Cullen, P. and Seedorf, U.
TITLE Coronary chip
JOURNAL Patent: WO 02072882-A 3128 19-SEP-2002;
OGHAM GmbH (DE)
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AX612100/c 48 bp DNA linear PAT 17-FEB-2003
LOCUS AX612100
DEFINITION Sequence 3125 from Patent WO02072882.
ACCESSION AX612100
VERSION AX612100.1 GI:28407529
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
AUTHORS Cullen, P. and Seedorf, U.
TITLE Coronary chip
JOURNAL Patent: WO 02072882-A 3125 19-SEP-2002;
OGHAM GmbH (DE)
FEATURES
source
1. .48
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RESULT 7				
AX612101/c				
LOCUS	AX612101	48 bp	DNA	linear
DEFINITION	Sequence 3126 from Patent WO02072882.			PAT 17-FEB-2003
ACCESSION	AX612101			
VERSION	AX612101.1	GI:28407530		
KEYWORDS				
SOURCE				
ORGANISM	Homo sapiens (human)			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1			
AUTHORS	Cullen,P. and Seedorf,U.			
TITLE	Coronary chip			
JOURNAL	Patent: WO 02072882-A 3126 19-SEP-2002;			
FEATURES	OGHAM GmbH (DE)			
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LOCUS	AR017890	50 bp	DNA	linear
DEFINITION	Sequence 37 from patent US 5780269.			PAT 05-DEC-1998
ACCESSION	AR017890			
VERSION	AR017890.1	GI:3973493		
KEYWORDS				
SOURCE				
ORGANISM	Unknown.			
	Unclassified.			
REFERENCE	1 (bases 1 to 50)			
AUTHORS	Inouye,S. and Inouye,M.			
TITLE	Hybrid molecules			
JOURNAL	Patent: US 5780269-A 37 14-JUL-1998;			
FEATURES	location/Qualifiers			
source	1..50			
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Db	41	GCTCCACTCCCGACGCTGCTGCTACCTGCTTTTCCAAAC 82		
	2	GATAAACCTCCACCTGCGTGTCTACCTGCGTTGGACACC 43		

LOCUS	AR681730	50 bp	DNA	linear	PAT 12-SEP-2005
DEFINITION	Sequence 1159 from patent US 6905827.				
ACCESSION	AR681730				
VERSION	AR681730.1	GI:74463500			
KEYWORDS					
SOURCE	unknown.				
ORGANISM	unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 50)				
TITLE	Wohlgenuth, J., Fry, K., Woodward, R. and Ly, N.				
JOURNAL	Methods and compositions for diagnosing or monitoring auto immune and chronic inflammatory diseases				
FEATURES	Patent: US 6905827-A 1159 14-JUN-2005;				
source	Expression Diagnostics, Inc.; So. San Francisco, CA				
ORIGIN	Location/Qualifiers				
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	/organism="unknown"				
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Query Match	8.1%; Score 19.6; DB 2; Length 50;				
Best Local Similarity	66.7%; Pred. No. 8.6e+05;				
Matches	28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;				
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Db	50 CTGTGCGCTTCCCTTCCAGTTACAGCCCGACGCTCTTC 9				
RESULT 10					
LOCUS	AR016521	39 bp	DNA	linear	PAT 05-DEC-1998
AR016521/c					
DEFINITION	Sequence 35 from patent US 5776746.				
ACCESSION	AR016521				
VERSION	AR016521.1	GI:3972798			
KEYWORDS					
SOURCE	unknown.				
ORGANISM	unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 39)				
TITLE	Denney, D.W. Jr.				
JOURNAL	Gene amplification methods				
FEATURES	Patent: US 5776746-A 35 07-JUL-1998;				
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Best Local Similarity	75.0%; Pred. No. 1.1e+06;				
Matches	24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;				
DY	211 TGTATCAGATPCCCACTAAACTGATTCAC 242				
Db	37 TGAACAGATPCCCACTAAACTGATTCAC 6				
RESULT 11					
LOCUS	AR096904	39 bp	DNA	linear	PAT 08-SEP-2000
AR096904/c					
DEFINITION	Sequence 35 from patent US 5972334.				
ACCESSION	AR096904				
VERSION	AR096904.1	GI:10009428			
KEYWORDS					
SOURCE	unknown.				
ORGANISM	unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 39)				
TITLE	Denney, D.W. Jr.				
JOURNAL	Vaccines for treatment of lymphoma and leukemia				
FEATURES	Patent: US 5972334-A 35 26-OCT-1999;				
	Location/Qualifiers				

Mon Oct 2 13:05:56 2006

us-10-642-946-6_copy_1967_2208.sz50.rge

Page 5

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Job time : 2027.61 secs

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

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(without alignments)
3748.870 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 2795665780 residues
Total number of hits satisfying chosen parameters: 194034

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_est7:*
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8: gb_est9:*
9: gb_est10:*
10: gb_est11:*
11: gb_est12:*
12: gb_est13:*
13: gb_est14:*
14: gb_est15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19.6	8.1	50	14	AT520369 Arabidops
2	19.4	8.0	45	7	AV960508 Arabidops
3	19.2	7.9	47	14	DUS32846 YHB292 Ba
4	19	7.9	42	2	BM392535 50071-2-1
5	19	7.9	42	2	BM392535 50072-2-1
6	19	7.9	42	2	BM392535 50072-2-1
7	18.8	7.8	44	11	BH801643 100811861
8	18.6	7.7	45	5	CF297420 30DGS--08
9	18.6	7.7	50	14	CR294949 Reverse 8
10	18.4	7.6	46	12	CG892412 01S0720-0
11	18.4	7.6	50	1	AUI05790 AUI05790
12	18.2	7.5	44	13	CZ294180 P063E09 G
13	18.2	7.5	46	1	AT179194 at06008 x
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17	18	7.4	50	1	AUI02351 AUI02351
18	18	7.4	50	13	CZ473637 d03923-3P
19	18	7.4	50	14	AJ622111 Drosophila

c	20	18	7.4	50	14	AJ622124 Drosophila
c	21	17.8	7.4	50	1	AUI06364 AUI06364
c	22	17.8	7.4	50	1	AUI07219 AUI07219
c	23	17.6	7.3	41	11	AZ423755 IM0203C23
c	24	17.6	7.3	49	2	BI790793 i609D08-Y
c	25	17.4	7.2	43	2	BM392587 50071-2-1
c	26	17.4	7.2	43	2	BM392587 50071-2-1
c	27	17.4	7.2	43	2	BM392587 50072-2-1
c	28	17.4	7.2	43	2	BM392587 50072-2-1
c	29	17.4	7.2	46	1	AA876150 nx21a04.s
c	30	17.4	7.2	50	14	AL765665 Arabidops
c	31	17.4	7.2	50	14	CR148431 Forward s
c	32	17.2	7.1	39	1	AA961533 oc79c11.s
c	33	17.2	7.1	50	1	AUI04401 AUI04401
c	34	17.2	7.1	50	1	AUI04421 AUI04421
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c	36	17.2	7.1	50	1	AUI07392 AUI07392
c	37	17.2	7.1	50	1	AUI07394 AUI07394
c	38	17.2	7.1	50	13	CZ194618 PST2433-N
c	39	17	7.0	42	11	BH799794 1008110B1
c	40	17	7.0	48	1	AI115696 uc34C06.r
c	41	17	7.0	49	1	AI1799548 tr49603.x
c	42	17	7.0	49	11	AZ430158 IM0214E05
c	43	17	7.0	50	1	AUI06897 AUI06897
c	44	16.8	6.9	38	11	AZ476034 1M0294F02
c	45	16.8	6.9	39	11	AZ803216 2M0063D02

ALIGNMENTS

RESULT 1
ATHS20369
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

ATHS20369
Arabidopsis thaliana T-DNA flanking sequence, left border, clone
027A07, genomic survey sequence.
AJ520369
AJ520369.1 GI:26788605
GSS, left border; T-DNA flanking sequence.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidops.

REFERENCE

AUTHORS

1
Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F.,
Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,
Lepoint, L., Caboche, M. and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.inbio.gen.fr).

FEATURES

source

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misc_feature

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Best Local Similarity 62.0%; Pred. No. 7.5e+05;
Matches 31; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 69 TGTAAAGCTACTACATTTCGGCCACTAGCCCTGTTCCATCTCT 138
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RESULT 2
AV960508 45 bp mRNA linear EST 26-MAY-2005
DEFINITION AV960508 Nori Satoh unpublished cDNA library, cleavage stage embryo
Ciona intestinalis cDNA clone cici12n17 5', mRNA sequence.
ACCESSION AV960508
VERSION AV960508.1 GI:19448807
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Clonidae; Ciona.
1 (bases 1 to 45)
Satoh,N., Satoh,Y., Kohara,Y. and Shin-i,T.
Expressed genes in Ciona intestinalis
Unpublished (2000)
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-Ku, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
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/clone_lib="Nori Satoh unpublished cDNA library, cleavage
stage embryo"

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Best Local Similarity 70.3%; Pred. No. 8.5e+05;
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 52 CCAGCTGCTGCTCACCTGTTTCCAAACCCACC 88
1 CCTGCAGCTGCCCAACAGCTGTACCAAGTCCAAACAC 37

Db

RESULT 3
DUS32846 47 bp mRNA linear GSS 06-OCT-2005
DEFINITION YHB292 BayGenomics Gene Trap Library pGT0Lxf Mus musculus cDNA,
mRNA sequence.
ACCESSION DUS32846
VERSION DUS32846.1 GI:77358565
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 47)
BayGenomics.
http://baygenomics.ucsf.edu/
Unpublished (2001)
Contact: BayGenomics
Bay Area Functional Genomics Consortium (BayGenomics)
Email: info@baygenomics.ucsf.edu
Sequence tag generated by 5' RACE of total RNA from gene trap ES
cell line. ES cell lines harboring insertion mutation of target
gene are available upon request from BayGenomics. Annotation
information available from
http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACT&TYPE=
CELL_LINEKEY=YHB292
Class: Gene trap.
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Matches 27; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 38 GGAAGTCACCTCCCGAGCTGCTGCCTCAGCTGTTTCC 77
1 GGGCTCTCGCGCGCGCTGCGCTCCGCGCTTCC 40

Db

RESULT 4
BM392535 42 bp mRNA linear EST 17-JAN-2002
DEFINITION 50071-2-10-A02.f.1 Chilcoat/Turkewitz cDNA (small fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM392535
VERSION BM392535.1 GI:18192573
KEYWORDS EST.
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
1 (bases 1 to 42)
Turkewitz,A.P., Karer,K.M., Jahn,C., Orlas,E., Kirk,K.E.,
Frankel,U. and Klobutcher,U.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apurkew@midway.uchicago.edu
Seq primer: T3.
Location/Qualifiers
1. .42
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (small fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Query Match	Similarity	7.9%	Score 19	DB 2	Length 42
Best Local	Similarity	71.4%	Pred. No. 1.1e+06		
Matches	25	Conservative	0	Mismatches	10
				Indels	0
				Gaps	0
Db	1	GGACACAAAGCTGGAGCTCCACCGCGGTGGCGGC	35		
RESULT 5	BM393595	42 bp	mRNA	linear	EST 17-JAN-2002
LOCUS	50072-2-10-A02.f.1	Chilicoat/Turkewitz cDNA (large fraction)			
DEFINITION	Tetrahymena thermophila cDNA, mRNA sequence.				
ACCESSION	BM393595				
VERSION	BM393595.1	GI:18193648			
KEYWORDS	EST.				
SOURCE	Tetrahymena thermophila				
ORGANISM	Eukaryota; Alveolata; Ciliophora; Oligohymenophora; Hymenotomastix; Tetrahymenina; Tetrahymenidae; Tetrahymena.				
REFERENCE	1 (bases 1 to 42)				
AUTHORS	Turkewitz,A.P., Karter,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel,J. and Klobutcher,L.				
TITLE	EST from Tetrahymena thermophila, strain CU428.1, growing cells				
JOURNAL	Unpublished (2002)				
COMMENT	Contact: Turkewitz AP Molecular Genetics and Cell Biology University of Chicago 920 E. 58th Street, Chicago, IL 60637, USA Tel: 773 702 4374 Fax: 773 702 3172 Email: apturkew@midway.uchicago.edu Seq primer: 13.				
FEATURES	Location/Qualifiers				
source	1..42				
	/organism="Tetrahymena thermophila"				
	/mol_type="mRNA"				
	/strain="CU428.1"				
	/db_xref="taxon:5911"				
	/clone_11b="Chilicoat/Turkewitz cDNA (large fraction)"				
	/note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilicoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."				
ORIGIN					
Query Match	7.9%	Score 19	DB 2	Length 42	
Best Local	Similarity	71.4%	Pred. No. 1.1e+06		
Matches	25	Conservative	0	Mismatches	10
				Indels	0
				Gaps	0
Db	1	GGACACAAAGCTGGAGCTCCACCGCGGTGGCGGC	35		
RESULT 6	CZ550492	49 bp	DNA	linear	GSS 24-MAY-2005
LOCUS	02F0151-11C2-B12	UniformMu MutAIL Library			
DEFINITION	02F0151-11C2-B12, genomic survey sequence.				
ACCESSION	CZ550492				
VERSION	CZ550492.1	GI:66476962			
KEYWORDS	GSS.				
SOURCE	Zea mays				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.				
REFERENCE	1 (bases 1 to 49)				
AUTHORS	latschew,S., Tan,B.-C., Settles,A.M. and McCarty,D.R.				
TITLE	Sequence tagged transposon insertions from the UniformMu maize population				

```

JOURNAL      Unpublished (2003)
COMMENT      Contact: Donald R. McCarty
              Plant Molecular and Cellular Biology Program
              University of Florida
              PO 110690 Gainesville, FL 32611-0690, USA
              Tel: 352-392-1928 x322
              Email: drmc@ufl.edu
              Sequence flanking probable Mu insertion site in UniformMu line:
              02F0151-1
              Class: transposon insertion site.
              Location/Qualifiers
                1..49
                /organism="Zea mays"
                /mol_type="genomic DNA"
                /strain="W22 (ACR, bz1-m9)"
                /cultivar="UniformMu"
                /db_xref="taxon:4577"
                /clone="02F0151-13C2-B12"
                /clone_lib="UniformMu MutAIL library"
                /note="Vector: TOPO-PCR4; DNA flanking Mu transposon
                insertions in Mu inactive lines were extracted from the
                UniformMu maize population by the thermo asymmetric
                interlaced PCR (TAIL) protocol using primers specific for
                the Mu terminal inverted repeat and a set of 16 arbitrary
                primers. Amplicons were size enriched using Sepharose 400
                spin columns and cloned into the TOPO PCR4 vector."

ORIGIN
Query Match      7.9%; Score 19; DB 13; Length 49;
Best Local Similarity 71.4%; Pred. No. 1.1e+06;
Matches 25; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Oy      125  CGTTTCATCTCTTTGGAGCACCTCTCAGCGGAG 159
          || ||||| ||||| ||||| ||||| |||||
Db      1  CGCCTCATTTGTCGAATCCCTTTCGCGGAG 35

RESULT 7
BH801643
LOCUS      1008118G10.JBL.X1.1008 - Rescuemu Grid I Zea mays genomic, genomic
DEFINITION survey sequence.
ACCESSION  BH801643
VERSION    BH801643.1 GI:20314925
KEYWORDS   GSS.
SOURCE     Zea mays
ORGANISM   Zea mays
REFERENCE  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
TITLE      Clade; Panicoideae; Andropogoneae; Zea.
JOURNAL    1 (bases 1 to 44)
COMMENT    Walbot,V.
            Maize genomic sequences found using engineered Rescuemu transposon
            Unpublished (2001)
            Contact: Walbot V
            Department of Biological Sciences
            Stanford University
            855 California Ave, Palo Alto, CA 94304, USA
            Tel: 650 723 2237
            Fax: 650 725 8221
            Email: walbot@stanford.edu
            Very probable ligation site of ends cut by single endonuclease.
            Reverse complemented post-ligation sequence from source sequence.
            Plate: 1008118 row: 21
            Class: transposon-tagged.
            Location/Qualifiers
              1..44
              /organism="Zea mays"
              /mol_type="genomic DNA"
              /cultivar="mixed background W23/A188/B73"
              /db_xref="taxon:4577"
              /tissue_type="leaf"
              /dev_stage="adult"
FEATURES
SOURCE

```


JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estw@wustl.edu
This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.lml.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..46
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2354367"
/sex="male"
/dev_stage="adult, age 64"
/lab_host="DH10B (phage resistant)"
/clone_lib="Barestead aorta HPLRB6"
/note="Organ: aorta; Vector: pT73D-Pac1; Site 1: EcoRI;
Site 2: NotI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer (5'
TCTTACGATCTGAACTGGAGCGGCCCTTTTCTTTTCTTTTCTTTT
3') ; double-stranded cDNA was ligated to Eco RI adaptors
5' AATTCGATCGAAC 3' and 5' GTTGGATCGG 3', digested
with Not I and cloned into the Not I and Eco RI sites of
the modified pT73 vector. Library constructed by Bob
Barestead."

ORIGIN
Query Match 7.5%; Score 18.2; DB 1; Length 46;
Best Local Similarity 66.7%; Pred. No. 1.9e+06;
Matches 26; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 18 GGATTTTGTCTACCTGCTGGAGCTCCACCTCCACG 56
DB 39 GGGTTTGTCTCCCGTTGGGGCCCCCCCCCGGCGC 1

RESULT 14
CF661282 49 bp mRNA linear EST 28-JUL-2004
LOCUS CCLM09a34120f1 Carp muscle library 1 Cyprinus carpio cDNA clone
DEFINITION 34120 5', mRNA sequence.
ACCESSION CF661282
VERSION CF661282.2 GI:50743501
KEYWORDS EST.
SOURCE Cyprinus carpio (common carp)
ORGANISM Cyprinus carpio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Cyprinus.
1 (bases 1 to 49)
Gracey,A.Y., Frazer,E.J., Li,W., Fang,Y., Taylor,R.R., Rogers,J.,
Brase,A., and Cossins,A.R.
Cloning with cold: An integrative, multiissue analysis of the
transcriptome of a poikilothermic vertebrate
Proc. Natl. Acad. Sci. U.S.A. 101 (48), 16970-16975 (2004)
15550548
On Oct 7, 2003 this sequence version replaced gi:37558440.
CONTACT: Andrew R. Cossins
Laboratory for Environmental Gene Regulation
University of Liverpool
School of Biological Sciences, The Biosciences Building, Crown
Street, Liverpool, United Kingdom, L69 7ZB
Tel: +44(0)151-795-4510
Fax: +44(0)151-795-4431
Email: cossins@lly.ac.uk
Vector has been trimmed from this EST.

JOURNAL
COMMENT

Plate: 34 row: 1 column: 20
Seq primer: Triplex 5' LD (5'-CTCGGAGAGCGCGCATGTGTGGT-3')
High quality sequence stop: 49
POLYA=No.
Location/Qualifiers
1..49
/organism="Cyprinus carpio"
/mol_type="mRNA"
/db_xref="taxon:7962"
/clone="34120"
/sex="Male & female"
/tissue_type="Muscle"
/dev_stage="Adult"
/lab_host="E. coli Electromax DH10B"
/clone_lib="Carp muscle library 1"
/note="Vector: triplex2; Site 1: SfiI GGCCATTACGCC;
Site 2: SfiI GGCGGCTGGCG; Serially subcloned cDNA
library prepared from muscle of warm, cold and hypoxia
challenged animals"

ORIGIN
Query Match 7.5%; Score 18.2; DB 5; Length 49;
Best Local Similarity 74.2%; Pred. No. 2e+06;
Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 32 TGCGTGGAGCTCCACCTCCCGAGCTGCTGC 62
DB 2 TAGCGGGAACCTCAGCTGCACCACTTCTGC 32

RESULT 15
AUI02840/c 50 bp mRNA linear EST 28-JAN-2004
LOCUS AUI02840
DEFINITION AUI02840 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
ACCESSION CAS09777, mRNA sequence.
VERSION AUI02840
KEYWORDS AUI02840.1 GI:13552361
EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isegai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
11375929
CONTACT: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokane-dai, Minatoku, Tokyo 108-8639, Japan
Tel: 81-3-5449-5343
Fax: 81-3-5449-5416
Email: ysuzuki@hgc.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).
Location/Qualifiers
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CAS09777"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN
Query Match 7.5%; Score 18.2; DB 1; Length 50;
Best Local Similarity 66.7%; Pred. No. 2e+06;

Matches 26; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 QY 165 CAGACGACCTGTTAAGCCCAACCGTGTCTGTAGGTTG 203
 Db 41 CAGAGCAGCCTGTGTGCGCTCCGCTCGAAGAGTTTG 3

Search completed: October 1, 2006, 06:42:19
 Job time : 3612.75 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 1, 2006, 00:15:33 ; Search time 324.377 Seconds
(without alignments)
5072.656 Million cell updates/sec

Title: US-10-642-946-6_COPY_3002_3237

Perfect score: 236
Sequence: 1 tgcctggtcctgctggtgcaaaactg 236

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 5218826

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: N_Geneseq_8: *
2: geneseqn1980s: *
3: geneseqn1980s: *
4: geneseqn2001as: *
5: geneseqn2001as: *
6: geneseqn2002as: *
7: geneseqn2002as: *
8: geneseqn2003as: *
9: geneseqn2003as: *
10: geneseqn2003as: *
11: geneseqn2003as: *
12: geneseqn2004as: *
13: geneseqn2004as: *
14: geneseqn2005s: *
15: geneseqn2006s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32.6	13.8	50	13	ADU25047 Retroelem
2	32.6	13.8	50	13	ADU22514 Human tra
3	32	13.6	50	13	ADU25299 Retroelem
4	32	13.6	50	13	ADU22766 Human tra
5	29	12.3	50	13	ADU24578 Retroelem
6	29	12.3	50	13	ADU22045 Human tra
7	22.6	9.6	50	13	ADU25274 Retroelem
8	22.6	9.6	50	13	ADU25263 Retroelem
9	22.6	9.6	50	13	ADU22741 Human tra
10	22.6	9.6	50	13	ADU22730 Human tra
11	22.4	9.3	41	8	AB279597 Quinoprot
12	22	9.3	41	6	AB248086 Human tra
13	22	9.3	41	6	AB248256 Human tra
14	22	9.3	50	13	ADU25276 Retroelem
15	22	9.3	50	13	ADU22743 Human tra
16	21.8	9.2	27	2	AAV33949 Human tra
17	21.8	9.2	50	13	ADU25275 Retroelem
18	21.8	9.2	50	13	ADU22742 Human tra

C 19	21.2	9.0	37	10	ADF41823	Adf41823 Bacillus
C 20	21.2	9.0	49	2	AAV36530	Aav36530 Self-cler
C 21	21.2	9.0	50	13	ADU25169	Adu25169 Retroelem
C 22	21.2	9.0	50	13	ADU22636	Adu22636 Human tra
C 23	21	8.9	31	2	AAV06442	Aav06442 Human tra
C 24	21	8.9	50	14	AEC34323	Aec34323 Human tra
C 25	20.8	8.6	41	6	AB279598	Ab279598 Quinoprot
C 26	20.4	8.6	41	6	ABV76589	Abv76589 Human DNA
C 27	20.2	8.6	50	14	AEE04164	Aee04164 Cinamyl
C 28	20	8.5	33	8	AB279595	Ab279595 Quinoprot
C 29	19.8	8.4	50	4	AAV29722	Aav29722 Human SNP
C 30	19.6	8.3	38	12	ADM68781	Adm68781 Ryanodine
C 31	19.6	8.3	50	6	AB200593	Ab200593 Human leu
C 32	19.4	8.2	45	2	ADH29805	Adh29805 Swinepox
C 33	19.4	8.2	45	2	AAV26212	Aav26212 Swinepox
C 34	19.4	8.2	50	6	AB204255	Ab204255 Human leu
C 35	19.4	8.2	50	6	AB204421	Ab204421 Human leu
C 36	19.2	8.1	41	5	AAH49686	Aah49686 Scathin
C 37	19.2	8.1	50	4	AAI79051	Aai79051 Human sll
C 38	19.2	8.1	50	6	AB201446	Ab201446 Human leu
C 39	19.2	8.1	50	14	AEC04715	Aec04715 Human Dre
C 40	19	8.1	36	2	AAV03157	Aav03157 PCR prime
C 41	19	8.1	42	4	AAH48668	Aah48668 Anti-Crop
C 42	19	8.1	42	5	AAH21345	Aah21345 CSC-F ove
C 43	19	8.1	42	8	AB221455	Ab221455 Chicken i
C 44	19	8.1	43	3	AAC81286	Aac81286 Human/mou
C 45	19	8.1	50	2	AAV79171	Aav79171 Oligonuci

ALIGNMENTS

RESULT 1	ADU25047	standard; DNA; 50 BP.
ID	ADU25047	
AC	ADU25047	
XX		
DT	27-JAN-2005	(first entry)
XX		
DE		Retroelement consensus sequence identifier oligonucleotide #517.
XX		
KW		Expression pattern; transposable element; developmental potential;
KW		stem cell; cellular differentiation induction factor;
KW		methylation pattern; chromatin status pattern; endogenous retrovirus;
KW		ERV; short interspersed nuclear element; SINE;
XX		long interspersed nuclear element; LINE; retroelement; ss.
OS		Synthetic.
XX		
PN	WO2004097005-A2.	
XX		
PD	11-NOV-2004.	
XX		
PF	29-APR-2004; 2004WO-US013667.	
XX		
PR	29-APR-2003; 2003US-0466801P.	
XX		
PA	(UYGE-) UNIV GEORGIA RES FOUND INC.	
XX		
PI	McDonald JF.	
XX		
DR	WPI; 2004-804756/79.	
XX		
PT		Assigning an expression pattern of transposable elements to the level of
PT		developmental potential of a cell comprises determining expression of one
PT		or more families of transposable elements, and assigning the expression
PT		pattern.
XX		
PS		Disclosure; SEQ ID NO 518; 50bp; English.
XX		
CC		The invention relates to a method of assigning an expression pattern of
CC		transposable elements to the level of developmental potential of a cell.

The method comprises determining the expression of one or more families of transposable elements, and assigning the expression pattern obtained to the level of developmental potential of a cell. Also disclosed are a method of determining the developmental potential of a stem cell, a method of identifying a cellular differentiation induction factor, a method of identifying a factor that increases the developmental potential of a cell, a method of assigning a methylation pattern of transposable elements to the level of developmental potential of a cell, and a method of assigning a chromatin status pattern of transposable elements to the level of developmental potential of a cell. In assigning an expression pattern of transposable elements to the level of developmental potential of a cell, the cell is a fully pluripotent stem cell, a pluripotent stem cell, or a differentiated cell. The expression pattern is determined by microarray analysis. One or more of the families of transposable elements are retroelement families, or DNA element families. One or more of the families of retroelements is selected from the group consisting of endogenous retroviruses (ERVs), a family of short interspersed nuclear elements (SINES) and a family of long interspersed nuclear elements (LINEs). The expression of the transposable elements is measured by assaying for the mRNA transcribed from the genes or proteins translated from an mRNA transcribed from the genes. The expression of two or more families of transposable elements is determined and used to form the pattern of expression. The methylation of the transposable element genes is monitored by enzymatic means, microarray analysis, or methylation-specific PCR. The methylation pattern is determined by microarray analysis. The methods of the invention are useful for assigning an expression pattern of transposable elements to the level of developmental potential of a cell. This sequence represents an oligonucleotide identifier of a retroelement consensus sequence.

Query Match	13.8%	Score 32.6	DB 13	Length 50
Best Local Similarity	79.2%	Pred. No. 1.5	10	Indels 0
Matches	38	Mismatches	0	Gaps 0
Oy	61	GTGACTTACCTGAGAGCTGTTGTTTGAAGAGCCTGAGCCCTCTCTC	108	
Db	2	GTGAGTTACAGCGAGACTGTGTTGTTTAAAGAGTNTGGCACTCTCCC	49	

xx	RESULT 2
xx	ADU22514
ID	ADU22514 standard; DNA, 50 BP.
xx	
xx	ADU22514;
AC	
xx	
D7	27-JAN-2005 (first entry)
DE	
xx	Human transposable element representative sequence, SEQ ID 518.
xx	
KW	Human; B6; transposable element; DNA methylation; cancer
KM	LINE; long interspersed nuclear element; SINE;
KV	short interspersed nuclear element; HERV; human endogenous retrovi-
microarray.	
xx	
OS	Homo sapiens.
xx	
PN	WO2004096021-A2.
xx	
PD	11-NOV-2004.
xx	
XX	29-APR-2004; 2004WO-USO13522.
PF	
xx	
PR	29-APR-2003; 2003US-0466798P.
xx	
PA	(UYGE-) UNIV GEORGIA RES FOUND INC.
PI	
xx	Mcdonald JF;
xx	
DR	WPI; 2004-804580/79.
PT	
xx	Determining expression, methylation or chromatin status pattern of

PT families of transposable elements in a sample e.g. for diagnosing cancer.
PT comprises determining the expression, methylation or chromatin status of
PT the elements.

PS Disclosure; SEQ ID NO 518; 68bp; English.

The invention relates to determining expression, methylation or chromatin status pattern of one or more families of transposable elements in a sample comprising determining expression, methylation or chromatin status of one or more families of transposable elements. Also included are a method of assigning an expression pattern of transposable elements to a type of cancerous cell in a sample, a method of diagnosing cancer, a method of determining the effectiveness of an anti-cancer therapeutic in a subject, a method of assigning a methylation pattern of one or more families of transposable elements to a type of cancerous cell in a sample and a method of assigning a chromatin status pattern of transposable elements to a type of cancerous cell in a sample. The method is useful in determining an expression, methylation or chromatin status pattern of one or more families of transposable elements (e.g. LINE, long interspersed nuclear element, SINE, short interspersed nuclear element, or HERV, human endogenous retrovirus) in a sample for diagnosing cancer or determining the effectiveness of an anti-cancer therapeutic. The present sequence is a representative sequence for a human transposable element, used in a microarray to study the expression, methylation or chromatin status pattern of the transposable elements.

Sequence 50 BP; 10 A; 12 C; 12 G; 15 T; 0 U; 1 Other;

Query Match	13.8%	Score 32.6;	DB 13;	Length 50;
Best Local Similarity	79.2%;	Pred. No. 1.5;		
Matches 38; Conservative	0;	Mismatches 10;	Indels 0;	Gaps 0

```
QY      61 GTGAGTTCACGTGAGAGCGCTGGTTGTTGAAGAAGCCGCCCCCCCCTCTC   108
       ||||| | | | | | | | | | | | | | | | | | | | | | |
Db     2 GTTAGTTCACCCGAGATCTGGTGTGTTAAAAAGAGTNTGGCACCTCCCC   49
```

RESULT 3	
ADU25299	
ID	ADU25299 standard; DNA; 50 BP.

```

DT 27-JAN-2005 (first entry)
DE Retroelement consensus sequence identifier oligonucleotide #769.
XX
XX Expression pattern; transposable element; developmental potential;
XX stem cell; cellular differentiation induction factor;
KM methylation pattern; chromatin status pattern; endogenous retrovirus;
KM ERV; short interspersed nuclear element; SINE;
KM long interspersed nuclear element; LINE; retroelement; ss.
XX
OS Synthetic.
XX
XX
XX WO2004097005-A2.
XX
XX 11-NOV-2004.
XX
XX 29-APR-2004; 2004WO-US013667.
XX
XX 29-APR-2003; 2003US-0466801P.
XX
XX
XX (UYGE-) UNIV GEORGIA RES FOUND INC.
XX
XX McDonald JF;
XX
XX
XX WI; 2004-804756/79.
XX
XX
XX
XX
XX Assigning an expression pattern of transposable elements to the level of
XX developmental potential of a cell comprises determining expression of one
XX or more families of transposable elements, and assigning the expression
XX pattern.
PT

```


XX Assigning an expression pattern of transposable elements to the level of
PT developmental potential of a cell comprises determining expression of one
PT or more families of transposable elements, and assigning the expression
PT pattern.

XX Disclosure; SEQ ID NO 48; 50bp; English.

XX The invention relates to a method of assigning an expression pattern of
CC transposable elements to the level of developmental potential of a cell.
CC The method comprises determining the expression of one or more families
CC of transposable elements, and assigning the expression pattern obtained
CC to the level of developmental potential of a cell. Also disclosed are a
CC method of determining the developmental potential of a stem cell, a
CC method of identifying a cellular differentiation induction factor, a
CC method of identifying a factor that increases the developmental potential
CC of a cell, a method of assigning a methylation pattern of transposable
CC elements to the level of developmental potential of a cell, and a method
CC of assigning a chromatin status pattern of transposable elements to the
CC level of developmental potential of a cell. In assigning an expression
CC pattern of transposable elements to the level of developmental potential
CC of a cell, the cell is a fully pluripotent stem cell, a pluripotent stem
CC cell, or a differentiated cell. The expression pattern is determined by
CC microarray analysis. One or more of the families of transposable elements
CC are retroelement families, or DNA element families. One or more of the
CC families of retroelements is selected from the group consisting of
CC endogenous retroviruses (ERVs), a family of short interspersed nuclear
CC elements (SINES) and a family of long interspersed nuclear elements
CC (LINEs). The expression of the transposable elements is measured by
CC assaying for the mRNA transcribed from the genes or proteins translated
CC from an mRNA transcribed from the genes. The expression of two or more
CC families of transposable elements is determined and used to form the
CC pattern of expression. The methylation of the transposable element genes
CC is monitored by enzymatic means, microarray analysis, or methylation-
CC specific PCR. The methylation pattern is determined by microarray
CC analysis. The methods of the invention are useful for assigning an
CC expression pattern of transposable elements to the level of developmental
CC potential of a cell. This sequence represents an oligonucleotide
CC identifier of a retroelement consensus sequence.

XX Sequence 50 BP; 6 A; 11 C; 16 G; 17 T; 0 U; 0 Other;

Query Match 12.3%; Score 29; DB 13; Length 50;
Best Local Similarity 77.8%; Pred. No. 23;
Matches 35; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 37 TTATGCCATCCCTTGTGATGAGTGAGTTCACGTGAGACTGG 81
DB 6 TTGGTGTCTGCTCGATGATGAGTGAGTTCCTCGAGACTCTGG 50

RESULT 6
ADU22045
ID ADU22045 standard; DNA; 50 BP.

AC ADU22045;

XX 27-JAN-2005 (first entry)

XX Human transposable element representative sequence, SEQ ID 48.

XX Human; ss; transposable element; DNA methylation; chromatin; cancer;

XX LINE; long interspersed nuclear element; SINE;

XX short interspersed nuclear element; HERV; human endogenous retrovirus;

XX microarray.

XX Homo sapiens.

XX WO2004096021-A2.

XX 11-NOV-2004.

XX 29-APR-2004; 2004WO-US013522.

XX 29-APR-2003; 2003US-0466798P.

XX (UTGE-) UNIV GEORGIA RES FOUND INC.

XX McDonald JF;

XX WPI, 2004-804580/79.

XX Determining expression, methylation or chromatin status pattern of
PT families of transposable elements in a sample e.g. for diagnosing cancer,
PT comprises determining the expression, methylation or chromatin status of
PT the elements.

XX Disclosure; SEQ ID NO 48; 68bp; English.

XX The invention relates to determining expression, methylation or chromatin
CC status pattern of one or more families of transposable elements in a
CC sample comprises determining expression, methylation or chromatin status
CC of one or more families of transposable elements. Also included are a
CC method of assigning an expression pattern of transposable elements to a
CC type of cancerous cell in a sample, a method of diagnosing cancer, a
CC method of determining the effectiveness of an anti-cancer therapeutic in
CC a subject, a method of assigning a methylation pattern of one or more
CC families of transposable elements to a type of cancerous cell in a sample
CC and a method of assigning a chromatin status pattern of transposable
CC elements to a type of cancerous cell in a sample. The method is useful in
CC determining an expression, methylation or chromatin status pattern of one
CC or more families of transposable elements (e.g. LINE, long interspersed
CC nuclear element, SINE, short interspersed nuclear element, or HERV, human
CC endogenous retrovirus) in a sample for diagnosing cancer or determining
CC the effectiveness of an anti-cancer therapeutic. The present sequence is
CC a representative sequence for a human transposable element, used in a
CC microarray to study the expression, methylation or chromatin status
CC pattern of the transposable elements.

XX Sequence 50 BP; 6 A; 11 C; 16 G; 17 T; 0 U; 0 Other;

Query Match 12.3%; Score 29; DB 13; Length 50;
Best Local Similarity 77.8%; Pred. No. 23;
Matches 35; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 37 TTATGCCATCCCTTGTGATGAGTGAGTTCACGTGAGACTGG 81
DB 6 TTGGTGTCTGCTCGATGATGAGTGAGTTCCTCGAGACTCTGG 50

RESULT 7
ADU25274
ID ADU25274 standard; DNA; 50 BP.

AC ADU25274;

XX 27-JAN-2005 (first entry)

XX Retroelement consensus sequence identifier oligonucleotide #744.

XX Expression pattern; transposable element; developmental potential;

XX stem cell; cellular differentiation induction factor;

XX methylation pattern; chromatin status pattern; endogenous retrovirus;

XX ERV; short interspersed nuclear element; SINE;

XX long interspersed nuclear element; LINE; retroelement; ss.

XX Synthetic.

XX WO2004097005-A2.

XX 11-NOV-2004.

XX 29-APR-2004; 2004WO-US013667.

XX 29-APR-2003; 2003US-0466801P.

PA (UYGE-) UNIV GEORGIA RES FOUND INC.
XX
XX McDonald JF;
XX
XX WPI, 2004-804756/79.
XX
XX Assigning an expression pattern of transposable elements to the level of
PT developmental potential of a cell comprises determining expression of one
PT or more families of transposable elements, and assigning the expression
PT pattern.
XX
XX Disclosure; SEQ ID NO 745; 50bp; English.
XX
XX The invention relates to a method of assigning an expression pattern of
CC transposable elements to the level of developmental potential of a cell.
CC The method comprises determining the expression of one or more families
CC of transposable elements, and assigning the expression pattern obtained
CC to the level of developmental potential of a cell. Also disclosed are a
CC method of determining the developmental potential of a stem cell, a
CC method of identifying a cellular differentiation induction factor, a
CC method of identifying a factor that increases the developmental potential
CC of a cell, a method of assigning a methylation pattern of transposable
CC elements to the level of developmental potential of a cell, and a method
CC of assigning a chromatin status pattern of transposable elements to the
CC level of developmental potential of a cell. In assigning an expression
CC pattern of transposable elements to the level of developmental potential
CC of a cell, the cell is a fully pluripotent stem cell, a pluripotent stem
CC cell, or a differentiated cell. The expression pattern is determined by
CC microarray analysis. One or more of the families of transposable elements
CC are retroelement families, or DNA element families. One or more of the
CC families of retroelements is selected from the group consisting of
CC endogenous retroviruses (ERVs), a family of short interspersed nuclear
CC elements (SINES) and a family of long interspersed nuclear elements
CC (LINES). The expression of the transposable elements is measured by
CC assaying for the mRNA transcribed from the genes or proteins translated
CC from an mRNA transcribed from the genes. The expression of two or more
CC families of transposable elements is determined and used to form the
CC pattern of expression. The methylation of the transposable element genes
CC is monitored by enzymatic means, microarray analysis, or methylation-
CC specific PCR. The methylation pattern is determined by microarray
CC analysis. The methods of the invention are useful for assigning an
CC expression pattern of transposable elements to the level of developmental
CC potential of a cell. This sequence represents an oligonucleotide
CC identifier of a retroelement consensus sequence.
XX
XX Sequence 50 BP; 10 A; 11 C; 12 G; 17 T; 0 U; 0 Other;
SQ
Query Match 9.6%; Score 22.6; DB 13; Length 50;
Best Local Similarity 86.2%; Pred. No. 2.9e+03;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 149 CTTCTCCTTCTGCCATGATTAAAGATTTC 177
DB 22 CTTCCCTTCGCCCATGATTGAAGTTTC 50
RESULT 8
ADU25263
ID ADU25263 standard; DNA; 50 BP.
XX
XX
XX ADU25263;
AC
XX
XX 27-JAN-2005 (first entry)
XX
XX Retroelement consensus sequence identifier oligonucleotide #733.
XX
XX Expression pattern; transposable element; developmental potential;
XX stem cell; cellular differentiation induction factor;
XX methylation pattern; chromatin status pattern; endogenous retroviruses;
XX ERV; short interspersed nuclear element; SINE;
XX long interspersed nuclear element; LINE; retroelement; ss.
XX
XX Synthetic.

XX
XX PN M02004097005-A2.
XX
XX 11-NOV-2004.
XX
XX 29-APR-2004; 2004WO-US013667.
XX
XX 29-APR-2003; 2003US-0466801P.
XX
XX (UYGE-) UNIV GEORGIA RES FOUND INC.
XX
XX McDonald JF;
XX
XX WPI, 2004-804756/79.
XX
XX Assigning an expression pattern of transposable elements to the level of
PT developmental potential of a cell comprises determining expression of one
PT or more families of transposable elements, and assigning the expression
PT pattern.
XX
XX Disclosure; SEQ ID NO 734; 50bp; English.
XX
XX The invention relates to a method of assigning an expression pattern of
CC transposable elements to the level of developmental potential of a cell.
CC The method comprises determining the expression of one or more families
CC of transposable elements, and assigning the expression pattern obtained
CC to the level of developmental potential of a cell. Also disclosed are a
CC method of determining the developmental potential of a stem cell, a
CC method of identifying a cellular differentiation induction factor, a
CC method of identifying a factor that increases the developmental potential
CC of a cell, a method of assigning a methylation pattern of transposable
CC elements to the level of developmental potential of a cell, and a method
CC of assigning a chromatin status pattern of transposable elements to the
CC level of developmental potential of a cell. In assigning an expression
CC pattern of transposable elements to the level of developmental potential
CC of a cell, the cell is a fully pluripotent stem cell, a pluripotent stem
CC cell, or a differentiated cell. The expression pattern is determined by
CC microarray analysis. One or more of the families of transposable elements
CC are retroelement families, or DNA element families. One or more of the
CC families of retroelements is selected from the group consisting of
CC endogenous retroviruses (ERVs), a family of short interspersed nuclear
CC elements (SINES) and a family of long interspersed nuclear elements
CC (LINES). The expression of the transposable elements is measured by
CC assaying for the mRNA transcribed from the genes or proteins translated
CC from an mRNA transcribed from the genes. The expression of two or more
CC families of transposable elements is determined and used to form the
CC pattern of expression. The methylation of the transposable element genes
CC is monitored by enzymatic means, microarray analysis, or methylation-
CC specific PCR. The methylation pattern is determined by microarray
CC analysis. The methods of the invention are useful for assigning an
CC expression pattern of transposable elements to the level of developmental
CC potential of a cell. This sequence represents an oligonucleotide
CC identifier of a retroelement consensus sequence.
XX
XX Sequence 50 BP; 14 A; 13 C; 10 G; 12 T; 0 U; 1 Other;
SQ
Query Match 9.6%; Score 22.6; DB 13; Length 50;
Best Local Similarity 71.8%; Pred. No. 2.9e+03;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
QY 197 AATGCTAACGCCATGCTTTGTTGTCGTGCAAACT 235
DB 1 AGATGCTCGACCAATGCTTTTGTCCAGCCACAGAAAT 39
RESULT 9
ADU22741
ID ADU22741 standard; DNA; 50 BP.
XX
XX ADU22741;
AC
XX
XX 27-JAN-2005 (first entry)
XX
XX

PN CN1380401-A.
XX
PD 20-NOV-2002.
XX
PF 10-APR-2001; 2001CN-00105895.
XX
PR 10-APR-2001; 2001CN-00105895.
XX
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI Mao Y, Xie Y;
XX
PS WPI; 2003-230985/23.
XX
PT A polypeptide-quinoprotein dehydrogenase-12.10 and polynucleotide for
PT coding this polypeptide.
XX
XX Example 7; Page 22 (disclosure); 30pp; Chinese.
XX
XX The present invention discloses a polypeptide for a quinoprotein
CC dehydrogenase 12.10, the polynucleotide for coding the polypeptide, and a
CC method for producing this polypeptide using DNA recombination technology.
CC Also disclosed is a method for curing several diseases, such as malignant
CC tumour, haemopathy, Human Immunodeficiency virus (HIV) infection,
CC immunological disease and various inflammation. The invention also
CC discloses the antagonist for resisting this polypeptide, and its
CC therapeutic action. The current sequence represents a quinoprotein
CC dehydrogenase 12.10 related probe
XX
SQ Sequence 41 BP; 11 A; 7 C; 18 G; 5 T; 0 U; 0 Other;
XX
Query Match 9.5%; Score 22.4; DB 8; Length 41;
Best Local Similarity 81.2%; Pred. No. 3.1e+03;
Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 132 TGAGACACCTGCTCCCTCTCTCTCTGCGCA 163
DB 32 TGCTACACCGGCTTCCCTTGTGCTTGTGCA 1
XX
RESULT 12
AB246086
ID AB246086 standard; DNA; 41 BP.
XX
AC AB246086;
XX
XX 26-JUN-2003 (first entry)
XX
DE Human organic anion transporter OATP2 gene polymorphic site, #2870.
XX
XX Human; drug metabolising enzyme; gene; drug metabolism; chromosome 12;
XX polymorphic site; drug evaluation; drug screening; genotyping;
XX genetic profiling; therapeutic customisation; adverse reaction;
XX clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT replace(21,A)
XX FT /*tag= a
XX FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX
XX WO200252044-A2.
XX
XX 04-JUL-2002.
XX
XX 27-DEC-2001; 2001WO-JP011592.
XX
XX 27-DEC-2000; 2000JP-00399443.
XX
XX 02-MAY-2001; 2001JP-00135256.
XX
XX 27-MAY-2001; 2001JP-00256862.
XX
XX (RIKE) RIKEN KK.

XX
PI Nakamura Y, Sekine A, Iida A, Saito S;
XX
XX WPI; 2002-583571/62.
XX
XX Identifying individuals having a polymorphism, useful for determining the
PT effectiveness or side effect of a drug or treatment protocol, comprises
PT detecting at least one polymorphism in the drug metabolizing enzyme
PT nucleic acid.
XX
XX Claim 23; Page 112; 2785pp; English.
XX
XX Sequences AB243217-AB250887 represent polymorphic sites within genes
CC encoding enzymes associated with drug metabolism. The invention relates
CC to methods and compositions for identifying individuals who have at least
CC one polymorphism in such drug metabolising enzyme-encoding genes. The
CC polymorphisms may be identified in a nucleic acid sample using probes or
CC primers specific for a sequence selected from AB243217-AB250887 using a
CC variety of detection assays, including hybridisation assays, nucleic acid
CC arrays and PCR-based methods. The invention also encompasses methods of
CC evaluating and screening drugs using genetic polymorphism data. Genetic
CC polymorphisms (SNPs), may be used in studying the relationship between
CC DNA sequence variations and human diseases, conditions, and responses to
CC drugs. SNPs are also useful as polymorphism markers for discovering genes
CC that cause or exacerbate certain diseases. SNPs are particularly useful
CC in the above respects as they are stable in populations, occur
CC frequently, and have lower mutation rates than other genome variations
CC such as repeating sequences. The detection and analysis of polymorphisms
CC in genes encoding drug metabolising enzymes allows the customisation of
CC drug therapies based upon the genetic profile of individual patients.
CC This would not only take the guesswork out of selecting the drug with the
CC greatest therapeutic effect for a particular patient, but would also
CC reduce the likelihood of adverse reactions, thereby increasing safety.
CC Methods of the invention are also useful in the drug discovery and
CC approval processes. For example, individuals could be selected for
CC clinical trials only if their genetic profiles indicate that they are
CC capable of responding to a particular drug or drug class, and previously
CC failed drug candidates could be revived if they were matched with more
CC appropriate patient populations. The methods, data and compositions of
CC the invention may therefore lead to an increase in the range of
CC possible drug targets and decreases in the number of adverse drug
CC reactions, failed drug trials, the time taken for a drug to be approved,
CC the length of time patients are on medication and the number of different
CC medications a patient needs to take before finding an effective therapy
XX
SQ Sequence 41 BP; 4 A; 16 C; 7 G; 14 T; 0 U; 0 Other;
XX
Query Match 9.3%; Score 22; DB 6; Length 41;
Best Local Similarity 73.7%; Pred. No. 4.3e+03;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 141 TGCTCCCTCTCTGTCATGATGATTTAGATTC 178
DB 2 TGCTCTTCTTATCTTCGCGCATGATGTGAGGCC 39
XX
RESULT 13
AB248256
ID AB248256 standard; DNA; 41 BP.
XX
AC AB248256;
XX
XX 26-JUN-2003 (first entry)
XX
DE Human organic anion transporter OATP2 gene polymorphic site, #5039.
XX
XX Human; drug metabolising enzyme; gene; drug metabolism; chromosome 12;
XX polymorphic site; drug evaluation; drug screening; genotyping;
XX genetic profiling; therapeutic customisation; adverse reaction;
XX clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
XX
OS Homo sapiens.

XX Key Location/Qualifiers
FH replacement(21,A)
FT /tag= a
FT /standard_name= "Single nucleotide polymorphism (SNP)"
XX
XX WO200252044-A2.
XX
XX 04-JUL-2002.
XX
XX 27-DEC-2001; 2001WO-JP011592.
XX
XX 27-DEC-2000; 2000JP-00399443.
XX 02-MAY-2001; 2001JP-00135256.
XX 27-AUG-2001; 2001JP-00256862.
XX
XX (RIKE) RIKEN KK.
XX
XX Nakamura Y, Sekine A, Iida A, Saito S;
XX
XX WPI; 2002-563571/62.
XX
XX Identifying individuals having a polymorphism, useful for determining the
XX effectiveness or side effect of a drug or treatment protocol, comprises
XX detecting at least one polymorphism in the drug metabolizing enzyme
XX nucleic acid.
XX
XX Claim 23; Page 161; 2785pp; English.
XX
XX Sequences AB243217-AB250887 represent polymorphic sites within genes
XX encoding enzymes associated with drug metabolism. The invention relates
XX to methods and compositions for identifying individuals who have at least
XX one polymorphism in such drug metabolizing enzyme-encoding genes. The
XX polymorphisms may be identified in a nucleic acid sample using probes or
XX primers specific for a sequence selected from AB243217-AB250887 using a
XX variety of detection assays, including hybridisation assays, nucleic acid
XX arrays and PCR-based methods. The invention also encompasses methods of
XX evaluating and screening drugs using genetic polymorphism data. Genetic
XX polymorphism data, particularly that relating to single nucleotide
XX polymorphisms (SNPs), may be used in studying the relationship between
XX DNA sequence variations and human diseases, conditions, and responses to
XX drugs. SNPs are also useful as polymorphism markers for discovering genes
XX that cause or exacerbate certain diseases. SNPs are particularly useful
XX in the above respects as they are stable in populations, occur
XX frequently, and have lower mutation rates than other genome variations
XX such as repeating sequences. The detection and analysis of polymorphisms
XX in genes encoding drug metabolizing enzymes allows the customisation of
XX drug therapies based upon the genetic profile of individual patients.
XX This would not only take the guesswork out of selecting the drug with the
XX greatest therapeutic effect for a particular patient, but would also
XX reduce the likelihood of adverse reactions, thereby increasing safety.
XX Methods of the invention are also useful in the drug discovery and
XX approval processes. For example, individuals could be selected for
XX clinical trials only if their genetic profiles indicate that they are
XX capable of responding to a particular drug or drug class, and previously
XX failed drug candidates could be revived if they were matched with more
XX appropriate patient populations. The methods, data and compositions of
XX the invention may therefore lead to an increase in the range of
XX possible drug targets and decreases in the number of adverse drug
XX reactions, failed drug trials, the time taken for a drug to be approved,
XX the length of time patients are on medication and the number of different
XX medications a patient needs to take before finding an effective therapy
XX
XX Sequence 41 BP; 4 A; 16 C; 7 G; 14 T; 0 U; 0 Other;
SQ
Query Match 9.3%; Score 22; DB 6; Length 41;
Best Local Similarity 73.7%; Pred. No. 4.3e+03;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 141 TGTCTCCCTTCTCTGCGCCATGATTTTAAATTC 178
DB 2 TGTCTTCTCTCATCTTCCGCGCATGATGTGAGCCCC 39

RESULT 14
ADU25276
ID ADU25276 standard; DNA; 50 BP.
XX
XX ADU25276;
XX
XX 27-JAN-2005 (first entry)
XX
XX Retroelement consensus sequence identifier oligonucleotide #746.
XX
XX Expression pattern; transposable element; developmental potential;
XX stem cell; cellular differentiation induction factor;
XX methylation pattern; chromatin status pattern; endogenous retrovirus;
XX ERV; short interspersed nuclear element; SINE;
XX long interspersed nuclear element; LINE; retroelement; SE.
XX
XX Synthetic.
XX
XX WO2004097005-A2.
XX
XX 11-NOV-2004.
XX
XX 29-APR-2004; 2004WO-US013667.
XX
XX 29-APR-2003; 2003US-0466801P.
XX
XX (UYGE-) UNIV GEORGIA RES FOUND INC.
XX
XX McDonald JF;
XX
XX WPI; 2004-804756/79.
XX
XX Assigning an expression pattern of transposable elements to the level of
XX developmental potential of a cell comprises determining expression of one
XX or more families of transposable elements, and assigning the expression
XX pattern.
XX
XX Disclosure; SEQ ID NO 747; 50pp; English.
XX
XX The invention relates to a method of assigning an expression pattern of
XX transposable elements to the level of developmental potential of a cell.
XX The method comprises determining the expression of one or more families
XX of transposable elements, and assigning the expression pattern obtained
XX to the level of developmental potential of a cell. Also disclosed are a
XX method of determining the developmental potential of a stem cell, a
XX method of identifying a cellular differentiation induction factor, a
XX method of identifying a factor that increases the developmental potential
XX of a cell, a method of assigning a methylation pattern of transposable
XX elements to the level of developmental potential of a cell, and a method
XX of assigning a chromatin status pattern of transposable elements to the
XX level of developmental potential of a cell. In assigning an expression
XX pattern of transposable elements to the level of developmental potential
XX of a cell, the cell is a fully pluripotent stem cell, a pluripotent stem
XX cell, or a differentiated cell. The expression pattern is determined by
XX microarray analysis. One or more of the families of transposable elements
XX are retroelement families, or DNA element families. One or more of the
XX families of retroelements is selected from the group consisting of
XX endogenous retroviruses (ERVs), a family of short interspersed nuclear
XX elements (SINES) and a family of long interspersed nuclear elements
XX (LINEs). The expression of the transposable elements is measured by
XX assaying for the mRNA transcribed from the genes or proteins translated
XX from an mRNA transcribed from the genes. The expression of two or more
XX families of transposable elements is determined and used to form the
XX pattern of expression. The methylation of the transposable element genes
XX is monitored by enzymatic means, microarray analysis, or methylation-
XX specific PCR. The methylation pattern is determined by microarray
XX analysis. The method of the invention are useful for assigning an
XX expression pattern of transposable elements to the level of developmental
XX potential of a cell. This sequence represents an oligonucleotide
XX identifier of a retroelement consensus sequence.
SQ
Sequence 50 BP; 13 A; 15 C; 9 G; 13 T; 0 U; 0 Other;

Query Match 9.3%; Score 22; DB 13; Length 50;
Best Local Similarity 83.3%; Pred. No. 4.6e+03;
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 207 GCCATGCTTCTTGTCTGTCTGCAAACTG 236
Db 1 GCCATGCTTCTTGTCTGTCTGCAAACTG 30

Qy 207 GCCATGCTTCTTGTCTGTCTGCAAACTG 236
Db 1 GCCATGCTTCTTGTCTGTCTGCAAACTG 30
Search completed: October 1, 2006, 00:26:41
Job time : 325.377 secs

RESULT 15
ID ADU22743 standard; DNA: 50 BP.
XX
AC ADU22743;
XX
DT 27-JAN-2005 (first entry)
XX
DE Human transposable element representative sequence, SEQ ID 747.
XX
KM Human; ss; transposable element; DNA methylation; chromatin; cancer;
KM LINE; long interspersed nuclear element; SINE;
KM short interspersed nuclear element; HERV; human endogenous retrovirus;
XX microarray.
XX
OS Homo sapiens.
XX
PN WO2004096021-A2.
XX
PD 11-NOV-2004.
XX
PF 29-APR-2004; 2004MO-US013522.
XX
PR 29-APR-2003; 2003US-0466798P.
XX
PA (UYGE-) UNIV GEORGIA RES FOUND INC.
XX
PI McDonald JF;
XX
DR WPI; 2004-804580/79.
XX
PT Determining expression, methylation or chromatin status pattern of
PT families of transposable elements in a sample e.g. for diagnosing cancer.
PT comprises determining the expression, methylation or chromatin status of
PT the elements.
XX
PS Disclosure; SEQ ID NO 747; 68bp; English.
XX
CC The invention relates to determining expression, methylation or chromatin
CC status pattern of one or more families of transposable elements in a
CC sample comprises determining expression, methylation or chromatin status
CC of one or more families of transposable elements. Also included are a
CC method of assigning an expression pattern of transposable elements to a
CC type of cancerous cell in a sample, a method of diagnosing cancer, a
CC method of determining the effectiveness of an anti-cancer therapeutic in
CC a subject, a method of assigning a methylation pattern of one or more
CC families of transposable elements to a type of cancerous cell in a sample
CC and a method of assigning a chromatin status pattern of transposable
CC elements to a type of cancerous cell in a sample. The method is useful in
CC determining an expression, methylation or chromatin status pattern of one
CC or more families of transposable elements (e.g. LINE, long interspersed
CC nuclear element, SINE, short interspersed nuclear element, or HERV, human
CC endogenous retrovirus) in a sample for diagnosing cancer or determining
CC the effectiveness of an anti-cancer therapeutic. The present sequence is
CC a representative sequence for a human transposable element, used in a
CC microarray to study the expression, methylation or chromatin status
CC pattern of the transposable elements.
XX
SQ Sequence 50 BP; 13 A; 15 C; 9 G; 13 T; 0 U; 0 Other;

Query Match 9.3%; Score 22; DB 13; Length 50;
Best Local Similarity 83.3%; Pred. No. 4.6e+03;
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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```
/ CURRENT FILING DATE: 2005-07-05
/ PRIOR APPLICATION NUMBER: US 60/585,352
/ PRIOR FILING DATE: 2004-07-02
/ NUMBER OF SEQ ID NOS: 116251
/ SOFTWARE: Patent version 3.2
/ SEQ ID NO 68606
/ LENGTH: 50
/ TYPE: DNA
/ ORGANISM: homo sapien
US-11-175-859-68606
```

```
Query Match 11.4%; Score 26.8; DB 16; Length 50;
Best Local Similarity 77.5%; Pred. No. 73;
Matches 31; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
```

```
Qy 14 GGGGCGATCCCTCATGATGATTAGTGCATCCCTTG 53
Db 11 GAGGCTGCTCTTGATGATGATTAGAGCCATCCCTCG 50
```

RESULT 3

```
US-11-175-859-51557/c
/ Sequence 51557, Application US/11175859
/ Publication No. US20060024715A1
/ GENERAL INFORMATION:
/ APPLICANT: Affymetrix, Inc.
/ APPLICANT: Liu, Guoying et al.
/ TITLE OF INVENTION: Method of Analysis of Human Polymorphism
/ FILE REFERENCE: 3690.1
/ CURRENT APPLICATION NUMBER: US/11/175, 859
/ CURRENT FILING DATE: 2005-07-05
/ PRIOR APPLICATION NUMBER: US 60/585,352
/ PRIOR FILING DATE: 2004-07-02
/ NUMBER OF SEQ ID NOS: 116251
/ SOFTWARE: Patent version 3.2
/ SEQ ID NO 51557
/ LENGTH: 50
/ TYPE: DNA
/ ORGANISM: homo sapien
US-11-175-859-51557
```

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Query Match 10.8%; Score 25.4; DB 16; Length 50;
Best Local Similarity 71.1%; Pred. No. 2.3e+02;
Matches 32; Conservative 1; Mismatches 12; Indels 0; Gaps 0;
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Qy 136 ACACCTGCTCCCTCTCTCCATGATTTTATGATTCAG 180
Db 45 ACACCCACTGCTACTGCTCTACTACCATTTGATTCAG 1
```

RESULT 4

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US-10-891-260-437
/ Sequence 437, Application US/10891260
/ Publication No. US2005022724A1
/ GENERAL INFORMATION:
/ APPLICANT: Affymetrix, Inc.
/ APPLICANT: Matsuzaki, Hajime
/ APPLICANT: Mei, Rui
/ TITLE OF INVENTION: Methods of Analysis of Human Polymorphisms
/ FILE REFERENCE: 3522.3
/ CURRENT APPLICATION NUMBER: US/10/891,260
/ CURRENT FILING DATE: 2004-07-13
/ PRIOR APPLICATION NUMBER: 10/681,773
/ PRIOR FILING DATE: 2003-10-07
/ NUMBER OF SEQ ID NOS: 10244
/ SOFTWARE: Patent version 3.2
/ SEQ ID NO 437
/ LENGTH: 33
/ TYPE: DNA
/ ORGANISM: homo sapien
US-10-891-260-437
```

```
Query Match 9.8%; Score 23.2; DB 10; Length 33;
```

```
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 25; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy 14 GGGGCGATCCCTCATGATGATTAGTGC 43
Db 1 GGGGCGATCCCTCATGATGATTAGTGC 30
```

RESULT 5

```
US-10-891-260-1034/c
/ Sequence 1034, Application US/10891260
/ Publication No. US2005022724A1
/ GENERAL INFORMATION:
/ APPLICANT: Affymetrix, Inc.
/ APPLICANT: Matsuzaki, Hajime
/ APPLICANT: Mei, Rui
/ TITLE OF INVENTION: Methods of Analysis of Human Polymorphisms
/ FILE REFERENCE: 3522.3
/ CURRENT APPLICATION NUMBER: US/10/891,260
/ CURRENT FILING DATE: 2004-07-13
/ PRIOR APPLICATION NUMBER: 10/681,773
/ PRIOR FILING DATE: 2003-10-07
/ NUMBER OF SEQ ID NOS: 10244
/ SOFTWARE: Patent version 3.2
/ SEQ ID NO 1034
/ LENGTH: 33
/ TYPE: DNA
/ ORGANISM: homo sapien
US-10-891-260-1034
```

```
Query Match 9.6%; Score 22.6; DB 10; Length 33;
Best Local Similarity 80.6%; Pred. No. 1.9e+03;
Matches 25; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
```

```
Qy 70 CCGAGAGCTGCTGTTTGAAGAAGCTGCG 100
Db 32 CATGAGACTGATGTTGTAAGAGCTGCG 2
```

RESULT 6

```
US-11-175-859-57653/c
/ Sequence 57653, Application US/11175859
/ Publication No. US20060024715A1
/ GENERAL INFORMATION:
/ APPLICANT: Affymetrix, Inc.
/ APPLICANT: Liu, Guoying et al.
/ TITLE OF INVENTION: Method of Analysis of Human Polymorphism
/ FILE REFERENCE: 3690.1
/ CURRENT APPLICATION NUMBER: US/11/175, 859
/ CURRENT FILING DATE: 2005-07-05
/ PRIOR APPLICATION NUMBER: US 60/585,352
/ PRIOR FILING DATE: 2004-07-02
/ NUMBER OF SEQ ID NOS: 116251
/ SOFTWARE: Patent version 3.2
/ SEQ ID NO 57653
/ LENGTH: 50
/ TYPE: DNA
/ ORGANISM: homo sapien
US-11-175-859-57653
```

```
Query Match 9.5%; Score 22.4; DB 16; Length 50;
Best Local Similarity 72.5%; Pred. No. 2.6e+03;
Matches 29; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
```

```
Qy 105 TCTCATTTCTCTGCTCCCACTCTTGATGAGACACTGCT 144
Db 48 TCTCTCATTTCTGTTCCAAATTCATACATGACACAGCTCT 9
```

RESULT 7

```
US-10-310-914A-1140145/c
/ Sequence 1140145, Application US/10310914A
/ Publication No. US20060003322A1
```

GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CFUS01
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1140145
LENGTH: 28
TYPE: RNA
ORGANISM: Human
US-10-310-914A-1140145

Query Match 9.4%; Score 22.2; DB 11; Length 28;
Best Local Similarity 88.9%; Pred. No. 2.5e+03;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 13 GGGGCGAGATCCCTCATGATGTTTA 39
DB 27 GAGGCGAGATCCCTTATGATGTTCA 1

RESULT 8
US-11-175-859-55008/c
Sequence 55008, Application US/11175859
Publication No. US20060024715A1
GENERAL INFORMATION:
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Method of Analysis of Human Polymorphism
FILE REFERENCE: 3690.1
CURRENT APPLICATION NUMBER: US/11/175,859
CURRENT FILING DATE: 2005-07-05
PRIOR APPLICATION NUMBER: US 60/585,352
PRIOR FILING DATE: 2004-07-02
NUMBER OF SEQ ID NOS: 116251
SOFTWARE: PatentIn version 3.2
SEQ ID NO 55008
LENGTH: 50
TYPE: DNA
ORGANISM: homo sapien
US-11-175-859-55008

Query Match 9.4%; Score 22.2; DB 16; Length 50;
Best Local Similarity 66.7%; Pred. No. 3.1e+03;
Matches 30; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

OY 1 TGTCTGGTCAATGGGCGAGATCCCTCATGATGTTTAAAGTCCCA 45
DB 50 TGTCTGGTCAATGAGAAATTCACACSTCATGATGATTAATGATGCA 6

RESULT 9
US-11-060-756-81484/c
Sequence 81484, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 81484
LENGTH: 25
TYPE: DNA
ORGANISM: probe

US-11-060-756-81484

Query Match 9.2%; Score 21.8; DB 13; Length 25;
Best Local Similarity 92.0%; Pred. No. 3.2e+03;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 149 CTTCTCCTTCGCGATGATTTTAAG 173
DB 25 CTTACCTTCGCGATGATTTTAAG 1

RESULT 10
US-11-060-756-81500/c
Sequence 81500, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 81500
LENGTH: 25
TYPE: DNA
ORGANISM: probe
US-11-060-756-81500

Query Match 9.2%; Score 21.8; DB 13; Length 25;
Best Local Similarity 92.0%; Pred. No. 3.2e+03;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 148 CTTCTCCTTCGCGATGATTTTAAG 172
DB 25 CTTACCTTCGCGATGATTTTAAG 1

RESULT 11
US-11-060-756-81511/c
Sequence 81511, Application US/11060756
Publication No. US20050221354A1
GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 81511
LENGTH: 25
TYPE: DNA
ORGANISM: probe
US-11-060-756-81511

Query Match 9.2%; Score 21.8; DB 13; Length 25;
Best Local Similarity 92.0%; Pred. No. 3.2e+03;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 154 CTTCTCCTTCGCGATGATTTTAAGTTC 178
DB 25 CTTCTCCTTCGCGATGATTTTAAGTTC 1

RESULT 12
US-11-175-859-75179
Sequence 75179, Application US/11175859
Publication No. US20060024715A1


```
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 75179
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-175-859-75179

Query Match
Best Local Similarity 9.2%; Score 21.6; DB 16; Length 50;
Best Local Similarity 74.3%; Pred. No. 4.3e+03;
Matches 26; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Cy 103 CCTCTCATTTCTCCGCTCCCACTTTGACAGAGC 137
Db 10 CCTCTCATTTCTCCGCTCCCACTTTGACAGAGC 44

RESULT 13
US-10-035-833A-2870
; Sequence 2870, Application US/10035833A
; Publication No. US20040072156A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yuho
; APPLICANT: Sekine, Akihito
; APPLICANT: Iida, Aritoshi
; APPLICANT: Saito, Osamu
; TITLE OF INVENTION: Detection of Genetic Polymorphisms
; FILE REFERENCE: FORS-06904
; CURRENT APPLICATION NUMBER: US/10/035,833A
; CURRENT FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 7669
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2870
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-035-833A-2870

Query Match
Best Local Similarity 9.2%; Score 21.6; DB 8; Length 41;
Best Local Similarity 71.1%; Pred. No. 4.7e+03;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Cy 141 TGCCTCCCTTCCTTCGCGATGATTTAAGATTCC 178
Db 2 TGCCTTCCTTCATCTTCRCATGATTTGAGGCCCC 39

RESULT 14
US-10-035-833A-5039
; Sequence 5039, Application US/10035833A
; Publication No. US20040072156A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yuho
; APPLICANT: Sekine, Akihito
; APPLICANT: Iida, Aritoshi
; APPLICANT: Saito, Osamu
; TITLE OF INVENTION: Detection of Genetic Polymorphisms
; FILE REFERENCE: FORS-06904
; CURRENT APPLICATION NUMBER: US/10/035,833A
; CURRENT FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 7669
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5039
; LENGTH: 41
```

```
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-035-833A-5039

Query Match
Best Local Similarity 9.2%; Score 21.6; DB 8; Length 41;
Best Local Similarity 71.1%; Pred. No. 4.7e+03;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Cy 141 TGCCTCCCTTCCTTCGCGATGATTTAAGATTCC 178
Db 2 TGCCTTCCTTCATCTTCRCATGATTTGAGGCCCC 39

RESULT 15
US-10-310-914A-1072814/C
; Sequence 1072814, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kivuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 138402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1072814
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1072814

Query Match
Best Local Similarity 9.1%; Score 21.4; DB 11; Length 23;
Best Local Similarity 95.7%; Pred. No. 4.3e+03;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 44 CATCCCTTGTGATGAGTAGT 66
Db 23 CATCTCTTGATGATGAGT 1
```

Search completed: October 1, 2006, 01:09:51
Job time : 773.184 secs


```
; TITLE OF INVENTION: as Molecular Markers of the Developmental Potential of Stem
; TITLE OF INVENTION: Cells
; FILE REFERENCE: 21099.0077P1
; CURRENT APPLICATION NUMBER: US/10/554,759
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,801
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 518
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
; NAME/KEY: mlec_feature
; LOCATION: 37
; OTHER INFORMATION: n=G, A, T, or C
US-10-554-759-518
```

```
Query Match 13.8%; Score 32.6; DB 6; Length 50;
Best Local Similarity 79.2%; Pred. No. 0.27;
Matches 38; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
```

```
OY 61 GTGAGTTCAGCGAGAGCGTGTGTTGAAGAGCCGCGCCCTCTC 108
DB 2 GTTAGTTCAGCGAGATCTGCTGTTAAAGAGTTGGACCTCCCC 49
```

```
RESULT 3
US-10-554-711-770
; Sequence 770, Application US/10554711
; Publication No. US20060115806A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: as Molecular Markers of Cancer
; FILE REFERENCE: 21099.0075P1
; CURRENT APPLICATION NUMBER: US/10/554,711
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,798
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 778
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 770
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
US-10-554-711-770
```

```
Query Match 13.6%; Score 32; DB 6; Length 50;
Best Local Similarity 79.2%; Pred. No. 0.43;
Matches 38; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
```

```
OY 139 CTTGCTCCCCCTTCTCTTCCATGATTTTAAGATTCAGGACTT 186
DB 3 CTTGCTCCCCCTTCTCTTCCATGATTTTAAGATTCAGGACTT 50
```

```
RESULT 4
US-10-554-759-770
; Sequence 770, Application US/10554759
; Publication No. US20060177825A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
```

```
; TITLE OF INVENTION: as Molecular Markers of the Developmental Potential of Stem
; TITLE OF INVENTION: Cells
; FILE REFERENCE: 21099.0077P1
; CURRENT APPLICATION NUMBER: US/10/554,759
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,801
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 770
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
US-10-554-759-770
```

```
Query Match 13.6%; Score 32; DB 6; Length 50;
Best Local Similarity 79.2%; Pred. No. 0.43;
Matches 38; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
```

```
OY 139 CTTGCTCCCCCTTCTCTTCCATGATTTTAAGATTCAGGACTT 186
DB 3 CTTGCTCCCCCTTCTCTTCCATGATTTTAAGATTCAGGACTT 50
```

```
RESULT 5
US-10-554-711-48
; Sequence 48, Application US/10554711
; Publication No. US20060115806A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: as Molecular Markers of Cancer
; FILE REFERENCE: 21099.0075P1
; CURRENT APPLICATION NUMBER: US/10/554,711
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,798
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 778
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
US-10-554-711-48
```

```
Query Match 12.3%; Score 29; DB 6; Length 50;
Best Local Similarity 77.8%; Pred. No. 4.4;
Matches 35; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
```

```
OY 37 TTATGCGCATCCCTTGTGATGATGATGATTCAGGAGCTGG 81
DB 6 TTGATGCTGCTCTGATGATGATGATGATTCGATGAGTCTGG 50
```

```
RESULT 6
US-10-554-759-48
; Sequence 48, Application US/10554759
; Publication No. US20060177825A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: as Molecular Markers of the Developmental Potential of Stem
; FILE REFERENCE: 21099.0077P1
; CURRENT APPLICATION NUMBER: US/10/554,759
```

```
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,801
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
US-10-554-759-48
```

```
Query Match          12.3%; Score 29; DB 6; Length 50;
Best Local Similarity 77.8%; Pred. No. 4.4;
Matches 35; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
```

```
Qy      37  TTAGTCCATCCCTTGATGAGTGCAGTTCAGCTGAGACTGG 81
Db      6  TTGATCTCTCTCTCTGATAGTACTGAGTCTCTCTGAGATCTGG 50
```

```
RESULT 7
US-10-554-711-734
; Sequence 734, Application US/10554711
; Publication No. US20060115806A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: as Molecular Markers of Cancer
; FILE REFERENCE: 21099.0075P1
; CURRENT APPLICATION NUMBER: US/10/554,711
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,798
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 778
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 734
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
US-10-554-711-734
```

```
Query Match          9.6%; Score 22.6; DB 6; Length 50;
Best Local Similarity 71.8%; Pred. No. 6.2e+02;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
```

```
Qy      197  AATGCTAACGCCCATGCTTCTGTCTGTCGCAAACT 235
Db      1  AGATGCTGCGACCATGCTTTTGTGCGACGCGAGAAAT 39
```

```
RESULT 8
US-10-554-711-745
; Sequence 745, Application US/10554711
; Publication No. US20060115806A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: as Molecular Markers of Cancer
; FILE REFERENCE: 21099.0075P1
; CURRENT APPLICATION NUMBER: US/10/554,711
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: 60/466,798
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 778
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 745
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
US-10-554-711-745
```

```
Query Match          9.6%; Score 22.6; DB 6; Length 50;
Best Local Similarity 86.2%; Pred. No. 6.2e+02;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      149  CTCTCCTTCGCGCATGATTTTAAGATTC 177
Db      22  CTTCCTTCGCGCATGATTTTAAGATTC 50
```

```
RESULT 9
US-10-554-759-734
; Sequence 734, Application US/10554759
; Publication No. US20060177825A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: as Molecular Markers of the Developmental Potential of Stem
; TITLE OF INVENTION: Cells
; FILE REFERENCE: 21099.0077P1
; CURRENT APPLICATION NUMBER: US/10/554,759
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,801
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 734
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
US-10-554-759-734
```

```
Query Match          9.6%; Score 22.6; DB 6; Length 50;
Best Local Similarity 71.8%; Pred. No. 6.2e+02;
Matches 28; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
```

```
Qy      197  AATGCTAACGCCCATGCTTCTGTCTGTCGCAAACT 235
Db      1  AGATGCTGCGACCATGCTTTTGTGCGACGCGAGAAAT 39
```

```
RESULT 10
US-10-554-759-745
; Sequence 745, Application US/10554759
; Publication No. US20060177825A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: as Molecular Markers of the Developmental Potential of Stem
; FILE REFERENCE: 21099.0077P1
; CURRENT APPLICATION NUMBER: US/10/554,759
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,801
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 745
; LENGTH: 50
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
US-10-554-759-745
```

```
Query Match          9.6%; Score 22.6; DB 6; Length 50;
Best Local Similarity 86.2%; Pred. No. 6.2e+02;
Matches 25; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      149 CTTCTCTCTGCGCATGATTTTAAGATTC 177
Db      22 CTTCCCTTCGCGCATGATTTGAATTTC 50
```

```
RESULT 11
US-10-554-711-747
; Sequence 747, Application US/10554711
; Publication No. US20060115806A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: as Molecular Markers of Cancer
; FILE REFERENCE: 21099.0075P1
; CURRENT APPLICATION NUMBER: US/10/554,711
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,798
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 778
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 747
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
US-10-554-711-747
```

```
Query Match          9.3%; Score 22; DB 6; Length 50;
Best Local Similarity 83.3%; Pred. No. 9.9e+02;
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
Qy      207 GCCATGCTTCTGTGTCGCAAACTG 236
Db      1 GCCATGCTTCTGTACAGCTGCAGAACCG 30
```

```
RESULT 12
US-10-554-759-747
; Sequence 747, Application US/10554759
; Publication No. US20060177825A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: as Molecular Markers of the Developmental Potential of Stem
; TITLE OF INVENTION: Cells
; FILE REFERENCE: 21099.0077P1
; CURRENT APPLICATION NUMBER: US/10/554,759
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,801
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 747
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
```

```
US-10-554-759-747
```

```
Query Match          9.3%; Score 22; DB 6; Length 50;
Best Local Similarity 83.3%; Pred. No. 9.9e+02;
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
Qy      207 GCCATGCTTCTGTGTCGCAAACTG 236
Db      1 GCCATGCTTCTGTACAGCTGCAGAACCG 30
```

```
RESULT 13
US-10-554-711-746
; Sequence 746, Application US/10554711
; Publication No. US20060115806A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: as Molecular Markers of Cancer
; FILE REFERENCE: 21099.0075P1
; CURRENT APPLICATION NUMBER: US/10/554,711
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,798
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 778
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 746
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
; NAME/KEY: misc_feature
; LOCATION: 8
; OTHER INFORMATION: n=G, A, T, or C
US-10-554-711-746
```

```
Query Match          9.2%; Score 21.8; DB 6; Length 50;
Best Local Similarity 76.5%; Pred. No. 1.2e+03;
Matches 26; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

```
Qy      163 ATGATTTAAGATTCAGAGCACTTCACAGAAGC 196
Db      1 ATGATTTAAGATTCCTGAGGCTCTCACAGAACG 34
```

```
RESULT 14
US-10-554-759-746
; Sequence 746, Application US/10554759
; Publication No. US20060177825A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: as Molecular Markers of the Developmental Potential of Stem
; TITLE OF INVENTION: Cells
; FILE REFERENCE: 21099.0077P1
; CURRENT APPLICATION NUMBER: US/10/554,759
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,801
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 746
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
```

FEATURE:
NAME/KEY: misc_feature
LOCATION: 8
OTHER INFORMATION: n-G, A, T, or C
US-10-554-759-746

Query Match 9.2%; Score 21.8; DB 6; Length 50;
Best Local Similarity 76.5%; Pred. No. 1.2e+03;
Matches 26; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 163 ATGATTTAAGATTCAGGAGCTTCACAGAAGC 196
|||||
Db 1 ATGATGNAAGCTTCCTGAGGCTTCACCAAGC 34

RESULT 15
US-10-554-711-640
Sequence 640; Application US/10554711
Publication No. US20060115806A1
GENERAL INFORMATION:
APPLICANT: University of Georgia Research Foundation
APPLICANT: McDonald, John F.
TITLE OF INVENTION: Global Analysis of Transposable Elements
FILE REFERENCE: 21099.0075P1
CURRENT APPLICATION NUMBER: US/10/554,711
PRIOR FILING DATE: 2005-10-28
PRIOR APPLICATION NUMBER: 60/466,798
NUMBER OF SEQ ID NOS: 778
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 640
LENGTH: 50
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:/note =
OTHER INFORMATION: Synthetic Construct
US-10-554-711-640

Query Match 9.0%; Score 21.2; DB 6; Length 50;
Best Local Similarity 76.5%; Pred. No. 1.8e+03;
Matches 26; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 163 ATGATTTAAGATTCAGGAGCTTCACAGAAGC 196
|||||
Db 1 ATGATGTAAGTTCTGAGGCTTCACCAAGC 34

Search completed: October 1, 2006, 01:14:07
Job time : 123.925 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 1, 2006, 00:29:43 / Search time 3520.25 Seconds
(without alignments)
3748.870 Million cell updates/sec

Title: US-10-642-946-6_COPY_3002_3237

Perfect score: 236
Sequence: 1 tgcctcggcgacatgagggggcag.....tgcctcgcctgcaaacg 236

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 2795965780 residues

Total number of hits satisfying chosen parameters: 194034

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_hic:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_gsa1:*
12: gb_gsa2:*
13: gb_gsa3:*
14: gb_gsa4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21.2	9.0	45	13	CL529018 HIV55C09
2	19.8	8.4	44	11	AZ862104 2M0169D04
3	19.6	8.3	44	11	BH804777 1008098B1
4	19.4	8.2	31	1	A1022023
5	19.2	8.1	49	10	DT933089 BH006A10
6	19.2	8.1	50	10	DV774160 MCG1intoc
7	19.2	8.1	37	11	AZ836826 2M0131A20
8	19.2	8.1	41	14	BX128197 Dancio rer
9	18.8	8.0	44	11	AZ368544 2M0240C20
10	18.8	8.0	46	14	BX650405 Arabidops
11	18.8	8.0	50	11	AZ765968 1M0563N12
12	18.8	8.0	50	13	CZ194703 PST6723-N
13	18.6	7.9	43	11	AZ862121 2M0169H01
14	18.6	7.9	47	11	AZ331496 1M0059P21
15	18.6	7.9	50	8	CX001254 1V40A04.D
16	18.4	7.8	46	1	A1941313 6D87E01.Y
17	18.4	7.8	48	1	A1749566 AC30F01.X
18	18.2	7.7	40	1	AA257023 zR84E02.S
19	18.2	7.7	49	4	CA966474 CCLX05a17

20	18.2	7.7	50	7	BE882523 601507265
21	18	7.6	45	11	AZ504116
22	18	7.6	49	1	A1521631 C065H01.X
23	18	7.6	49	11	AZ407440
24	18	7.6	50	7	BE299660
25	17.8	7.5	33	9	D45809 HUMS03027
26	17.8	7.5	40	11	AZ789792 2M0037J19
27	17.8	7.5	45	5	CF334268 JMT--03-H
28	17.8	7.5	48	7	BF507210 3659P-23
29	17.8	7.5	49	1	A1334100 GP97C03.X
30	17.8	7.5	49	11	AZ324079
31	17.8	7.5	50	1	AU104247
32	17.6	7.5	43	5	CF306079
33	17.6	7.5	44	2	BU001599
34	17.6	7.5	45	5	CF304467 ABF1--05-
35	17.6	7.5	47	8	CV721217 YBH--03-F
36	17.6	7.5	48	5	CF304105 ABF1--04-
37	17.6	7.5	49	1	AV674036 AV674036
38	17.6	7.5	49	5	CF322787 HDN--02-B
39	17.6	7.5	49	7	AV965544
40	17.6	7.5	50	1	AJ920737
41	17.4	7.4	32	11	AZ387638
42	17.4	7.4	34	1	A1561118 tG26e11.X
43	17.4	7.4	38	11	AZ479185 1M0299J11
44	17.4	7.4	40	11	AZ328467 1M0052E18
45	17.4	7.4	40	11	AZ793917 2M0047L24

ALIGNMENTS

RESULT 1
CL529018
LOCUS
DEFINITION
CL529018 HIV55C09.fwd HIV-vector integration sites in human IMR90 primary lung fibroblasts Homo sapiens genomic clone HIV55C09.fwd, genomic survey sequence.
ACCESSION
CL529018
VERSION
CL529018.1 GI:47422229
KEYWORDS
GSS.
SOURCE
Homo sapiens
ORGANISM
Homo sapiens (human)
REFERENCE
1 (bases 1 to 45)
AUTHORS
Mitchell,R.S., Betzel, B.F., Schroder,A.R.W., Shin,P., Chen,H., Berry,C.C., Becker,J.R. and Bushman,F.
TITLE
Retroviral DNA Integration: ASLV, HIV and MLV Show Distinct Target Site Preferences
JOURNAL
Unpublished (2004)
COMMENT
Contact: Frederic Bushman
Salk Institute Infectious Disease Laboratory
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1630
Fax: 858 554 0341
Email: bushman@salk.edu
Class: PCR with specific primers.
Location/Qualifiers
1. 45
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone.lib="HIV55C09.fwd"
/clone.lib="HIV-vector integration sites in human IMR90 primary lung fibroblasts"
/note="Human primary lung fibroblasts (IMR90) were infected with an HIV-based vector. DNA was isolated and cleaved with restriction enzymes; linkers were ligated onto the cleaved DNA and DNAs were amplified using one primer that bound to the linker DNA and one that bound to the HIV cDNA. Junctions between integrated HIV proviruses

ORIGIN and cellular DNA were cloned and sequenced."

Query Match 9.0%; Score 21.2; DB 13; Length 45;
Best Local Similarity 88.5%; Pred. No. 2.5e+05;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 GGGTCATGGGGCAGATCCCTCATGA 31
||||| ||||| ||||| ||||| |||||
DB 14 GGGTCATGAGGCGAGCAGCCCTCATGA 39

RESULT 2 44 bp DNA linear GSS 21-FEB-2001
LOCUS AZ862104/c
DEFINITION 2M0169D04R Mouse 10kb plasmid UGCGIM library Mus musculus genomic
ACCESSION AZ862104
VERSION AZ862104.1 GI:13059089
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 44)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weles, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0169 row: D column: 04
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 44.
Location/Qualifiers

FEATURES
source 1..44
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCG2M0169D04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_1lb="Mouse 10kb plasmid UGCGIM library"
/note="Vector: PWD42nv. Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptor complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into

ORIGIN chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 8.4%; Score 19.8; DB 11; Length 44;
Best Local Similarity 69.2%; Pred. No. 6.5e+05;
Matches 27; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 137 CACCGCTCCCGCTTCCTCTGCCATGATTTAAGAT 175
||||| ||||| ||||| ||||| |||||
DB 39 CCCCTCCCTCCCTTCCTCTGCCATGATTTAATAT 1

RESULT 3 44 bp DNA linear GSS 25-APR-2002
LOCUS BH804777/c
DEFINITION 1008096B10.2EL_x1 1008 - Rescuedu Grid I Zea mays genomic, genomic
survey sequence.
ACCESSION BH804777
VERSION BH804777.1 GI:20321384
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 44)
Walbot, V.
Maize genomic sequences found using engineered Rescuedu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1008098 row: 14
Class: transposon-tagged.
Location/Qualifiers

FEATURES
source 1..44
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/Al88/B73"
/db_xref="taxon:4577"
/issue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_1lb="1008 - Rescuedu Grid I"
/note="Organ: leaf; Vector: Rescuedu (engineered from
pBluescript backbone); Site: 1: BamHI, Site 2: BglII;
Rescuedu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on Rescuedu, go to the web
site www.zmdb.iastate.edu and follow the links for
'Rescuedu'. Grid I was grown at Berkeley in 2001. DNA was
extracted from leaf punches, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

ORIGIN

Query Match 8.3%; Score 19.6; DB 11; Length 44;
Best Local Similarity 66.7%; Pred. No. 7.5e+05;
Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 20 GATCCCTATGATAGTTAGTCATCCCTTGATGATGAG 61
||||| ||||| ||||| ||||| |||||
DB 44 GATCCGAATTAATGAGCTGTGCTTCTGATGATGAGG 3

RESULT 4
LOCUS AI022023
DEFINITION 31 bp mRNA linear EST 28-AUG-1998
ov72a02.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA
clone IMAGE:1652330 3' similar to TR:069340 069340 ORF1, ORF2, AND
ORF3; contains TARI.13 TARI repetitive element; mRNA sequence.
ACCESSION AI022023
VERSION
KEYWORDS
SOURCE EST. Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo
1 (bases 1 to 31)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: ega@rs-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert length: 864 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..31
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1652330"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_fetal_liver_spleen_INFLS_S1"
/note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
this is a subcloned version of the original Soares fetal
liver spleen INFLS library. 1st strand cDNA was primed
with a Pac I - oligo(dT) primer [5',
AAGTGAAGATTAATTAAGACTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Library
constructed by Benito Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 8.2%; Score 19.4; DB 1; Length 31;
Best Local Similarity 79.3%; Pred. No. 1e+05;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 94 GCCTGGCCCTCTCATCTCCCTGCC 122
|||||
3 GCCTGGCCCTCTCTCCCTCTGCC 31

RESULT 5
LOCUS DT933089
DEFINITION 49 bp mRNA linear EST 20-SEP-2005
BH006A10 Leptosphaeria starvation library Leptosphaeria maculans
cDNA, mRNA sequence.
ACCESSION DT933089
VERSION DT933089.1 GI:75966345
KEYWORDS EST.
SOURCE Leptosphaeria maculans (blackleg of rapeseed fungus)
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
Pleosporales; Leptosphaeriaceae; Leptosphaeria; Leptosphaeria
maculans complex.

REFERENCE 1 (bases 1 to 49)
AUTHORS Gardiner, D.M., Cozijnsen, A.J. and Howlett, B.J.
TITLE Leptosphaeria maculans EST's
JOURNAL Unpublished (2005)
COMMENT Contact: Cozijnsen A.J.
Blackleg Group
The School of Botany, The University of Melbourne
The University of Melbourne, Victoria 3010, Australia
Tel: + 61 3 8344 5056
Fax: + 61 3 9347 5406
Email: a.cozijnsen@unimelb.edu.au.
Location/Qualifiers
1..49
/organism="Leptosphaeria maculans"
/mol_type="mRNA"
/strain="IBCN18 (M)"
/db_xref="taxon:5022"
/sex="MART-2"
/tissue_type="mycelium"
/clone_lib="Leptosphaeria starvation library"

ORIGIN

Query Match 8.1%; Score 19.2; DB 10; Length 49;
Best Local Similarity 70.6%; Pred. No. 1e+06;
Matches 24; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 167 TTTTAAGATTCAGGACTTCACAGAGCAANT 200
|||||
3 TTTTAAGATTCAGGACTTCACAGATTAAT 36

RESULT 6
LOCUS DV774160/c 50 bp mRNA linear EST 23-NOV-2005
DEFINITION MCclintock24_C06.ab1 Homarus EST library project Homarus americanus
cDNA clone MCclintock24_C06.ab1, mRNA sequence.
ACCESSION DV774160
VERSION DV774160.1 GI:82627020
KEYWORDS EST.
SOURCE Homarus americanus (American lobster)
ORGANISM Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Decapoda; Pleocyemata; Astacidae;
Homarus
1 (bases 1 to 50)
Nephropidae; Nephropidae; Homarus.
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidae;
Nephropidae; Nephropidae; Homarus.
Stepanyan, R., Day, K., Urban, J.J., Hardin, D.L., Shetty, R.S.,
Derby, C.D., Ache, B.W. and MCclintock, T.S.
Gene expression and specificity in the mature zone of the lobster
olfactory organ
Unpublished (2005)
Contact: MCclintock TS
Department of Physiology
University of Kentucky
800 Rose St., Lexington, KY 40536-0298, USA
Tel: 859 323 1083
Fax: 859 323 1070
Email: mcclint@uky.edu.
Location/Qualifiers
1..50
/organism="Homarus americanus"
/mol_type="mRNA"
/db_xref="taxon:6706"
/clone="MCclintock24_C06.ab1"
/sex="male and female"
/tissue_type="mature zone"
/dev_stage="adult"
/lab_host="Dh5alpha"
/clone_lib="Homarus EST library project"
/note="Organ: Olfactory organ; lateral ramus of first
antennae; Vector: pBluescript; Site_1: NotI; Site_2: SalI;
5'-end sequences from a subcloned cDNA library. The
frequency of common sequences in this library was reduced
by screening filter lifts of colonies with complex probes"

/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGGCM0169H01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCLIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGGCM0059P21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCLIM library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 7.9%; Score 18.6; DB 11; Length 43;
Best Local Similarity 65.9%; Pred. No. 1.5e+06;
Matches 27; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

ORIGIN

Query Match 7.9%; Score 18.6; DB 11; Length 47;
Best Local Similarity 72.7%; Pred. No. 1.5e+06;
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 112 CTCCTGCTCCCACTCTTGATGAGACCGCTCCCTTC 152
DB 42 CACATGCTCACACATGCTCCACACATGCGGATTC 2

QY 71 GTGAGAGCTGCTGTTTGAAGAGCTGGCCCC 103
DB 33 GTGGATGTGCTGCTTGAATGAATGATGCCCC 1

RESULT 14
LOCUS AZ331496 47 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0059P21F Mouse 10kb plasmid UGCLIM library Mus musculus genomic
ACCESSION AZ331496
VERSION AZ331496.1 GI:10394261
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 47)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE Plasmid whole genome scaffolding with paired end reads from 10kb
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112 USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0059 row: P column: 21
Seq primer: CGTTGTAACGACGCGCACT
Class: plasmid inserts
High quality sequence stop: 47.
Location/Qualifiers
1..47
/organism="Mus musculus"

RESULT 15
LOCUS CX001254 50 bp mRNA linear EST 03-DEC-2004
DEFINITION 1v40a04.b1 Left Cardiac Ventricle (DOGEST7) Canis familiaris cDNA,
mRNA sequence.
ACCESSION CX001254
VERSION CX001254.1 GI:56272670
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
REFERENCE 1 (bases 1 to 50)
AUTHORS Balija, V.S., Nascento, L.V. and McCombie, W.R.
TITLE ESTs from Canis familiaris left cardiac ventricle (dog)
JOURNAL Unpublished (2004)
COMMENT Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Location/Qualifiers
1..50
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"
/sex="Unknown"
/tissue_type="Cardiac muscle"
/dev_stage="3 month old normal canine"
/lab_host="XL10 Gold"
/clone_lib="Left Cardiac Ventricle (DOGEST7)"
/note="Organ: Heart; Vector: pBluescript II SK; Site 1:
EORI; Site 2: XhoI; Library constructed using pBluescript

XR kit from Stratagene. Cloned cDNA was size selected between 1-3 kb. Tissue supplied by Mark Haskins VMD, PhD, Pathology and Medical Genetics, School of Veterinary Medicine, University of Pennsylvania, 3800 Spruce Street, Philadelphia, PA 19104-6051"

ORIGIN

Query Match 7.9%; Score 18.6; DB 8; Length 50;
 Best Local Similarity 72.7%; Pred. No. 1.5e+06;
 Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Oy 95 CCTGGCCCCCTCATCTCTCTGCTCCCACTCT 127
 |||||
 Db 5 CCGGCCCCCTCTCTCTCTCTCTCTCTCTCT 37

Search completed: October 1, 2006, 06:42:23
 Job time : 3524.25 secs


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/ CURRENT FILING DATE: 2005-10-28
/ PRIOR APPLICATION NUMBER: 60/466,801
/ PRIOR FILING DATE: 2003-04-29
/ NUMBER OF SEQ ID NOS: 778
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 527
/ LENGTH: 50
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:/note =
/ OTHER INFORMATION: Synthetic Construct
US-10-554-759-527
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Best Local Similarity 64.6%; Pred. No. 9.1e+02;
Matches 31; Conservative 1; Mismatches 16; Indels 0; Gaps 0;
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Db      1 TTTGTTTGGACACCAAGAGCCTGGAACCTGCACGCAKCTGTAA 48
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RESULT 3
US-11-155-444-16/c
/ Sequence 16, Application US/11155444
/ Publication No. US20060104971A1
/ GENERAL INFORMATION:
/ APPLICANT: GABER, ELLEN
/ APPLICANT: BAILLY, VERONIQUE
/ APPLICANT: BROWNING, JEFFREY L.
/ TITLE OF INVENTION: MULTIVALENT LYMPHOTOXIN BETA RECEPTOR AGONISTS AND
/ TITLE OF INVENTION: THERAPEUTIC USES THEREOF
/ FILE REFERENCE: BGNA168CN
/ CURRENT APPLICATION NUMBER: US/11/155,444
/ CURRENT FILING DATE: 2005-06-17
/ PRIOR APPLICATION NUMBER: PCT/US03/041393
/ PRIOR FILING DATE: 2003-12-22
/ PRIOR APPLICATION NUMBER: 60/435,154
/ PRIOR FILING DATE: 2002-12-20
/ PRIOR APPLICATION NUMBER: 60/435,185
/ PRIOR FILING DATE: 2002-12-20
/ NUMBER OF SEQ ID NOS: 23
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 16
/ LENGTH: 50
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: primer
US-11-155-444-16
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Query Match          8.6%; Score 20.8; DB 8; Length 50;
Best Local Similarity 70.0%; Pred. No. 2.3e+03;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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OY      37 GGGAGCTCCACCTCCGAGCTGCTGCTCACCTGCTTTTC 76
Db      50 GGATCTTCACCTCTGAGCGCGCCGCTCATTTATCTCC 11
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```
RESULT 4
US-10-554-711-343
/ Sequence 343, Application US/10554711
/ Publication No. US20060115806A1
/ GENERAL INFORMATION:
/ APPLICANT: University of Georgia Research Foundation
/ APPLICANT: McDonald, John F.
/ TITLE OF INVENTION: Global Analysis of Transposable Elements
/ TITLE OF INVENTION: as Molecular Markers of Cancer
/ FILE REFERENCE: 21099.0075P1
/ CURRENT APPLICATION NUMBER: US/10/554,711
```

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/ CURRENT FILING DATE: 2005-10-28
/ PRIOR APPLICATION NUMBER: 60/466,798
/ PRIOR FILING DATE: 2003-04-29
/ NUMBER OF SEQ ID NOS: 778
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 343
/ LENGTH: 50
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:/note =
/ OTHER INFORMATION: Synthetic Construct
US-10-554-711-343
```

```
Query Match          7.9%; Score 19.2; DB 6; Length 50;
Best Local Similarity 75.0%; Pred. No. 8e+03;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

```
OY      39 GAGCTCCACCTCCCGAGCTGCTGCTCACCTG 70
Db      12 GACCTTCACCTCCCGAGCTGCTGCTCACCAATTG 43
```

```
RESULT 5
US-10-554-711-723
/ Sequence 723, Application US/10554711
/ Publication No. US20060115806A1
/ GENERAL INFORMATION:
/ APPLICANT: University of Georgia Research Foundation
/ APPLICANT: McDonald, John F.
/ TITLE OF INVENTION: Global Analysis of Transposable Elements
/ TITLE OF INVENTION: as Molecular Markers of Cancer
/ FILE REFERENCE: 21099.0075P1
/ CURRENT APPLICATION NUMBER: US/10/554,711
/ CURRENT FILING DATE: 2005-10-28
/ PRIOR APPLICATION NUMBER: 60/466,798
/ PRIOR FILING DATE: 2003-04-29
/ NUMBER OF SEQ ID NOS: 778
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 723
/ LENGTH: 50
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:/note =
/ OTHER INFORMATION: Synthetic Construct
US-10-554-711-723
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```
Query Match          7.9%; Score 19.2; DB 6; Length 50;
Best Local Similarity 75.0%; Pred. No. 8e+03;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

```
OY      39 GAGCTCCACCTCCCGAGCTGCTGCTCACCTG 70
Db      12 GACCTTCACCTCCCGAGCTGCTGCTCACCAATTG 43
```

```
RESULT 6
US-10-554-759-343
/ Sequence 343, Application US/10554759
/ Publication No. US20060177825A1
/ GENERAL INFORMATION:
/ APPLICANT: University of Georgia Research Foundation
/ APPLICANT: McDonald, John F.
/ TITLE OF INVENTION: Global Analysis of Transposable Elements
/ TITLE OF INVENTION: as Molecular Markers of the Developmental Potential of Stem
/ FILE REFERENCE: 21099.0077P1
/ CURRENT APPLICATION NUMBER: US/10/554,759
/ CURRENT FILING DATE: 2005-10-28
/ PRIOR APPLICATION NUMBER: 60/466,801
/ PRIOR FILING DATE: 2003-04-29
/ NUMBER OF SEQ ID NOS: 770
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SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 343
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
US-10-554-759-343

Query Match 7.9%; Score 19.2; DB 6; Length 50;
Best Local Similarity 75.0%; Pred. No. 8e+03; Mismatches 8; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 39 GAGCTCCACTCCCGAGCTGCTGCTCCTCAGCTG 70
Db 12 GACCTTCACTTCCCGAGCTCCTCCCACTTGG 43

RESULT 7
US-10-554-759-723
; Sequence 723; Application US/10554759
; Publication No. US20060177825A1
; GENERAL INFORMATION:
; APPLICANT: University of Georgia Research Foundation
; APPLICANT: McDonald, John F.
; TITLE OF INVENTION: Global Analysis of Transposable Elements
; TITLE OF INVENTION: as Molecular Markers of the Developmental Potential of Stem
; TITLE OF INVENTION: Cells
; FILE REFERENCE: 21099.0077P1
; CURRENT APPLICATION NUMBER: US/10/554,759
; CURRENT FILING DATE: 2005-10-28
; PRIOR APPLICATION NUMBER: 60/466,801
; PRIOR FILING DATE: 2003-04-29
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 723
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic Construct
US-10-554-759-723

Query Match 7.9%; Score 19.2; DB 6; Length 50;
Best Local Similarity 75.0%; Pred. No. 8e+03; Mismatches 8; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Oy 39 GAGCTCCACTCCCGAGCTGCTGCTCCTCAGCTG 70
Db 12 GACCTTCACTTCCCGAGCTCCTCCCACTTGG 43

RESULT 8
US-11-370-584-2387/c
; Sequence 2387; Application US/11370584
; Publication No. US20060177863A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Ballelic markers for use in constructing a high
; TITLE OF INVENTION: density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/11/370,584
; CURRENT FILING DATE: 2006-03-08
; PRIOR APPLICATION NUMBER: US/10/349,143
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: 1999-04-21

; PRIOR APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 2387
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-10720-63 : polymorphic base A or G
US-11-370-584-2387

Query Match 7.4%; Score 17.8; DB 7; Length 47;
Best Local Similarity 67.6%; Pred. No. 2.3e+04; Mismatches 12; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Oy 161 TGAACAGACGACCTGTTAAGCCGCTGCTGTTA 197
Db 39 TTATCGAAGACCAAGTGAAGCCCTGTTCTTTAA 3

RESULT 9
US-11-217-529-49117
; Sequence 49117; Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIRO
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIRO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 49117
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-49117

Query Match 7.3%; Score 17.6; DB 8; Length 25;
Best Local Similarity 83.3%; Pred. No. 2e+04; Mismatches 4; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 97 GTAACATATTGTCGCCACTAC 120
Db 1 GAAGTACATTGGTCCCACTAC 24

RESULT 10
US-11-370-584-1835
; Sequence 1835; Application US/11370584
; Publication No. US20060177863A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Ballelic markers for use in constructing a high
; TITLE OF INVENTION: density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/11/370,584
; CURRENT FILING DATE: 2006-03-08
; PRIOR APPLICATION NUMBER: US/10/349,143
; PRIOR FILING DATE: 2003-01-21

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; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 1835
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-6730-356 : polymorphic base A or G
US-11-370-584-1835
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Query Match          7.2%; Score 17.4; DB 7; Length 47;
Best Local Similarity 60.0%; Pred. No. 3.1e+04;
Matches 27; Conservative 1; Mismatches 17; Indels 0; Gaps 0;
```

```
QY      5 CCAGCAGACGACGTGATTTGGTCACTGCTGGAGCTCCACT 49
Db      3 CTAGACCAGAACTAATTTCTCCTCTTCTTGAATTTCTTCA 47
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```

RESULT 11
US-11-217-529-22009/c
; Sequence 22009, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 22009
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-22009
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Best Local Similarity 86.4%; Pred. No. 2.8e+04;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
QY      180 AGCCACCGCTCTGTAGGCT 201
Db      25 AGCCACCGCTCTGTAAAGT 4
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```

RESULT 12
US-11-217-529-99537
; Sequence 99537, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
```

```

; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 99537
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-99537
```

```
Query Match          7.1%; Score 17.2; DB 8; Length 25;
Best Local Similarity 86.4%; Pred. No. 2.8e+04;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      203 GTCTAGGCTGTATCAATACCC 224
Db      1 GTCCAGGCTGTATCAGACAACC 22
```

```

RESULT 13
US-10-511-937-263
; Sequence 263, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 263
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-263
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```
Query Match          7.0%; Score 17; DB 6; Length 50;
Best Local Similarity 69.7%; Pred. No. 4.4e+04;
Matches 23; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
```

```
QY      149 CTCACGTGAGCTGACAGACGACCTGTTAAG 181
Db      9 CCCAAGTGAGACAGAACGAGGATTTGGGAGG 41
```

```

RESULT 14
US-11-348-413-461909
; Sequence 461909, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
```

Search completed: October 1, 2006, 01:14:07
Job time : 128.075 secs

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; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 461909
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 13836; WANDIUPTD; Start 105; Stop 129;
; US-11-348-413-461909
```

Query Match 6.9%; Score 16.8; DB 9; Length 25;
Best Local Similarity 90.0%; Pred. No. 3.8e+04;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 94 ACGGTAACATTTTGTGC 113
|||
Db 5 ACTATACTACATTTTGTGC 24

```
RESULT 15
US-11-348-413-461910
; Sequence 461910, Application US/11348413
; Publication No. US2006016012A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276209
; SEQ ID NO 461910
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 13836; WANDIUPTD; Start 106; Stop 130;
; OTHER INFORMATION: 000000000011110
; US-11-348-413-461910
```

Query Match 6.9%; Score 16.8; DB 9; Length 25;
Best Local Similarity 90.0%; Pred. No. 3.8e+04;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 94 ACGGTAACATTTTGTGC 113
|||
Db 4 ACTATACTACATTTTGTGC 23

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: October 1, 2006, 00:15:33 : Search time 332.623 Seconds
(without alignments)
5072.656 Million cell updates/sec

Title: US-10-642-946-6_COPY_1967_2208

Perfect score: 242
Sequence: 1 tctctcagcagcagcactgga.....ccaactaaactgattcac 242

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 5218826

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_8:*

1:	geneseqn1980s:*
2:	geneseqn1990s:*
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4:	geneseqn2001as:*
5:	geneseqn2001bs:*
6:	geneseqn2002as:*
7:	geneseqn2002bs:*
8:	geneseqn2003as:*
9:	geneseqn2003bs:*
10:	geneseqn2003cs:*
11:	geneseqn2003ds:*
12:	geneseqn2004as:*
13:	geneseqn2004bs:*
14:	geneseqn2005s:*
15:	geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	22	9.1	50	13	ADU25056	ADU25056 Retroelem
2	22	9.1	50	13	ADU22523	ADU22523 Human tra
3	20.8	8.6	50	6	ABZ07908	ABZ07908 Human leu
4	20.8	8.6	50	13	ADQ12194	ADQ12194 Primer of
5	20.4	8.4	41	6	ABZ47186	ABZ47186 Human ATP
6	20.4	8.4	41	6	ABZ47186	ABZ47186 Human ATP
7	20.2	8.3	48	6	ABK97936	ABK97936 DNA encod
8	19.6	8.1	31	3	AAAS1766	AAAS1766 31-mer CT
9	19.6	8.1	42	2	AAQ74160	AAQ74160 Mouse hea
10	19.6	8.1	50	6	ABZ01168	ABZ01168 Human leu
11	19.2	7.9	39	2	AAAT97180	AAAT97180 T cell re
12	19.2	7.9	42	2	AAV16931	AAV16931 Sense PCR
13	19.2	7.9	42	2	AAV16931	AAV16931 Antisense
14	19.2	7.9	42	2	AAV16801	AAV16801 Pea Rubis
15	19.2	7.9	42	2	AAV16811	AAV16811 Pea Rubis
16	19.2	7.9	50	13	ADU25252	ADU25252 Retroelem
17	19.2	7.9	50	13	ADU24873	ADU24873 Retroelem
18	19.2	7.9	50	13	ADU22340	ADU22340 Human tra

19	19.2	7.9	50	13	ADU22719	ADU22719 Human tra
20	19	7.9	39	8	ABX79718	ABX79718 EST polym
21	19	7.9	41	6	ABK97985	ABK97985 Human zln
22	19	7.9	41	12	ADH05426	ADH05426 Gene poly
23	19	7.9	41	12	ADH91213	ADH91213 I-beta-me
24	19	7.9	50	4	AAI28699	AAI28699 Human SNP
25	19	7.9	50	6	ABZ06403	ABZ06403 Human leu
26	19	7.9	50	6	ABZ06793	ABZ06793 Human leu
27	19	7.9	50	9	AAZ56821	AAZ56821 MT413 VL
28	18.8	7.8	46	4	ABJ51688	ABJ51688 Human GFR
29	18.6	7.7	25	14	ABE90482	ABE90482 127B prob
30	18.6	7.7	43	5	AAZ09540	AAZ09540 Antibody
31	18.6	7.7	47	2	AAV02490	AAV02490 B-ridge o1
32	18.6	7.7	47	2	AAV02469	AAV02469 Primer MP
33	18.6	7.7	47	4	AAZ81686	AAZ81686 Chimeric
34	18.6	7.7	50	2	AAZ069754	AAZ069754 Herpes s1
35	18.6	7.7	50	2	AAZ64216	AAZ64216 HSV-1 b'8
36	18.6	7.7	50	2	AAZ17504	AAZ17504 Test sequ
37	18.6	7.7	50	6	ABK82995	ABK82995 DNA blind
38	18.6	7.7	50	12	ADE80534	ADE80534 Duplex o1
39	18.4	7.6	24	6	ABL40677	ABL40677 ParKinson
40	18.4	7.6	28	13	ADZ48190	ADZ48190 Cutaneous
41	18.4	7.6	40	3	AAZ96036	AAZ96036 Polynucle
42	18.4	7.6	41	6	ABV72866	ABV72866 Mouse bra
43	18.4	7.6	41	6	ABV72867	ABV72867 Mouse bra
44	18.4	7.6	45	5	AAZ10797	AAZ10797 Bovine MH
45	18.4	7.6	45	5	AAI71381	AAI71381 Bovine MH

ALIGNMENTS

RESULT 1						
ID	ADU25056	standard; DNA; 50 BP.				
XX	ADU25056;					
XX	27-JUN-2005	(first entry)				
DE	Retroelement consensus sequence identifier oligonucleotide #526.					
XX	Expression pattern: transposable element; developmental potential;					
KW	stem cell; cellular differentiation induction factor;					
KW	methylation pattern; chromatin status pattern; endogenous retrovirus;					
KW	ERV; short interspersed nuclear element; SINE;					
KW	long interspersed nuclear element; LINE; retroelement; ss.					
OS	Synthetic.					
XX	PN	WO2004097005-A2.				
XX	PD	11-NOV-2004.				
XX	PF	29-APR-2004; 2004WO-US013667.				
XX	PR	29-APR-2003; 2003US-0466801P.				
PA	(UYGE-) UNIV GEORGIA RES FOUND INC.					
XX	PI	Mcdonald JF.				
XX	DR	WPI, 2004-804756/79.				
PT	Assigning an expression pattern of transposable elements to the level of					
PT	developmental potential of a cell comprises determining expression of one					
PT	or more families of transposable elements, and assigning the expression					
PT	pattern.					
XX	Disclosure; SEQ ID NO 527; 50bp; English.					
XX	The invention relates to a method of assigning an expression pattern of					
CC	transposable elements to the level of developmental potential of a cell.					

The method comprises determining the expression of one or more families of transposable elements, and assigning the expression pattern obtained to the level of developmental potential of a cell. Also disclosed are a method of determining the developmental potential of a stem cell, a method of identifying a cellular differentiation induction factor, a method of identifying a factor that increases the developmental potential of a cell, a method of assigning a methylation pattern of transposable elements to the level of developmental potential of a cell, and a method of assigning a chromatin status pattern of transposable elements to the level of developmental potential of a cell. In assigning an expression pattern of transposable elements to the level of developmental potential of a cell, the cell is a fully pluripotent stem cell, a pluripotent stem cell, or a differentiated cell. The expression pattern is determined by microarray analysis. One or more of the families of transposable elements are retroelement families, or DNA element families. One or more of the families of retroelements is selected from the group consisting of endogenous retroviruses (ERVs), a family of short interspersed nuclear elements (SINES) and a family of long interspersed nuclear elements (LINES). The expression of the transposable elements is measured by assaying for the mRNA transcribed from the genes or proteins translated from an mRNA transcribed from the genes. The expression of two or more families of transposable elements is determined and used to form the pattern of expression. The methylation of the transposable element genes is monitored by enzymatic means, microarray analysis, or methylation-specific PCR. The methylation pattern is determined by microarray analysis. The methods of the invention are useful for assigning an expression pattern of transposable elements to the level of developmental potential of a cell. This sequence represents an oligonucleotide identifier of a retroelement consensus sequence.

Query Match	9.1%	Score 22;	DB 13;	Length 50;
Best Local Similarity	64.6%	Pred. No. 4e+03;		
Matches 31; Conservative	1;	Mismatches 16;	Indels 0;	Gaps 0;

QY 133 TCCTTTGGAGCACTCTCAGCTGGAGCTGAA CAGAACGACTGTAA 180
| | | | | | | | : | | | | |
Db 1 TTTGTTTGGGACACCAGAGCCTGGA ACTGCACRGACCACTGTGTA 48

RESULT 2	
ADU22523	
ID	ADU22523 standard; DNA; 50 BP.

XX
AC ADU22523;

XX	
DT	27-JAN-2005 (first entry)

XX Human transposable element representative sequence, SEQ ID 527.

Human; ss; transposable element; DNA methylation; chromatin; cancer;
 LINE; long interspersed nuclear element; SINE;
 short interspersed nuclear element; HBRV; human endogenous retrovirus;
 microarray.

xx
os Homo sapiens.

AA
PN WO2004096021-A2.

AA PD 11-NOV-2004

AA 29-APR-2004; 2004WO-US013522.
PF

PR 29-APR-2003; 2003US-0466798P.

PA (UYGE-) UNIV GEORGIA RES FOUND INC.

PI McDonald JF;

AA WPI; 2004-804580/79.
DR

XX Determining expression, methylation or chromatin status pattern of PT

PT families of transposable elements in a sample e.g. for diagnosing cancer.
PT comprises determining the expression, methylation or chromatin status of
PT the elements.

PS Disclosure; SEQ ID NO 527; 68bp; English

The invention relates to determining expression, methylation or chromatin status pattern of one or more families of transposable elements in a sample comprises determining expression, methylation or chromatin status of one or more families of transposable elements. Also included are a method of assigning an expression pattern of transposable elements to a type of cancerous cell in a sample, a method of diagnosing cancer, a method of determining the effectiveness of an anti-cancer therapeutic in a subject, a method of assigning a methylation pattern of one or more families of transposable elements to a type of cancerous cell in a sample and a method of assigning a chromatin status pattern of transposable elements to a type of cancerous cell in a sample. The method is useful in determining an expression, methylation or chromatin status pattern of one or more families of transposable elements (e.g. LINE, long interspersed nuclear element, SINE, short interspersed nuclear element, or HENV, human endogenous retrovirus) in a sample for diagnosing cancer or determining the effectiveness of an anti-cancer therapeutic. The present sequence is a representative sequence for a human transposable element, used in a microarray to study the expression, methylation or chromatin status pattern of the transposable elements.

Sequence 50 BP; 13 A; 13 C; 12 G; 10 T; 0 U; 2 Other;

Query Match	9.1%	Score 22;	DB 13;	length 50;
Best Local Similarly	64.6%	Pred. No. 4e+03;		
Matches 31; Conservative	1;	Mismatches	0;	Gaps 0

```

Qy      133 TCTCTTTGGAGCACCTCTCAGGTGAGCTGAACAGAACGACCTGTTAA 180
          | | | | | | | | | | | | | | | | | | | | | |
Db      1 TTTGTTTGGACACCAAGACCTGGAATGCACRGACCAKCTGTGTA 48

```

RESULT 3
ABZ07908
ID ABZ07908 standard; DNA; 50 BP.

AA ABZ07908;
AC

DT 09-JAN-2003 (first entry)

Human leukocyte gene expression profiling probe SEQ ID NO 7899.

AA T7; leukocyte; gene expression profiling; allograft rejection;
KW

KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;

KW	T
S	

OS Homo sapiens.

AA WO200257414-A2.
PN

PD 25-JUL-2002.

22-OCT-2001; 2001WO-US047856.

PR 20-OCT-2000; 2000US-0241994P.

XX
EN
XX

[illegible]

PI Ly N, Woodward R, Quertermous T, Johnson F;

WPI; 2002-636525/68.

PT New system for leukocyte expression profiling, diagnosing a disease, or

PT or congestive heart failure, comprises diagnostic oligonucleotides.

XX Claim 1; Page 582; Opp; English.

XX PS The invention relates to a system for detecting gene expression, which
CC comprises one or two isolated DNA molecules that detect expression of a
CC gene, where the two corresponds to any of 8143 oligonucleotides
CC (AB200010-AB208152) each having 50 base pairs (bp). The system is useful
CC for leukocyte expression profiling. It is particularly useful for
CC diagnosing a disease, monitoring (rate of) progression of a disease,
CC predicting therapeutic outcome, determining prognosis for a patient,
CC predicting disease complications in an individual or monitoring response
CC to treatment in an individual. The diseases include cardiac allograft
CC rejection, kidney allograft rejection, liver allograft rejection,
CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection

XX SQ Sequence 50 BP; 12 A; 11 C; 8 G; 19 T; 0 U; 0 Other;

Query Match 8.6%; Score 20.8; DB 6; Length 50;
Best Local Similarity 70.0%; Pred. No. 1e+04;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 54 AGCTGCTGCTCCTCAGCTGCTTTTCCAAACCCACCTGTAA 93
DB 1 AGCTGCTGCTTCTCTTTCAGTTCGAATGCAACCTGTAA 40

RESULT 4
ADQ12194/c
ID ADQ12194 standard; DNA; 50 BP.

AC ADQ12194;

DT 07-OCT-2004 (first entry)
XX Primer of the invention #6.

DE Lymphotoxin-beta receptor; LT-Edgr-R; Cytostatic; cancer; tumour;
KM hucB211; hucB1A10; primer; ss.

XX Unidentified.

OS WO2004058191-A2.

PN 15-JUL-2004.

XX 22-DEC-2003; 2003WO-US041393.

XX 20-DEC-2002; 2002US-0435154P.

XX (BIOG-) BIOGEN IDEC MA INC.

XX Garder E, Bailly V, Browning JL;

DR MPI; 2004-525790/50.

XX New multivalent antibody constructs specific for the human lymphotoxin-
PT beta receptor, useful for diagnosing or treating cancer or for inhibiting
PT tumour volume.

XX Example 5; SEQ ID NO 16; 85pp; English.

XX The present invention relates to a multivalent antibody comprising at
CC least one antigen recognition site specific for a lymphotoxin-beta
CC receptor (LT-Edgr-R) epitope. The antibody is useful for preparing a
CC medicament for the treatment of cancer. The composition and method are
CC used for diagnosing or treating cancer and for inhibiting tumour volume.
CC The present sequence represents a primer of the invention.

XX Sequence 50 BP; 13 A; 12 C; 19 G; 6 T; 0 U; 0 Other;

Query Match 8.6%; Score 20.8; DB 13; Length 50;
Best Local Similarity 70.0%; Pred. No. 1e+04;

Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 37 GGAGCTCCACCTCCCGCAGCTGCTGCTCCTTTC 76
DB 50 GGATCTCCACCTCTCGAGCGCGCTCATTTGATCTCC 11

RESULT 5

ID AB247186/c
AB247186 standard; DNA; 41 BP.

AC AB247186;

DT 26-JUN-2003 (first entry)

XX Human ATP-binding cassette ABCB9 gene polymorphic site, #3970.

XX Human; drug metabolizing enzyme; gene; drug metabolism; chromosome 12;

KM polymorphic site; drug evaluation; drug screening; genotyping;

KW genetic profiling; therapeutic customisation; adverse reaction;

XX clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.

OS Homo sapiens.

XX Key Location/Qualifiers

FT variation replace(21,T)

FT /*tag a /standard_name= "Single nucleotide polymorphism (SNP)"

PN WO200252044-A2.

XX 04-JUL-2002.

XX 27-DEC-2001; 2001WO-JP011592.

XX 27-DEC-2000; 2000JP-00399443.

PR 02-MAY-2001; 2001JP-00135256.

PR 27-AUG-2001; 2001JP-00256862.

XX (RIKE) RIKEN KK.

XX Nakamura Y, Sekine A, Iida A, Saito S;

PI MPI; 2002-583571/62.

XX Claim 23; Page 136; 2785pp; English.

XX Sequences AB243217-AB250887 represent polymorphic sites within genes

XX encoding enzymes associated with drug metabolism. The invention relates

XX to methods and compositions for identifying individuals who have at least

XX one polymorphism in such drug metabolizing enzyme-encoding genes. The

XX polymorphisms may be identified in a nucleic acid sample using probes or

XX primers specific for a sequence selected from AB243217-AB250887 using a

XX variety of detection assays, including hybridisation assays, nucleic acid

XX arrays and PCR-based methods. The invention also encompasses methods of

XX evaluating and screening drugs using genetic polymorphism data. Genetic

XX polymorphism data, particularly that relating to single nucleotide

XX polymorphisms (SNPs), may be used in studying the relationship between

XX DNA sequence variations and human diseases, conditions, and responses to

XX drugs. SNPs are also useful as polymorphism markers for discovering genes

XX that cause or exacerbate certain diseases. SNPs are particularly useful

XX in the above respects as they are stable in populations, occur

XX frequently, and have lower mutation rates than other genome variations

XX such as repeating sequences. The detection and analysis of polymorphisms

XX in genes encoding drug metabolizing enzymes allows the customisation of

XX drug therapies based upon the genetic profile of individual patients.

XX This would not only take the guesswork out of selecting the drug with the

XX greatest therapeutic effect for a particular patient, but would also

CC	reduces the likelihood of adverse reactions, thereby increasing safety.
CC	Methods of the invention are also useful in the drug discovery and
CC	approval processes. For example, individuals could be selected for
CC	clinical trials only if their genetic profiles indicate that they are
CC	capable of responding to a particular drug or drug class, and previously
CC	failed drug candidates could be revived if they were matched with more
CC	appropriate patient populations. The methods, data and compositions of
CC	the invention may therefore lead to a an increase in the range of
CC	possible drug targets and decreases in the number of adverse drug
CC	reactions, failed drug trials, the time taken for a drug to be approved,
CC	the length of time patients are on medication and the number of different
CC	medications a patient needs to take before finding an effective therapy
XX	
XX	Sequence 41 BP; 9 A; 10 C; 20 G; 2 T; 0 U; 0 Other;
XX	
XX	Query Match 8.4%; Score 20.4; DB 6; Length 41;
XX	Best Local Similarity 71.1%; Pred. No. 1.3e+04;
XX	Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0
XX	
XX	21 TTTTGTCACTGTGCTGGAGCTCCACTTCCCCAGCTG 58
XX	
XX	41 TTTTGCACCGCTGTGGCGGTACCCCTCCCGCCTG 4
XX	
XX	RESULT 6
XX	ABZ44689/C
XX	ID ABZ44689 standard; DNA; 41 BP.
XX	AC ABZ44689;
XX	DT 26-JUN-2003 (first entry)
XX	DE Human ATP-binding cassette ABCB9 gene polymorphic site, #1473.
XX	XX
XX	Human; drug metabolizing enzyme; gene; drug metabolism; chromosome 12;
XX	polymorphic site; drug evaluation; drug screening; genotyping;
XX	genetic profiling; therapeutic customization; adverse reaction;
XX	clinical trial; drug approval; single nucleotide polymorphism; SNP; ds.
XX	OS Homo sapiens.
XX	XX
XX	Key Location/Qualifiers
XX	FT variation replace(21..T)
XX	FT /*tag= a
XX	XX /standard_name= "Single nucleotide polymorphism (SNP)"
XX	PN MO200252044-A2.
XX	PD 04-JUL-2002.
XX	XX
XX	27-DEC-2001; 2001WO-JP011592.
XX	XX
XX	27-DEC-2000; 2000JP-00399443.
XX	PR 02-MAY-2001; 2001JP-00135256.
XX	PR 27-AUG-2001; 2001JP-00256862.
XX	XX
XX	(RIKE) RIKEN KK.
XX	DT
XX	PI Nakamura Y, Sekine A, Iida A, Saito S;
XX	XX
XX	WPI; 2002-583571/62.
XX	DR
XX	PT Identifying individuals having a polymorphism, useful for determining the
XX	effectiveness or side effect of a drug or treatment protocol, comprises
XX	detecting at least one polymorphism in the drug metabolizing enzyme
XX	nucleic acid.
XX	PS
XX	Claim 23; Page 88; 2785pp; English.
XX	XX
XX	Sequences ABZ43217-ABZ50887 represent polymorphic sites within genes
XX	encoding enzymes associated with drug metabolism. The invention relates
XX	to methods and compositions for identifying individuals who have at least
XX	one polymorphism in such drug metabolizing enzyme-encoding genes. The

	CC	polymorphisms may be identified in a nucleic acid sample using probes or primers specific for a sequence selected from ABZ43217-ABZ50867 using a variety of detection assays, including hybridisation assays, nucleic acid arrays and PCR-based methods. The invention also encompasses methods of evaluating and screening drugs using genetic polymorphism data. Genetic polymorphism data, particularly that relating to single nucleotide polymorphisms (SNPs), may be used in studying the relationship between DNA sequence variations and human diseases, conditions, and responses to drugs. SNPs are also useful as polymorphism markers for discovering genes that cause or exacerbate certain diseases. SNPs are particularly useful in the above respects as they are stable in populations, occur frequently, and have lower mutation rates than other genome variations such as repeating sequences. The detection and analysis of polymorphisms in genes encoding drug metabolising enzymes allows the customisation of drug therapies based upon the genetic profile of individual patients.
	CC	CC would not only take the guesswork out of selecting the drug with the greatest therapeutic effect for a particular patient, but would also reduce the likelihood of adverse reactions, thereby increasing safety.
	CC	Methods of the invention are also useful in the drug discovery and approval processes. For example, individuals could be selected for clinical trials only if their genetic profiles indicate that they are capable of responding to a particular drug or drug class, and previously failed drug candidates could be revived if they were matched with more appropriate patient populations. The methods, data and compositions of the invention may therefore lead to an increase in the range of possible drug targets and decreases in the number of adverse drug reactions, failed drug trials, the time taken for a drug to be approved, the length of time patients are on medication and the number of different medications a patient needs to take before finding an effective therapy
SX	XX	Sequence 41 BP; 9 A, 10 C; 2 T; 0 U; 0 Other;
OY	Db	Query Match 8.4%; Score 20.4; DB 6; Length 41; Beet Local Similarity 71.1%; Pred.No. 1.3e+04; Matches 27; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
		21 TTTTGGTCACCTGCGTGAGACTCCACCCTCCCCCAGCTG 58 41 TTITGCCCA CGGTGTGGCGGTACCCCCTCCCCGCCTG 4
AKB97936/C		RESULT 7 ABK97936 standard; DNA; 48 BP.
AC	XX	ABK97936;
AD	XX	(first entry)
DE	XX	DNA encoding IFN-Con IRPPI peptide #1.
KM	XX	Cytosolic; vinctude; hepatotropic; antiinflammatory; neuroprotective; immunosuppressive; antihairctic; cytokine receptor; interferon; IFN; cancer; hematological malignancy; viral infection; hepatitis; human; multiple sclerosis; autoimmune disease; arthritis; ds; gene.
OS	XX	Synthetic.
PV	XX	WO200244197-A2.
PD	XX	06-JUN-2002.
PF	XX	30-NOV-2001; 200IWO-CA001701.
PR	XX	01-DEC-2000; 2000US-00727388.
PA	XX	(FISH/) FISH E N.
PJ	XX	Fish EN,
P	DR	WPT. 2002-547689/58. P-PADB; ABG68863.

PT Cytokine receptor binding peptide construct, in particular interferon
PT receptor binding peptide construct for use as an interferon mimetic,
PT comprises a cytokine receptor binding domain incorporated in a molecular
PT scaffold.
XX
XX
XX Example 8; Page 52; 105pp; English.
XX
CC This invention relates to a novel cytokine receptor binding peptide
CC construct comprising a cytokine receptor binding domain incorporated in a
CC suitable molecular scaffold so that the scaffold maintains the binding
CC domain in a configuration suitable for binding to the cytokine receptor.
CC The peptides of the invention may have cytosstatic, virucide,
CC hepatotropic, antiinflammatory, neuroprotective, immunosuppressive and
CC antitarrtic activities. A new interferon receptor binding peptide
CC construct is useful in the manufacture of a medicament as an interferon
CC (IFN) mimetic. A peptide that mimics the effect of IFN is useful in
CC medical therapies for cancer, haematological malignancies, viral
CC infections (hepatitis B or C), multiple sclerosis and autoimmune diseases
CC such as arthritis, to detect modulators of IFN action, in screening
CC assays to compare the activity and/or interaction with another molecule
CC or potential IFN modulator and also in the diagnosis of IFN activity
CC related disorders. A nucleic acid encoding the peptide of the invention
CC or is useful for the treatment and therapy of the mentioned medical
CC conditions. The peptide of the invention has less side effect than those
CC of native cytokines. The present sequence represents an interferon
CC receptor binding peptide associated DNA of the invention
CC
XX
SQ Sequence 48 BP; 5 A; 10 C; 25 G; 8 T; 0 U; 0 Other;
Query Match 8.3%; Score 20.2; DB 6; Length 48;
Best Local Similarity 68.3%; Pred. No. 1.6e+04;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 31 CTGGCTGGAGCTCCACCTCCCGAGCTGCTGCTCCTCACCCTGC 71
DB 45 CAGACAGAACTCCACCGCCGAGCCGCCGCTCCGCCG 5
RESULT 8
AA51766
ID AAA51766 standard; DNA; 31 BP.
XX
AC AAA51766;
XX
DT 31-OCT-2000 (first entry)
XX
DE 31-mer CYP3A5 wild-type -147A oligonucleotide.
XX
KM CYP3A5; Cytochrome P450; transcription regulatory region; polymorphism;
KM Activator protein-3 motif; AP-3; basic transcription element;
KM drug metabolism; phenotype; variant; ds.
XX
OS Homo sapiens.
XX
OS WO20039332-A1.
XX
PN 06-JUL-2000.
XX
PD 22-DEC-1999; 99WO-GB004380.
XX
PF 23-DEC-1998; 98GB-00028619.
XX
PR (JANC) JANSSEN PHARM NV.
XX
PA Paulussen ADC, Armstrong M;
XX
PI WPI; 2000-452418/39.
XX
DR Identifying subjects with a high drug metabolizing phenotype associated
PT with cytochrome CYP3A5 expression for establishing whether a drug will be
PT metabolized by the subject.
XX
PS Disclosure; Page 31; 68pp; English.

XX
CC 31-mer double stranded oligonucleotides corresponding to the cytochrome
CC P450 subfamily CYP3A5 5' untranslated region containing a polymorphism at
CC -147 (G) or wild-type (A) sequence were used in an electrophoretic
CC mobility shift assay (EMSA). The assay showed that -147 polymorphism
CC might create a binding site for the transcription factor Sp1. CYP3A5
CC transcription regulatory regions can be screened for the presence/absence
CC of a polymorphic variant, preferably at positions -475 or -147 of the DNA
CC of the 5' flanking region adjacent to the CYP3A5 coding sequence. The
CC variants are present in an activator protein-3 (AP-3) motif and/or a
CC basic transcription element (BRE). The polymorphisms cause increased
CC CYP3A5 gene expression and this has been linked to drug metabolic
CC activity. Screening for the presence of variants can be used to identify
CC subjects with a high or low drug metabolizing phenotype associated with
CC cytochrome CYP3A5 expression. Primers are used which in addition to
CC hybridizing to the site of interest, are capable of introducing a
CC restriction site which is absent in either the wild type sequence or
CC polymorphic variants. Restriction enzyme cleavage analysis can then be
CC used to indicate the presence or absence of the variant. The methods are
CC used to establish, before treatment with a drug, whether the drug will be
CC effectively metabolized by the patient, to identify compounds and
CC transcription factors that can bind to a DNA sequence encoding CYP3A5,
CC diagnosing susceptibility to a disease which is caused by toxins or
CC procarcinogens metabolized by CYP3A5 and for identifying mutagenic
CC effects of a compound
XX
SQ Sequence 31 BP; 5 A; 15 C; 6 G; 5 T; 0 U; 0 Other;
Query Match 8.1%; Score 19.6; DB 3; Length 31;
Best Local Similarity 84.6%; Pred. No. 2.1e+04;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 53 CAGCTGCTGCTCCTCCTCCTCTTCCA 78
DB 3 CAGCTGACGCCACCTCCTCTCCA 28
RESULT 9
AAQ74160/c
ID AAQ74160 standard; DNA; 42 BP.
XX
AC AAQ74160;
XX
DT 07-FEB-1996 (first entry)
XX
DE Mouse heavy chain 3' amplification primer ICG2a,b RIL.
XX
XX
KM Primer; amplification; PCR; mouse; kappa chain; heavy chain; Fab;
KM antibody; immunotolerance; animal; variegated display library;
KM variable region; antigen; immunorecessive; cell surface marker; foetal;
KM cancer; stem cell; variant; therapy; Alzheimer's disease; hybridoma;
KM familial hypercholesterolaemia; binding affinity; ss.
XX
XX
OS Synthetic.
XX
OS WO9515982-A2.
XX
PN 15-JUN-1995.
XX
PD 08-DEC-1994; 94WO-US014106.
XX
PF 08-DEC-1993; 93US-00164022.
XX
PR 06-DEC-1994; 94US-00350400.
XX
PA (GENZ) GENZYME CORP.
XX
PI Barsomian G, Copeland DP, Hillhouse D, Johnson T;
XX
DR WPI; 1995-224291/29.
XX
PT Generating new antibodies specific for immunorecessive epitopes - by
PT selection from variegated V gene library cloned from immuno-tolerance
PT derived antibody repertoire, useful in diagnosis, purifcn. and therapy,

XX e.g. of cancer.
XX
XX Example; Fig 1A, 109pp; English.
XX
XX primers AA074153-74 are a set of degenerate primers used to amplify 90%
CC of the mouse kappa chain and heavy chain Fab coding sequences from
CC antibodies in an immunotolerant animal. This primer binds to the 3' of
CC the heavy chain coding region. The amplified products are cloned to
CC produce a variegated display library (VDL) of antibody variable regions.
CC The antibodies are generated by an immunotolerant individual against an
CC antigen. The VDL can be used to generate an antibody against a
CC immunorecessive antigen e.g. a cell surface marker on a foetal, cancer or
CC stem cell, which can differentiate between variant or related forms of
CC the antigen. The antibodies generated can be used in the diagnosis, e.g.
CC detection of the immunorecessive antigen, or in therapy e.g. of cancer.
CC Alzheimer's disease or familial hypercholesterolaemia. The method of
CC production of the antibody allows rapid and sensitive isolation of
CC antibodies that would be difficult to isolate by standard methods. The
CC antibodies produced have greater binding affinity than those produced by
CC combinatorial/hybridoma methods
XX
SQ Sequence 42 BP; 7 A; 13 C; 13 G; 9 T; 0 U; 0 Other;
XX
Query Match 8.1%; Score 19.6; DB 2; Length 42;
Best Local Similarity 66.7%; Pred. No. 2.3e+04;
Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
XX
QY 177 TTAAGCCACCGCTGCTGTAGGCTTGTAGCTGATCAG 218
DB 42 TTGAGCCCGACGCGGCCCACTAGTGAATCTGGCGGACACAG 1
XX
RESULT 10
AB201168/C
ID AB201168 standard; DNA; 50 BP.
XX
XX AB201168;
XX
XX 09-JAN-2003 (first entry)
XX
XX Human leukocyte gene expression profiling probe SEQ ID NO 1159.
XX
XX T7; leukocyte; gene expression profiling; allograft rejection;
XX atherosclerosis; congestive heart failure; systemic lupus erythematosus;
XX rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;
XX ss.
XX
XX Homo sapiens.
XX OS
XX MO200257414-A2.
XX PN
XX 25-JUL-2002.
XX PD
XX 22-OCT-2001; 2001WO-US047856.
XX PF
XX 20-OCT-2000; 2000US-0241994P.
XX PR
XX 08-JUN-2001; 2001US-0296764P.
XX PT
XX (BIOC-) BIOCARDIA INC.
XX PA
XX
XX Wohlgenuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;
XX Ly N, Woodward R, Queternous T, Johnson F;
XX
XX WPI, 2002-636525/68.
XX
XX New system for leukocyte expression profiling, diagnosing a disease, or
XX monitoring (the rate of) progression of a disease, e.g. atherosclerosis
XX or congestive heart failure, comprises diagnostic oligonucleotides.
XX
XX Claim 1, Page 361; opp; English.
XX
XX The invention relates to a system for detecting gene expression, which
XX comprises one or two isolated DNA molecules that detect expression of a

CC gene, where the gene corresponds to any of 8143 oligonucleotides
CC (AB200010-AB208152) each having 50 base pairs (bp). The system is useful
CC for leukocyte expression profiling. It is particularly useful for
CC diagnosing a disease, monitoring (rate of) progression of a disease,
CC predicting therapeutic outcome, determining prognosis for a patient,
CC to treatment in an individual. The diseases include cardiac allograft
CC rejection, kidney allograft rejection, liver allograft rejection,
CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,
CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection
XX
SQ Sequence 50 BP; 15 A; 9 C; 20 G; 6 T; 0 U; 0 Other;
XX
Query Match 8.1%; Score 19.6; DB 6; Length 50;
Best Local Similarity 66.7%; Pred. No. 2.5e+04;
Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
XX
QY 35 CTGGAGCTCCACCTCCCGACCTGCTGCTCAGCTGCTTC 76
DB 50 CTGGCGCTTCCCTTCCAGTTACAGCCGACGCTTCTC 9
XX
RESULT 11
AAT97180/C
ID AAT97180 standard; DNA; 39 BP.
XX
XX AAT97180;
XX
XX 11-MAY-1998 (first entry)
XX
XX T cell receptor alpha chain 3' PCR primer.
XX
XX
XX Vaccine; B-cell malignancy; lymphoma; leukaemia; tumour;
XX gene amplification; immunotherapy; therapy; T cell receptor; human; PCR;
XX primer; ss.
XX KM
XX
XX Homo sapiens.
XX OS
XX Synthetic.
XX
XX WO9741244-A1.
XX PN
XX 06-NOV-1997.
XX PD
XX 25-APR-1997; 97WO-US007039.
XX PF
XX 01-MAY-1996; 96US-00644664.
XX PR
XX 06-DEC-1996; 96US-00761277.
XX PT
XX (GENI-) GENITOPE CORP.
XX PA
XX
XX Denney DW;
XX PI
XX
XX WPI, 1997-549743/50.
XX DR
XX
XX Multivalent vaccine to treat B cell lymphoma or leukaemia - comprises at
XX least 2 different recombinant variable regions of immunoglobulin
XX molecules derived from B cell lymphoma cells.
XX
XX Example 9, Page 86; 177pp; English.
XX
XX This 3' primer is used with a consensus 5' primer (see AAT97179) for the
XX PCR amplification of the human T cell receptor (TCR) alpha chain
XX extracellular domain DNA. The 3' connection for the TCR alpha chain is
XX made after Aen-110 of the constant region of the alpha chain. The methods
XX of the invention allow large quantities of soluble TCR to be produced in
XX a rapid manner. Customised tumour cell vaccines comprising soluble TCR
XX are obtained for the treatment of lymphoma and leukaemia
XX
SQ Sequence 39 BP; 9 A; 7 C; 9 G; 14 T; 0 U; 0 Other;
XX
Query Match 7.9%; Score 19.2; DB 2; Length 39;
Best Local Similarity 75.0%; Pred. No. 3.1e+04;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;


```
OS Synthetic.
OS Pisum sativum.
XX US5866394-A.
XX
XX 02-FEB-1999.
XX
XX 31-OCT-1996; 96US-00741931.
XX PF
XX 21-FEB-1995; 95US-00391000.
XX PR
XX (KENT ) UNIV KENTUCKY RES FOUND.
XX PA
XX Houtz RL;
XX
XX WPI; 1999-141928/12.
XX
XX Recombinant Rubisco LSMT methyltransferase enzyme - that methylates the
XX lysine epsilon-amino group of Rubisco.
XX
XX Example 4; Col 13-14; 28pp; English.
XX
XX This sequence represents a primer from a degenerate pool of primers
XX synthesized based on the peptide P18 (AAW75489) from the pea Rubisco
XX (Ribulose-1,5-bisphosphate carboxylase/oxygenase) large subunit epsilon-N
XX -methyltransferase (LSMT). The primer is based on the sense strand
XX encoding the peptide P18 and is used in the isolation of the pea Rubisco
XX LSMT from a cDNA library. The Rubisco LSMT gene encodes a protein of 489
XX amino acids with a predicted molecular weight of 55 kD. Recombinant
XX Rubisco LSMT enzyme is a methyltransferase that catalyses methylation of
XX the epsilon-amino group of Lys-14 in the large subunit of Rubisco
XX
XX Sequence 42 BP; 9 A; 14 C; 8 G; 11 T; 0 U; 0 Other;
XX
XX Query Match 7.9%; Score 19.2; DB 2; Length 42;
XX Best Local Similarity 75.0%; Pred. No. 3.2e+04;
XX Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
XX
QY 39 GAGCTCCACTCCCGAGCTGCTGCTTACCTG 70
DB 8 GAACCTGCTCTGCTGCTGCTGCTTACCTG 39
DB
RESULT 15
AA16811/c
ID AA16811 standard; DNA; 42 BP.
XX
XX AA16811;
XX
XX 27-APR-1999 (first entry)
XX
XX Pea Rubisco LSMT P18-derived degenerate primer #13.
XX
XX Pea; rubisco; ribulose-1,5-bisphosphate carboxylase/oxygenase; primer;
XX epsilon-N-methyltransferase; PCR; amplification; methyltransferase;
XX methylation; ss.
XX
XX Synthetic.
XX OS Pisum sativum.
XX
XX US5866394-A.
XX
XX 02-FEB-1999.
XX
XX 31-OCT-1996; 96US-00741931.
XX PF
XX 21-FEB-1995; 95US-00391000.
XX PR
XX (KENT ) UNIV KENTUCKY RES FOUND.
XX PA
XX Houtz RL;
XX
XX WPI; 1999-141928/12.
XX
XX
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```
XX
XX Recombinant Rubisco LSMT methyltransferase enzyme - that methylates the
XX lysine epsilon-amino group of Rubisco.
XX
XX Example 4; Col 13-14; 28pp; English.
XX
XX This sequence represents a primer from a degenerate pool of primers
XX synthesized based on the peptide P18 (AAW75489) from the pea Rubisco
XX (Ribulose-1,5-bisphosphate carboxylase/oxygenase) large subunit epsilon-N
XX -methyltransferase (LSMT). The primer is based on the antisense strand
XX encoding the peptide P18 and is used in the isolation of the pea Rubisco
XX LSMT from a cDNA library. The Rubisco LSMT gene encodes a protein of 489
XX amino acids with a predicted molecular weight of 55 kD. Recombinant
XX Rubisco LSMT enzyme is a methyltransferase that catalyses methylation of
XX the epsilon-amino group of Lys-14 in the large subunit of Rubisco
XX
XX Sequence 42 BP; 11 A; 8 C; 14 G; 9 T; 0 U; 0 Other;
XX
XX Query Match 7.9%; Score 19.2; DB 2; Length 42;
XX Best Local Similarity 75.0%; Pred. No. 3.2e+04;
XX Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
XX
QY 39 GAGCTCCACTCCCGAGCTGCTGCTTACCTG 70
DB 35 GAACCTGCTCTGCTGCTGCTGCTTACCTG 4
DB
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Job time : 334.623 secs
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OM nucleic - nucleic search, using sw model

Run on: October 1, 2006, 00:40:27 ; Search time 791.816 Seconds
(without alignments)
3755.428 Million cell updates/sec

Title: US-10-642-946-6_COPY_1967_2208

Perfect score: 242

Sequence: 1 ctctccagcacacgactgta.....ccaactaaactgattcac 242

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 24111450

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	9.9	50	16	US-11-175-859-40976
2	20.8	8.6	50	16	US-10-131-827-7899
3	20.8	8.6	50	16	US-11-175-859-61985
4	20.2	8.3	50	16	US-11-175-859-73641
5	20.2	8.3	50	16	US-11-175-859-75378
6	20.2	8.3	50	16	US-11-175-859-94006
7	20	8.3	41	8	US-10-035-833A-1473
8	20	8.3	41	8	US-10-035-833A-3970
9	20	8.3	25	13	US-11-175-859-61890
10	19.8	8.2	50	16	US-11-036-317-987319
11	19.8	8.2	50	16	US-11-175-859-40305
12	19.8	8.2	50	16	US-11-175-859-61232
13	19.6	8.1	50	7	US-10-131-827-1159
14	19.6	8.1	50	16	US-11-175-859-89374
15	19.6	8.1	50	16	US-11-175-859-96830
16	19.4	8.0	48	8	US-10-035-833A-1173
17	19.4	8.0	50	16	US-11-175-859-2047

18	19.4	8.0	50	16	US-11-175-859-9678	Sequence 9678, Ap
19	19.4	8.0	50	16	US-11-175-859-64743	Sequence 64743, A
20	19.4	8.0	50	16	US-11-175-859-100374	Sequence 100374, A
21	19.2	7.9	39	3	US-09-925-664-35	Sequence 35, Appl
22	19.2	7.9	39	3	US-09-925-664-35	Sequence 35, Appl
23	19.2	7.9	39	3	US-09-925-664-35	Sequence 35, Appl
24	19.2	7.9	39	3	US-09-925-664-35	Sequence 35, Appl
25	19.2	7.9	39	3	US-09-925-664-35	Sequence 35, Appl
26	19.2	7.9	39	3	US-09-925-664-35	Sequence 35, Appl
27	19.2	7.9	39	3	US-09-925-664-35	Sequence 35, Appl
28	19.2	7.9	39	3	US-09-925-664-35	Sequence 35, Appl
29	19.2	7.9	39	3	US-09-925-664-35	Sequence 35, Appl
30	19.2	7.9	39	3	US-09-925-664-35	Sequence 35, Appl
31	18.8	7.8	50	16	US-11-175-859-58714	Sequence 58714, A
32	18.8	7.8	50	16	US-11-175-859-111918	Sequence 111918, A
33	18.6	7.7	43	6	US-10-186-186-2	Sequence 2, Appl1
34	18.6	7.7	43	6	US-10-186-186-2	Sequence 2, Appl1
35	18.6	7.7	43	6	US-10-186-186-2	Sequence 2, Appl1
36	18.6	7.7	43	6	US-10-186-186-2	Sequence 2, Appl1
37	18.6	7.7	43	6	US-10-186-186-2	Sequence 2, Appl1
38	18.4	7.6	32	10	US-10-093-294A-18234	Sequence 3861, Ap
39	18.4	7.6	45	3	US-09-748-111B-12	Sequence 18234, A
40	18.4	7.6	45	3	US-09-748-111B-12	Sequence 12, Appl
41	18.4	7.6	50	16	US-11-175-859-3989	Sequence 3989, Ap
42	18.4	7.6	50	16	US-11-175-859-37922	Sequence 37922, A
43	18.4	7.6	50	16	US-11-175-859-80567	Sequence 80567, A
44	18.4	7.6	50	16	US-11-175-859-89058	Sequence 89058, A
45	18.2	7.5	24	11	US-10-310-914A-116991	Sequence 116991, A

ALIGNMENTS

RESULT 1
US-11-175-859-40976
Sequence 40976, Application US/11175859
Publication No. US20060024715A1
GENERAL INFORMATION:
APPLICANT: Affimetrix, Inc.
TITLE OF INVENTION: Method of Analysis of Human Polymorphism
FILE REFERENCE: 3690.1
CURRENT APPLICATION NUMBER: US/11/175,859
PRIOR FILING DATE: 2005-07-05
PRIOR APPLICATION NUMBER: US 60/585,352
NUMBER OF SEQ ID NOS: 116251
SOFTWARE: PatentIn version 3.2
SEQ ID NO 40976
LENGTH: 50
TYPE: DNA
ORGANISM: homo sapien
US-11-175-859-40976

Query Match 9.9%; Score 24; DB 16; Length 50;
Best Local Similarity 66.0%; Pred. No. 6.3e+07;
Matches 33; Conservative 1; Mismatches 16; Indels 0; Gaps 0;

Qy 56 CTGCTGCTCCTGCTGCTTTCCTCAACCCACCTGTAACCGTAAGCTACTACA 105
Db 1 CTGCTGCTCCTGCTGCTGCTGCTGCTTAAGCTTCAAGGACGAGACGCCCA 50

RESULT 2
US-10-131-827-7899
Sequence 7899, Application US/10131827
Publication No. US20040009479A1
GENERAL INFORMATION:
APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Nscc
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE

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; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7899
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-7899

Query Match
Best Local Similarity 70.0%; Score 20.8; DB 7; Length 50;
Matches 28; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Oy 54 AGCTGCTGCTCCTCACCCTGTTTCCAAACCCACCCCTGAA 93
Db 1 AGCTGCTGCTTCTCTTTCAGTTGCAATGCAAACTGTTA 40

RESULT 3
US-11-175-859-61985
; Sequence 61985, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61985
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapiens
US-11-175-859-61985

Query Match
Best Local Similarity 66.7%; Score 20.8; DB 16; Length 50;
Matches 28; Conservative 1; Mismatches 13; Indels 0; Gaps 0;

Oy 50 CCCGAGCTGCTGCTCCTCACCCTGTTTCCAAACCCACCCCTGT 91
Db 8 CCACAGCATCTGCCCTCTACATCTGCTCCAAATCAATACCTT 49

RESULT 4
US-11-175-859-73641/c
; Sequence 73641, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 73641
; LENGTH: 50
; TYPE: DNA

; ORGANISM: homo sapiens
US-11-175-859-73641

Query Match
Best Local Similarity 65.1%; Score 20.2; DB 16; Length 50;
Matches 28; Conservative 1; Mismatches 14; Indels 0; Gaps 0;

Oy 68 CTCGTTTCCAAACCCACCCCTGTAAACGTAACACTATTG 110
Db 47 CTCGTTTCCAAACCTCACTCTTGTGATGATTAATCTTTG 5

RESULT 5
US-11-175-859-75378/c
; Sequence 75378, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 75378
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapiens
US-11-175-859-75378

Query Match
Best Local Similarity 71.4%; Score 20.2; DB 16; Length 50;
Matches 25; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Oy 197 AGGGTGTCTAGGCTGTATCAGATACCAACTAA 231
Db 36 AAGCTGACTRATCTATCAAAAACCAAAATAA 2

RESULT 6
US-11-175-859-94006/c
; Sequence 94006, Application US/11175859
; Publication No. US20060024715A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Liu, Guoying et al.
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism
; FILE REFERENCE: 3690.1
; CURRENT APPLICATION NUMBER: US/11/175,859
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: US 60/585,352
; PRIOR FILING DATE: 2004-07-02
; NUMBER OF SEQ ID NOS: 116251
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 94006
; LENGTH: 50
; TYPE: DNA
; ORGANISM: homo sapiens
US-11-175-859-94006

Query Match
Best Local Similarity 68.3%; Score 20.2; DB 16; Length 50;
Matches 28; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Oy 69 TGCTTTCCAAACCCACCCCTGTAAACGTAACACTATT 109
Db 50 TGATTTCCAGATCTTACCTGTATATATATCAATTT 10

RESULT 7
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Db 50 GAGCTCCCATTCATCAAGTCTAGCTGACAGCTGATCCCAAGAACCC 2

RESULT 12

US-11-175-859-61232

; Sequence 61232, Application US/11175859

; Publication No. US20060024715A1

; GENERAL INFORMATION:

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Method of Analysis of Human Polymorphism

; FILE REFERENCE: 3690.1

; CURRENT APPLICATION NUMBER: US/11/175, 859

; PRIOR FILING DATE: 2005-07-05

; PRIOR APPLICATION NUMBER: US 60/585,352

; NUMBER OF SEQ ID NOS: 116251

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 61232

; LENGTH: 50

; TYPE: DNA

; ORGANISM: homo sapien

US-11-175-859-61232

Query Match 8.2%; Score 19.8; DB 16; Length 50;

Best Local Similarity 61.2%; Pred. No. 2e+04;

Matches 30; Conservative 1; Mismatches 18; Indels 0; Gaps 0;

OY 21 TTTTGTCACCTGCTGGAGCTCCACCTCCCAAGCTGCTGCTGACCT 69

Db 2 TTGTCGACCTGACCTGACCTGACCTGACCAACCCAGCTGCTGCTGCT 50

RESULT 13

US-10-131-827-1159/c

; Sequence 1159, Application US/10131827

; Publication No. US20040009479A1

; GENERAL INFORMATION:

; APPLICANT: Wohlgemuth, Jay

; APPLICANT: Fry, Kirk

; APPLICANT: Woodward, Robert

; APPLICANT: Ly, Ngoc

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE

; FILE REFERENCE: 506612000120

; CURRENT APPLICATION NUMBER: US/10/131, 827

; PRIOR FILING DATE: 2002-09-06

; PRIOR APPLICATION NUMBER: US 10/006,290

; PRIOR FILING DATE: 2001-10-22

; PRIOR APPLICATION NUMBER: US 60/296,764

; NUMBER OF SEQ ID NOS: 9090

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1159

; LENGTH: 50

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-131-827-1159

Query Match 8.1%; Score 19.6; DB 7; Length 50;

Best Local Similarity 66.7%; Pred. No. 2.3e+04;

Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 35 CTGGAGCTCCAGCTCCCAAGCTGCTGCTGCTGCTGCTTTTC 76

Db 50 CTGTGCGCTTCCTTCCTTCAGTTACAGCCCAAGCTGCTTC 9

RESULT 14

US-11-175-859-89374

; Sequence 89374, Application US/11175859

; Publication No. US20060024715A1

; GENERAL INFORMATION:

; APPLICANT: Affymetrix, Inc.

; APPLICANT: Liu, Guoying et al.

; TITLE OF INVENTION: Method of Analysis of Human Polymorphism

; FILE REFERENCE: 3690.1

; CURRENT APPLICATION NUMBER: US/11/175, 859

; PRIOR FILING DATE: 2005-07-05

; PRIOR APPLICATION NUMBER: US 60/585,352

; NUMBER OF SEQ ID NOS: 116251

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 89374

; LENGTH: 50

; TYPE: DNA

; ORGANISM: homo sapien

US-11-175-859-89374

Query Match 8.1%; Score 19.6; DB 16; Length 50;

Best Local Similarity 66.7%; Pred. No. 2.3e+04;

Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 201 TTGTCAGCTGTATCAGATACCACTAACTGATTCAC 242

Db 9 TGGGTAGGGCTGACATACCAATATAGACTGGGCTAC 50

RESULT 15

US-11-175-859-96830

; Sequence 96830, Application US/11175859

; Publication No. US20060024715A1

; GENERAL INFORMATION:

; APPLICANT: Affymetrix, Inc.

; APPLICANT: Liu, Guoying et al.

; TITLE OF INVENTION: Method of Analysis of Human Polymorphism

; FILE REFERENCE: 3690.1

; CURRENT APPLICATION NUMBER: US/11/175, 859

; PRIOR FILING DATE: 2005-07-05

; PRIOR APPLICATION NUMBER: US 60/585,352

; PRIOR FILING DATE: 2004-07-02

; NUMBER OF SEQ ID NOS: 116251

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 96830

; LENGTH: 50

; TYPE: DNA

; ORGANISM: homo sapien

US-11-175-859-96830

Query Match 8.1%; Score 19.6; DB 16; Length 50;

Best Local Similarity 69.4%; Pred. No. 2.3e+04;

Matches 25; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

OY 199 GGTGTCTAGCTGTATCAGATACCACTAACT 234

Db 2 GGGTGTATAATTGTTTCAGATAGTCAGGAAAGT 37

Search completed: October 1, 2006, 01:09:50

Job time : 792.816 secs

SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is 70%, *length 10-241 nt.*

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.

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Mon Oct 2 15:45:48 2006

GenCore version 5.1.9
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OW nucleic - nucleic search, using sw model

Run on: October 2, 2006, 15:40:32 ; Search time 0.001 Seconds
(without alignments)
333.232 Million cell updates/sec

Title: US-10-642-946-6_3002-3237

Perfect score: 236

Sequence: 1 tgcctggcgcacggggggcag.....ctgttcctgcgcacaaactg 236

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 35 seqs, 706 residues

Total number of hits satisfying chosen parameters: 70

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 35 summaries

Database : pubnewdb2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	18.2	7.7	25	1	US-11-348-413-1113015
C 2	17.6	7.5	25	1	US-11-217-529-168000
C 3	17.6	7.5	25	1	US-11-348-413-779975
C 4	17.4	7.4	23	1	US-11-078-073-81
C 5	17.4	7.4	23	1	US-11-078-073-82
C 6	17.4	7.4	23	1	US-11-078-073-83
C 7	17.4	7.4	23	1	US-11-078-073-84
C 8	17.4	7.4	23	1	US-11-078-073-85
C 9	16.4	6.9	23	1	US-11-078-073-80
C 10	16.4	6.9	23	1	US-11-078-073-86
C 11	15.6	6.6	22	1	US-11-323-061-4
C 12	15.2	6.4	20	1	US-10-511-937-2014
C 13	15.2	6.4	20	1	US-11-346-145-6
C 14	14.8	6.3	19	1	US-11-233-507-43
C 15	14.4	6.1	20	1	US-11-223-738-35
C 16	14.2	6.0	19	1	US-10-511-937-857
C 17	14.2	6.0	19	1	US-11-370-584-10001
C 18	14.2	6.0	19	1	US-11-233-507-15
C 19	14.2	6.0	19	1	US-11-233-495-7
C 20	14.2	6.0	20	1	US-11-370-584-11320
C 21	14.2	6.0	20	1	US-11-043-842-740
C 22	13.8	5.8	18	1	US-11-370-584-493
C 23	13.8	5.8	18	1	US-11-293-697-5018
C 24	13.8	5.8	18	1	US-11-321-991-8
C 25	13.4	5.7	17	1	US-11-255-139A-6881
C 26	13.4	5.7	17	1	US-11-255-139A-6882
C 27	13.4	5.7	18	1	US-11-370-584-11764
C 28	13.4	5.7	19	1	US-11-102-097-1540
C 29	13.4	5.7	19	1	US-11-102-097-1541
C 30	13.4	5.7	19	1	US-11-102-097-1542
C 31	13.2	5.6	18	1	US-11-370-584-7274
C 32	13.2	5.6	18	1	US-11-268-341-1
C 33	12.8	5.4	17	1	US-11-255-139A-3650

Published Application - NA-Ne

34 12.8 5.4 18 1 US-11-293-697-5010 Sequence 5010, Ap
35 12.6 5.3 18 1 US-11-177-646-509 Sequence 509, Ap

ALIGNMENTS

```

RESULT 1
US-11-348-413-1113015/c
; Sequence 1113015, Application US/11348413
; Publication No. US20060160121A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084100 (AM 101724)
; CURRENT APPLICATION NUMBER: US/11/348,413
; CURRENT FILING DATE: 2006-02-07
; PRIOR APPLICATION NUMBER: PCT/US05/035471
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 11/243,445
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US 60/615,573
; PRIOR FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 1276205
; SEQ ID NO 1113015
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: probe
; NAME/KEY: misc.feature
; LOCATION: (1)..(25)
; OTHER INFORMATION: SEQ ID NO: 14059; WANO1UQ4_at; Start 620; Stop 644;
; OTHER INFORMATION: 0000000000000000
US-11-348-413-1113015

Query Match      7.7%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 4.6;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy      159  TGCATGATTTTAAGATTCACG 181
Db      23  TGCATGATTTTAAGATTCACG 1

RESULT 2
US-11-217-529-168000/c
; Sequence 168000, Application US/11217529
; Publication No. US2006099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHITIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 168000
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-168000

```

Query Match 7.5%; Score 17.6; DB 1; Length 25;
 Best Local Similarity 83.3%; Pred. No. 5.6;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 174 ATTCAGGAGCTTCACAGAAGCA 197
 DB 25 ATACGAGGACTGCACAAAAGCA 2

RESULT 3
 US-11-348-413-779975
 ; Sequence 779975, Application US/11348413
 ; Publication No. US20060160121A1
 ; GENERAL INFORMATION:

APPLICANT: Wyeth
 APPLICANT: Mounts, William M
 APPLICANT: Murphy, Ellen
 TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
 FILE REFERENCE: 031896-084100 (Am 101724)
 CURRENT APPLICATION NUMBER: US/11/348,413
 CURRENT FILING DATE: 2006-02-07
 PRIOR APPLICATION NUMBER: PCT/US05/035471
 PRIOR FILING DATE: 2005-10-05
 PRIOR APPLICATION NUMBER: US 11/243,445
 PRIOR FILING DATE: 2005-10-05
 PRIOR APPLICATION NUMBER: US 60/615,573
 PRIOR FILING DATE: 2004-10-05
 NUMBER OF SEQ ID NOS: 1276209
 SEQ ID NO 779975

LENGTH: 25

TYPE: DNA

ORGANISM: Artificial

FEATURE:

FEATURE: OTHER INFORMATION: probe

NAME/KEY: msec feature

LOCATION: (1)_(25)

OTHER INFORMATION: SEQ ID NO: 5002; MAN01PA72_at; Start 23; Stop 47;

US-11-348-413-779975

Query Match 7.5%; Score 17.6; DB 1; Length 25;
 Best Local Similarity 83.3%; Pred. No. 5.6;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 188 ACAAGAACAATGCTAACGCCAT 211
 DB 2 ACAGAGAACAATCTTATGCCAT 25

RESULT 4
 US-11-078-073-81/c
 ; Sequence 81, Application US/11078073
 ; Publication No. US20060094032A1
 ; GENERAL INFORMATION:

APPLICANT: de Fougereolles, Antonin
 APPLICANT: Frank-Kamenetsky, Maria
 APPLICANT: Manoharan, Muthiah
 APPLICANT: Rajeev, Kallanthottathil G.
 APPLICANT: Hadwiger, Philipp
 TITLE OF INVENTION: RNA AGENTS TARGETING VEGF
 FILE REFERENCE: 14174-085001
 CURRENT APPLICATION NUMBER: US/11/078,073
 CURRENT FILING DATE: 2005-03-11
 PRIOR APPLICATION NUMBER: US 60/552,620
 PRIOR FILING DATE: 2004-03-12
 PRIOR APPLICATION NUMBER: US 60/559,824
 PRIOR FILING DATE: 2004-04-05
 PRIOR APPLICATION NUMBER: US 60/647,191
 PRIOR FILING DATE: 2005-01-25
 NUMBER OF SEQ ID NOS: 1061

SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 81
 ; LENGTH: 23
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-078-073-81

Query Match 7.4%; Score 17.4; DB 1; Length 23;
 Best Local Similarity 94.7%; Pred. No. 5.4;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 147 CCCTTCCTTCGCGCATG 165
 DB 23 CCCTTCCTTCGCGCATG 5

RESULT 5
 US-11-078-073-82/c
 ; Sequence 82, Application US/11078073
 ; Publication No. US20060094032A1
 ; GENERAL INFORMATION:

APPLICANT: de Fougereolles, Antonin
 APPLICANT: Frank-Kamenetsky, Maria
 APPLICANT: Manoharan, Muthiah
 APPLICANT: Rajeev, Kallanthottathil G.
 APPLICANT: Hadwiger, Philipp
 TITLE OF INVENTION: RNA AGENTS TARGETING VEGF
 FILE REFERENCE: 14174-085001
 CURRENT APPLICATION NUMBER: US/11/078,073
 CURRENT FILING DATE: 2005-03-11
 PRIOR APPLICATION NUMBER: US 60/552,620
 PRIOR FILING DATE: 2004-03-12
 PRIOR APPLICATION NUMBER: US 60/559,824
 PRIOR FILING DATE: 2004-04-05
 PRIOR APPLICATION NUMBER: US 60/647,191
 PRIOR FILING DATE: 2005-01-25
 NUMBER OF SEQ ID NOS: 1061

SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 82
 ; LENGTH: 23
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-078-073-82

Query Match 7.4%; Score 17.4; DB 1; Length 23;
 Best Local Similarity 94.7%; Pred. No. 5.4;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 147 CCCTTCCTTCGCGCATG 165
 DB 22 CCCTTCCTTCGCGCATG 4

RESULT 6
 US-11-078-073-83/c
 ; Sequence 83, Application US/11078073
 ; Publication No. US20060094032A1
 ; GENERAL INFORMATION:

APPLICANT: de Fougereolles, Antonin
 APPLICANT: Frank-Kamenetsky, Maria
 APPLICANT: Manoharan, Muthiah
 APPLICANT: Rajeev, Kallanthottathil G.
 APPLICANT: Hadwiger, Philipp
 TITLE OF INVENTION: RNA AGENTS TARGETING VEGF
 FILE REFERENCE: 14174-085001
 CURRENT APPLICATION NUMBER: US/11/078,073
 CURRENT FILING DATE: 2005-03-11
 PRIOR APPLICATION NUMBER: US 60/552,620
 PRIOR FILING DATE: 2004-03-12
 PRIOR APPLICATION NUMBER: US 60/559,824
 PRIOR FILING DATE: 2004-04-05
 PRIOR APPLICATION NUMBER: US 60/647,191
 PRIOR FILING DATE: 2005-01-25

```
; NUMBER OF SEQ ID NOS: 1061
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-078-073-83
```

```
Query Match          7.4%; Score 17.4; DB 1; Length 23;
Best Local Similarity 94.7%; Pred. No. 5.4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      147 CCCTTCCTCTCTGCCATG 165
Db      21 CCCTCCTCTCTCTGCCATG 3
```

```
RESULT 7
US-11-078-073-84/c
; Sequence 84, Application US/11078073
; Publication No. US20060094032A1
; GENERAL INFORMATION:
; APPLICANT: de Fougereolles, Antonin
; APPLICANT: Frank-Kamenevsky, Maria
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Rajeev, Kallanthottachil G.
; APPLICANT: Hadwiger, Philipp
; TITLE OF INVENTION: RNA AGENTS TARGETING VEGF
; FILE REFERENCE: 14174-085001
; CURRENT APPLICATION NUMBER: US/11/078,073
; PRIOR FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US 60/552,620
; PRIOR FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: US 60/559,824
; PRIOR FILING DATE: 2004-04-05
; PRIOR APPLICATION NUMBER: US 60/647,191
; PRIOR FILING DATE: 2005-01-25
; NUMBER OF SEQ ID NOS: 1061
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-078-073-84
```

```
Query Match          7.4%; Score 17.4; DB 1; Length 23;
Best Local Similarity 94.7%; Pred. No. 5.4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      147 CCCTTCCTCTCTGCCATG 165
Db      20 CCCTCCTCTCTCTGCCATG 2
```

```
RESULT 8
US-11-078-073-85/c
; Sequence 85, Application US/11078073
; Publication No. US20060094032A1
; GENERAL INFORMATION:
; APPLICANT: de Fougereolles, Antonin
; APPLICANT: Frank-Kamenevsky, Maria
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Rajeev, Kallanthottachil G.
; APPLICANT: Hadwiger, Philipp
; TITLE OF INVENTION: RNA AGENTS TARGETING VEGF
; FILE REFERENCE: 14174-085001
; CURRENT APPLICATION NUMBER: US/11/078,073
; PRIOR FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US 60/552,620
; PRIOR FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: US 60/559,824
; PRIOR FILING DATE: 2004-04-05
; PRIOR APPLICATION NUMBER: US 60/647,191
```

```
; PRIOR FILING DATE: 2005-01-25
; NUMBER OF SEQ ID NOS: 1061
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-078-073-85
```

```
Query Match          7.4%; Score 17.4; DB 1; Length 23;
Best Local Similarity 94.7%; Pred. No. 5.4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      147 CCCTTCCTCTCTGCCATG 165
Db      19 CCCTCCTCTCTCTGCCATG 1
```

```
RESULT 9
US-11-078-073-80/c
; Sequence 80, Application US/11078073
; Publication No. US20060094032A1
; GENERAL INFORMATION:
; APPLICANT: de Fougereolles, Antonin
; APPLICANT: Frank-Kamenevsky, Maria
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Rajeev, Kallanthottachil G.
; APPLICANT: Hadwiger, Philipp
; TITLE OF INVENTION: RNA AGENTS TARGETING VEGF
; FILE REFERENCE: 14174-085001
; CURRENT APPLICATION NUMBER: US/11/078,073
; PRIOR FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US 60/552,620
; PRIOR FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: US 60/559,824
; PRIOR FILING DATE: 2004-04-05
; PRIOR APPLICATION NUMBER: US 60/647,191
; PRIOR FILING DATE: 2005-01-25
; NUMBER OF SEQ ID NOS: 1061
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-078-073-80
```

```
Query Match          6.9%; Score 16.4; DB 1; Length 23;
Best Local Similarity 94.4%; Pred. No. 7.4;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      148 CCTTCCTCTCTGCCATG 165
Db      23 CCTCCTCTCTCTGCCATG 6
```

```
RESULT 10
US-11-078-073-86/c
; Sequence 86, Application US/11078073
; Publication No. US20060094032A1
; GENERAL INFORMATION:
; APPLICANT: de Fougereolles, Antonin
; APPLICANT: Frank-Kamenevsky, Maria
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Rajeev, Kallanthottachil G.
; APPLICANT: Hadwiger, Philipp
; TITLE OF INVENTION: RNA AGENTS TARGETING VEGF
; FILE REFERENCE: 14174-085001
; CURRENT APPLICATION NUMBER: US/11/078,073
; PRIOR FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US 60/552,620
; PRIOR FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: US 60/559,824
; PRIOR FILING DATE: 2004-04-05
```

; PRIOR APPLICATION NUMBER: US 60/647,191
; PRIOR FILING DATE: 2005-01-25
; NUMBER OF SEQ ID NOS: 1061
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-078-073-86

Query Match 6.9%; Score 16.4; DB 1; Length 23;
Best Local Similarity 94.4%; Pred. No. 7.4;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 147 CCCTTCCTCTCTGCAT 164
Db 18 CCCTCTCTCTCTGCAT 1

RESULT 11
US-11-323-061-4
; Sequence 4, Application US/11323061
; Publication No. US20060177851A1
; GENERAL INFORMATION:
; APPLICANT: Brennan, Mark David
; APPLICANT: Condra, Jodi Ann
; APPLICANT: Maesey, Amy Tabb
; APPLICANT: Wei, Wei
; APPLICANT: Neibergs, Holly
; TITLE OF INVENTION: GENETIC MARKERS OF SCHIZOPHRENIA
; FILE REFERENCE: 17929-002001
; CURRENT APPLICATION NUMBER: US/11/323,061
; CURRENT FILING DATE: 2005-12-30
; PRIOR APPLICATION NUMBER: US 60/640,707
; PRIOR FILING DATE: 2004-12-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-11-323-061-4

Query Match 6.6%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 9;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 144 TCCCTTCCTCTCTGCATG 165
Db 1 TTCTCTTCACTTCTCTGCATG 22

RESULT 12
US-10-511-937-2014/c
; Sequence 2014, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946

; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2014
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-2014

Query Match 6.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 9.1;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 134 AGACCTGCTCCCTCTCT 153
Db 20 AGACCTCTCTCTCTCT 1

RESULT 13
US-11-346-145-6/c
; Sequence 6, Application US/11346145
; Publication No. US20060178333A1
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Saidman, Shlomo
; APPLICANT: Evron, Tama
; TITLE OF INVENTION: Antisense Oligonucleotide Against Human Acetylcholinesterase
; TITLE OF INVENTION: (ACHE) and uses thereof
; FILE REFERENCE: 13122/US/01
; CURRENT APPLICATION NUMBER: US/11/346,145
; CURRENT FILING DATE: 2006-02-01
; PRIOR APPLICATION NUMBER: IL 143379
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: PCT/IL02/00411
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rat inverse EN102
US-11-346-145-6

Query Match 6.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 9.1;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 102 CCCTTCATCTCTCTGCTC 121
Db 20 CCCTCTCTCTCTCTCTC 1

RESULT 14
US-11-233-507-43/c
; Sequence 43, Application US/11233507
; Publication No. US20060099616A1
; GENERAL INFORMATION:
; APPLICANT: Ommen van, Garrit-Jan B.
; APPLICANT: Deutekom van, Judith C.T.
; APPLICANT: Dunnen den, Johannes T.
; APPLICANT: Aartsma-Rus, Annemeke
; TITLE OF INVENTION: Modulation of exon recognition in pre-mRNA by
; TITLE OF INVENTION: interfering with the secondary RNA structure
; FILE REFERENCE: P63917US00
; CURRENT APPLICATION NUMBER: US/11/233,507
; CURRENT FILING DATE: 2005-09-21
; PRIOR APPLICATION NUMBER: PCT/NL2004/00196

;; PRIOR FILING DATE: 2004-03-22 PCT/NL03/00214
;; PRIOR APPLICATION NUMBER: PCT
;; PRIOR FILING DATE: 2003-03-21
;; NUMBER OF SEQ ID NOS: 68
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 43
;; LENGTH: 19
;; TYPE: RNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: h59A0N2
US-11-233-507-43

Query Match 6.3%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 9.7;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 171 AAGATTCAGGAGCTTCA 188
Db 19 AAGACTCCAGGAACTTCA 2

RESULT 15
US-11-223-738-35
; Sequence 35, Application US/11223738
; Publication No. US2006009682A1
; GENERAL INFORMATION:
; APPLICANT: DELANY, Samantha
; APPLICANT: SANSEAU, Philippe
; APPLICANT: TATE, Simon Nicholas
; TITLE OF INVENTION: HUMAN VANILLOID RECEPTORS AND THEIR USES
; FILE REFERENCE: PG3606D1
; CURRENT APPLICATION NUMBER: US/11/223,738
; CURRENT FILING DATE: 2005-09-09
; PRIOR APPLICATION NUMBER: 09/857,123
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: PCT/EP99/09284
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: GB98265593
; PRIOR FILING DATE: 1998-12-01
; NUMBER OF SEQ ID NOS: 40
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-11-223-738-35

Query Match 6.1%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 12;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 115 CTGCTCCACCTCTTGC 130
Db 2 CTGCTCCATCTTGC 17

RESULT 16
US-10-511-937-857
; Sequence 857, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION

;; FILE REFERENCE: 506612000104
;; CURRENT APPLICATION NUMBER: US/10/511,937
;; CURRENT FILING DATE: 2004-10-15
;; PRIOR APPLICATION NUMBER: PCT/US2003/012946
;; PRIOR FILING DATE: 2003-04-24
;; PRIOR APPLICATION NUMBER: US 10/131,831
;; PRIOR FILING DATE: 2002-04-24
;; PRIOR APPLICATION NUMBER: US 10/325,899
;; PRIOR FILING DATE: 2002-12-20
;; NUMBER OF SEQ ID NOS: 3117
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 857
;; LENGTH: 19
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-511-937-857

Query Match 6.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 12;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 135 GACACCTGCTCCCTTCT 153
Db 1 GACCCCTCTTCCCTTCT 19

RESULT 17
US-11-370-584-10001/c
; Sequence 10001, Application US/11370584
; Publication No. US20060177863A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high
; TITLE OF INVENTION: density...
; FILE REFERENCE: GENSET.020Cp1
; CURRENT APPLICATION NUMBER: US/11/370,584
; CURRENT FILING DATE: 2006-03-08
; PRIOR APPLICATION NUMBER: US/10/349,143
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 10001
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: downstream amplification primer 99-8732 for SEQ 2136,
; OTHER INFORMATION: in complement
US-11-370-584-10001

Query Match 6.0%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 12;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 209 CATGCTCTGTCTGTCT 227
Db 19 CTTACTTCTGTGTCT 1

RESULT 18
US-11-233-507-15
; Sequence 15, Application US/11233507

RESULT 20
US-11-370-584-11320
; Sequence 11320, Application US/11370584
; Publication No. US20060177863A1

RESULT 22
US-11-370-584-4193/c
; Sequence 4193, Application US/11370584
; Publication No. US20060177863A1


```
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Balleistic markers for use in constructing a high
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/11/370,584
; CURRENT FILING DATE: 2006-03-08
; PRIOR APPLICATION NUMBER: US/10/349,143
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4193
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-13878 for SEQ 259,
US-11-370-584-4193

Query Match          5.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 12;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      110 TTCTCTGCTCTCCACTC 126
DB      17 TTCTCTATATCCACTC 1

RESULT 23
US-11-293-697-5018/c
; Sequence 5018, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5018
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: an artificially synthesized F
US-11-293-697-5018

Query Match          5.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 12;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      100 CCCCTCTCATCTCTCT 116
DB      18 CCCCTTCTCCTCTCTCT 2

RESULT 24
US-11-321-991-8
; Sequence 8, Application US/11321991
```

```
; Publication No. US20060115877A1
; GENERAL INFORMATION:
; APPLICANT: WEIGEL, PAUL E.
; APPLICANT: DEANGELIS, PAUL L.
; APPLICANT: PARACONSTANTINOU, JOHN
; TITLE OF INVENTION: HYALURONATE SYNTHASE GENES AND USES THEREOF
; FILE REFERENCE: 35541.069
; CURRENT APPLICATION NUMBER: US/11/321,991
; CURRENT FILING DATE: 2005-12-29
; PRIOR APPLICATION NUMBER: US/11/024,426
; PRIOR FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: 09/146,893
; PRIOR FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 19
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: OLIGONUCLEOTIDE PROBE
US-11-321-991-8

Query Match          5.8%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 13;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      32 ATGGTTAGTGCATTC 48
DB      2 ATGGCTTAGTGCATTC 18

RESULT 25
US-11-255-139A-6881/c
; Sequence 6881, Application US/11255139A
; Publication No. US20060154271A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/11/255,139A
; CURRENT FILING DATE: 2005-10-20
; NUMBER OF SEQ ID NOS: 8014
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6881
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-11-255-139A-6881

Query Match          5.7%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 13;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      148 CCTTCTCTCTTGCC 162
DB      16 CTGTCTCTCTTGCC 2

RESULT 26
US-11-255-139A-6882/c
; Sequence 6882, Application US/11255139A
; Publication No. US20060154271A1
; GENERAL INFORMATION:
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/11/255,139A
; CURRENT FILING DATE: 2005-10-20
```

```
; NUMBER OF SEQ ID NOS: 8014
; SOFTWARE: Patentin version 3.0
; SEQ ID NO: 6882
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-255-139A-6882
```

```
Query Match          5.7%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 13;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      148 CCTTCTCCTCTGCC 162
      ||| ||| ||| ||| |||
Db       15 CCTGCTCCTCTGCC 1
```

```
RESULT 27
US-11-370-584-11764
; Sequence 11764, Application US/11370584
; Publication No. US20060177863A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marra
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/11/370,584
```

```
; PRIOR FILING DATE: 2006-03-08
; PRIOR APPLICATION NUMBER: US/10/349,143
; PRIOR FILING DATE: 2003-01-21
```

```
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: US 09/298,850
```

```
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: 1998-11-23
```

```
; PRIOR APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
```

```
; SEQ ID NO 11764
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
```

```
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-889 for SEQ 3899, in
US-11-370-584-11764
```

```
Query Match          5.7%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 14;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      113 TCCTGCTCCCACTCT 127
      ||| ||| ||| ||| |||
Db       2 TCCTTCTCCCACTCT 16
```

```
RESULT 28
US-11-102-097-1540
; Sequence 1540, Application US/11102097
; Publication No. US20060160759A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Chen, et al.
; TITLE OF INVENTION: Influenza Therapeutic
; FILE REFERENCE: 0492611-0621
; CURRENT APPLICATION NUMBER: US/11/102,097
; CURRENT FILING DATE: 2005-04-08
; NUMBER OF SEQ ID NOS: 2926
; SOFTWARE: Patentin version 3.2
```

```
; SEQ ID NO 1540
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Sequences of functional target portions for RNAi to inhibit
US-11-102-097-1540
```

```
Query Match          5.7%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 15;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      190 AAGAGCAATGCTA 204
      ||| ||| ||| ||| |||
Db       4 AAGAGCAATGCTA 18
```

```
RESULT 29
US-11-102-097-1541
; Sequence 1541, Application US/11102097
; Publication No. US20060160759A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Chen, et al.
; TITLE OF INVENTION: Influenza Therapeutic
; FILE REFERENCE: 0492611-0621
; CURRENT APPLICATION NUMBER: US/11/102,097
```

```
; CURRENT FILING DATE: 2005-04-08
; NUMBER OF SEQ ID NOS: 2926
; SOFTWARE: Patentin version 3.2
```

```
; SEQ ID NO 1541
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
```

```
; OTHER INFORMATION: Sequences of functional target portions for RNAi to inhibit
US-11-102-097-1541
```

```
Query Match          5.7%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 15;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      190 AAGAGCAATGCTA 204
      ||| ||| ||| ||| |||
Db       3 AAGAGCAATGCTA 17
```

```
RESULT 30
US-11-102-097-1542
; Sequence 1542, Application US/11102097
; Publication No. US20060160759A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Chen, et al.
; TITLE OF INVENTION: Influenza Therapeutic
; FILE REFERENCE: 0492611-0621
; CURRENT APPLICATION NUMBER: US/11/102,097
```

```
; CURRENT FILING DATE: 2005-04-08
; NUMBER OF SEQ ID NOS: 2926
; SOFTWARE: Patentin version 3.2
```

```
; SEQ ID NO 1542
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
```

```
; OTHER INFORMATION: Sequences of functional target portions for RNAi to inhibit
US-11-102-097-1542
```

```
Query Match          5.7%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 15;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

Qy 190 AAGAGCAATGCTA 204
| | | | |
Db 1 AAGAGTAAATCTA 15

RESULT 31
US-11-370-584-7274/c
; Sequence 7274, Application US/11370584
; Publication No. US2006017763A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high
; TITLE OF INVENTION: density...
; FILE REFERENCE: GENSET 020CPI
; CURRENT APPLICATION NUMBER: US/11/370,584
; CURRENT FILING DATE: 2006-03-08
; PRIOR APPLICATION NUMBER: US/10/349,143
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 7274
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-3391 for SEQ 3340,
US-11-370-584-7274

Query Match 5.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 15;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 25 CTCATGATGCTTGTG 42
| | | | |
Db 18 CTCATCAATGCTGTG 1

RESULT 32
US-11-268-341-1/c
; Sequence 1, Application US/11268341
; Publication No. US20060099574A1
; GENERAL INFORMATION:
; APPLICANT: Omar, Abdul Rahman
; APPLICANT: Hair-Bejo, Mohd
; APPLICANT: Aini, Ideris
; APPLICANT: Hamzah, Hairul Aini
; TITLE OF INVENTION: DETECTION AND DISTINGUISHING INFECTIONS BURSAL DISEASE VIRUS
; TITLE OF INVENTION: (IBDV) STRAINS BY MOLECULAR BIOLOGY METHOD
; FILE REFERENCE: SI146.70010US00
; CURRENT APPLICATION NUMBER: US/11/268,341
; CURRENT FILING DATE: 2005-11-07
; PRIOR APPLICATION NUMBER: MY PI 20044610
; PRIOR FILING DATE: 2004-11-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 1
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
US-11-268-341-1

Query Match 5.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 15;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 90 AAGAGCTGGCCCTCT 107
| | | | |
Db 18 AATAGCTGGCACTCT 1

RESULT 33
US-11-255-139A-3650/c
; Sequence 3650, Application US/11255139A
; Publication No. US20060154271A1
; GENERAL INFORMATION:
; APPLICANT: Sigma Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR
; FILE REFERENCE: MBHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/11/255,139A
; CURRENT FILING DATE: 2005-10-20
; NUMBER OF SEQ ID NOS: 8014
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3650
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-255-139A-3650

Query Match 5.4%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 16;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 142 GCTCCCTCTCTCTT 157
| | | | |
Db 16 GCTCCCTCTCTCTT 1

RESULT 34
US-11-293-697-5010
; Sequence 5010, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5010
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: an artificially synthesized p
US-11-293-697-5010

Query Match 5.4%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 134 AGACACCTGCTCCCC 149
| | | | |
Db 3 ACACCTGCTCCAC 18

RESULT 35
US-11-177-646-509
; Sequence 509, Application US/11177646

```

; Publication No. US20060210967A1
; GENERAL INFORMATION:
; APPLICANT: AGAN, BRIAN
; APPLICANT: ROWLEY, ROBB
; APPLICANT: SETO, DONALD
; APPLICANT: STENGER, DAVID
; APPLICANT: THORNTON, JENNIFER
; APPLICANT: TIBBETTS, CLARK
; APPLICANT: THACH, DZUNG
; APPLICANT: VORA, GARY
; APPLICANT: WALTER, ELIZABETH
; APPLICANT: WANG, ZHENG
; TITLE OF INVENTION: RE-SEQUENCING PATHOGEN MICROARRAY
; FILE REFERENCE: AFD 735
; CURRENT APPLICATION NUMBER: US/11/177,646
; PRIOR FILING DATE: 2005-07-02
; PRIOR APPLICATION NUMBER: 60/590931
; NUMBER OF SEQ ID NOS: 587
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 509
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-11-177-646-509

Query Match      5.3%; Score 12.6; DB 1; Length 18;
Best Local Similarity 92.3%; Pred. No. 18;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      113 TCCGTCTCCCACT 125
DB      2  TCTGTCTCCCACT 14

Search completed: October 2, 2006, 15:40:32
Job time : 0.001 secs

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2006, 15:35:07 ; Search time 0.001 Seconds

(without alignments)
101.952 Million cell updates/sec

Title: US-10-642-946-6_3002-3237

Perfect score: 236
Sequence: 1 tgcctgggcatcaggggagcag.....ctgtctgtctgcaaacatg 236

Scoring table: IDENTITY_NUC
Gap 10.0 , Gapext 0.5

Searched: 11 seqs, 216 residues

Total number of hits satisfying chosen parameters: 22

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 11 summaries

Database : genbank*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	17.4	7.4	19	1	CS155865 ACCESSION:CS155865
C 2	17.4	7.4	19	1	CS155923 ACCESSION:CS155923
C 3	17.4	7.4	19	1	AX114935 ACCESSION:AX114935
C 4	16.4	6.9	19	1	CS155866 ACCESSION:CS155866
C 5	16.4	6.9	19	1	CS155924 ACCESSION:CS155924
C 6	16.4	6.9	20	1	ARI18904 ACCESSION:ARI18904
C 7	16.4	6.9	20	1	BD089856 ACCESSION:BD089856
C 8	16.4	6.9	20	1	AB068203 ACCESSION:AB068203
C 9	16	6.8	20	1	AR207191 ACCESSION:AR207191
C 10	15	6.8	20	1	AX590845 ACCESSION:AX590845
C 11	15.8	6.7	21	1	AB166649 ACCESSION:AB166649

ALIGNMENTS

RESULT 1
LOCUS CS155865 19 bp RNA
DEFINITION Sequence 56 from Patent WO2005078097.
ACCESSION CS155865
VERSION CS155865.1 GI:74271013
KEYWORDS
SOURCE
ORGANISM
SYNTHETIC CONSTRUCT
SYNTHETIC CONSTRUCT
other sequences; artificial sequences.
REFERENCE
AUTHORS
Jadhav, V.
Patent: WO 2005078097-A 56 25-AUG-2005;
JOURNAL
Sitra Therapeutics, Inc. (US)
Location/Qualifiers
FEATURES
source
1..19
/organism="synthetic construct"

/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Synthetic"

Query Match 7.4%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 2.7;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 147 CCCTTCCTTCCTTCGCATG 165
Db 19 CCCTTCCTTCCTTCGCATG 1

RESULT 2
LOCUS CS155923 19 bp RNA
DEFINITION Sequence 114 from Patent WO2005078097.
ACCESSION CS155923
VERSION CS155923.1 GI:74271071
KEYWORDS
SOURCE
ORGANISM
SYNTHETIC CONSTRUCT
SYNTHETIC CONSTRUCT
other sequences; artificial sequences.
REFERENCE
AUTHORS
Jadhav, V.
Patent: WO 2005078097-A 114 25-AUG-2005;
JOURNAL
Sitra Therapeutics, Inc. (US)
Location/Qualifiers
FEATURES
source
1..19
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Synthetic"

Query Match 7.4%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 2.7;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 147 CCCTTCCTTCCTTCGCATG 165
Db 1 CCCTTCCTTCCTTCGCATG 19

RESULT 3
LOCUS AX114935 19 bp DNA
DEFINITION Sequence 58 from Patent WO0129262.
ACCESSION AX114935
VERSION AX114935.1 GI:14031877
KEYWORDS
SOURCE
ORGANISM
SYNTHETIC CONSTRUCT
SYNTHETIC CONSTRUCT
other sequences; artificial sequences.
REFERENCE
Picolin-Newburg, L. and Pohl, M.
Genotyping reagents, kits and methods of use thereof
Patent: WO 0129262-A 58 26-APR-2001;
JOURNAL
Orchid Biosciences, Inc. (US)
Location/Qualifiers
FEATURES
source
1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 7.4%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 2.7;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 147 CCCTTCCTTCCTTCGCATG 165
Db 19 CCCTTCCTTCCTTCGCATG 1

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RESULT 4
LOCUS CS155866/c 19 bp RNA linear PAT 07-SEP-2005
DEFINITION Sequence 57 from Patent WO2005078097.
ACCESSION CS155866
VERSION CS155866.1 GI:74271014
KEYWORDS
SOURCE
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Jadhav,V.
AUTHORS Patent: WO 2005078097-A 57 25-AUG-2005;
JOURNAL Sirna Therapeutics, Inc. (US)
FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Synthetic"

Query Match 6.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 3.4;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 147 CCCTTCCTCTGCGCAT 164
Db 18 CCTCTCTCTCTGCGCAT 1

RESULT 5
LOCUS CS155924 19 bp RNA linear PAT 07-SEP-2005
DEFINITION Sequence 115 from Patent WO2005078097.
ACCESSION CS155924
VERSION CS155924.1 GI:74271072
KEYWORDS
SOURCE
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Jadhav,V.
AUTHORS Patent: WO 2005078097-A 115 25-AUG-2005;
JOURNAL Sirna Therapeutics, Inc. (US)
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/db_xref="taxon:32630"
/note="Synthetic"

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Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 147 CCCTTCCTCTGCGCAT 164
Db 2 CCTCTCTCTCTGCGCAT 19

RESULT 6
LOCUS ARI18904 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 30 from patent US 6150092.
ACCESSION ARI18904
VERSION ARI18904.1 GI:14100814
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 Unclonified.
AUTHORS Uchida,K., Uchida,T., Tanaka,Y., Matsuda,Y. and Kondo,S.

```

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TITLE Antisense nucleic acid compound targeted to VEGF
JOURNAL Patent: US 6150092-A 30 21-NOV-2000;
FEATURES
source
1..20
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Query Match 6.9%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 3.2;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 147 CCCTTCCTCTGCGCAT 164
Db 3 CCTCTCTCTCTGCGCAT 20

RESULT 7
LOCUS BD089856 20 bp DNA linear PAT 27-AUG-2002
DEFINITION A method of arraying genome clone.
ACCESSION BD089856
VERSION BD089856.1 GI:22635466
KEYWORDS JP 2001321190-A/2100.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1 (bases 1 to 20)
AUTHORS Soeda,E.
TITLE A method of arraying genome clone
JOURNAL Patent: JP 2001321190-A 2100 20-NOV-2001;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
COMMENT
OS Artificial Sequence
PN JP 2001321190-A/2100
PD 20-NOV-2001
PF 12-MAR-2001 JP 2001068285
PI EIICHI SOEDA
PC C12N15/09, C12N15/00, C12M1/68, G01N33/53, G01N33/566, PC
C12N15/00
PC C12N15/00
CC Description of Artificial Sequence:Synthetic DNA FH Key
FT source
FT 1..20
Location/Qualifiers
1..20
/organism="Artificial Sequence".
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/db_xref="taxon:32630"

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Best Local Similarity 94.4%; Pred. No. 3.2;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 104 CTCGCATCTCTGCTCC 121
Db 1 CTCGCATCTCTGCTCC 18

RESULT 8
LOCUS AB068203 20 bp DNA linear SYN 21-MAY-2003
DEFINITION Synthetic construct DNA, reverse primer for human STS sts-D1S1400
at 1936.
ACCESSION AB068203
VERSION AB068203.1 GI:15129007
KEYWORDS
SOURCE
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,

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Morohashi, A., Ohira, M., Nakagawara, A., Liu, S., Hoehi, M., Horii, A. and Soeda, E.
 A BAC-based STS-content map spanning a 35-Mb region of human chromosome 1p35-p36
 JOURNAL Genomics 74 (1), 55-70 (2001)
 PUBMED 11374902
 REFERENCE 2 (bases 1 to 20)
 AUTHORS Horii, A.
 TITLE Direct Submission
 JOURNAL Submitted (04-AUG-2001) Akira Horii, Tohoku University School of Medicine, Molecular Pathology, 2-1 Seiryomachi, Aoba-ku, Sendai, Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp, Tel:81-22-717-8042, Fax:81-22-717-8047)
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 /db_xref="taxon:32630"
 misc_feature
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 Query Match 6.9%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 3.2;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 104 CTCATCTCTCTCTCTCC 121
 Db 1 CTCATCTCTCTCTCTCC 18
 RESULT 9
 AR207191 20 bp DNA linear PAT 20-JUN-2002
 LOCUS AR207191 Sequence 85 from patent US 6372492.
 DEFINITION AR207191
 ACCESSION AR207191
 VERSION AR207191.1 GI:21506024
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Bennett, C. Frank, and Cowsett, L. M.
 TITLE Antisense modulation of talin expression
 JOURNAL Patent: US 6372492-A 85 16-APR-2002;
 FEATURES
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 /organism="unknown"
 /mol_type="unassigned DNA"
 Query Match 6.8%; Score 16; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.6;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 105 TCTCATTTCTCTGCTC 120
 Db 3 TCTCATTTCTCTGCTC 18
 RESULT 10
 AX590845/c 20 bp DNA linear PAT 27-JAN-2003
 LOCUS AX590845 Sequence 285 from Patent WO02086113.
 DEFINITION AX590845
 ACCESSION AX590845
 VERSION AX590845.1 GI:27949394
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE 1
 AUTHORS Cookson, W.O., Moffat, M.F., Allen, M. and Lench, N.

TITLE Enzyme and snp marker for disease
 JOURNAL Patent: WO 02086113-A 285 31-OCT-2002;
 FEATURES
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 /organism="synthetic construct"
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 /db_xref="taxon:32630"
 /note="Primer"
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 Best Local Similarity 100.0%; Pred. No. 3.6;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 191 AGAGCAAAATGCTAAC 206
 Db 18 AGAGCAAAATGCTAAC 3
 RESULT 11
 AB166649/c 21 bp DNA linear SYN 07-OCT-2004
 LOCUS AB166649 Synthetic construct DNA, reverse primer for microsatellite DIK4617.
 DEFINITION AB166649
 ACCESSION AB166649
 VERSION AB166649.1 GI:51850039
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE 1
 AUTHORS Ihara, N., Takasuga, A., Mizoshita, K., Takeda, H., Sugimoto, M., Mizoguchi, Y., Hirano, T., Itoh, T., Matanabe, T., Reed, K. M., Sneling, W. M., Kappes, S. M., Beattie, C. W., Bennett, G. L. and Sugimoto, Y.
 TITLE A comprehensive genetic map of the cattle genome based on 3802 microsatellites
 JOURNAL Genome Res. 14 (10), 1987-1998 (2004)
 PUBMED 15466297
 REFERENCE 2 (bases 1 to 21)
 AUTHORS Sugimoto, Y., Ihara, N. and Takasuga, A.
 TITLE Direct Submission
 JOURNAL Submitted (04-MAR-2004) Yoshikazu Sugimoto, Shiraoka Institute of Animal Genetics, Odakura, Nishigo, Nishi-Shirakawa, Fukushima 961-8061, Japan (E-mail: kazusugis@sig.or.jp, Tel:81-248-25-5641, Fax:81-248-25-5725)
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 Best Local Similarity 89.5%; Pred. No. 3.6;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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 Db 19 CTCCTCTCTCTCTCTCC 1
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OM nucleic - nucleic search, using bw model

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(without alignments)
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Title: US-10-642-946-6_COPY_3002_3237

Perfect score: 236
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 2296392

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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15: gb_da: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	22.6	9.6	45	7	BX545753	Arabidops
2	21.6	9.2	41	2	AX516672	Sequence
3	21.6	9.2	41	2	AX518841	Sequence
4	21.2	9.0	49	2	BD190591	Bioreact1
5	21.2	9.0	49	2	AR405844	Sequence
6	20.8	8.8	43	2	I41116	Sequence 19
7	20.8	8.8	43	2	I41117	Sequence 20
8	19.8	8.4	50	2	CQ004290	Sequence
9	19.6	8.3	50	2	AR681155	Sequence
10	19.4	8.2	45	2	AR147108	Sequence
11	19.4	8.2	45	2	AR158296	Sequence
12	19.4	8.2	45	2	AR267871	Sequence
13	19.4	8.2	45	2	AR365906	Sequence
14	19.4	8.2	50	2	AR684817	Sequence
15	19.4	8.2	50	2	AR684983	Sequence
16	19.2	8.1	50	2	AR682008	Sequence
17	19.2	8.1	50	2	AX162664	Sequence
18	19	8.1	36	2	E13977	PCR primer

19	19	8.1	36	2	E14911	E14911 PCR primer
20	19	8.1	36	2	E64709	E64709 Anti-pathog
21	19	8.1	36	2	AR559761	AR559761 Sequence
22	19	8.1	42	2	AX512498	AX512498 Sequence
23	19	8.1	42	2	AX573414	AX573414 Sequence
24	19	8.1	42	2	AX746300	AX746300 Sequence
25	19	8.1	43	2	AR238006	AR238006 Sequence
26	19	8.1	50	2	E25630	E25630 RNA-DNA chl
27	19	8.1	50	2	AR682371	AR682371 Sequence
28	18.8	8.0	37	2	CQ004681	CQ004681 Sequence
29	18.6	7.9	49	2	E29443	E29443 Oligonucleo
30	18.6	7.9	42	2	I05520	I05520 Sequence 8
31	18.6	7.9	50	2	CQ002636	CQ002636 Sequence
32	18.6	7.9	50	2	AR682820	AR682820 Sequence
33	18.4	7.8	50	2	AX516639	AX516639 Sequence
34	18.4	7.8	41	2	AX518809	AX518809 Sequence
35	18.4	7.8	47	2	AR289030	AR289030 Sequence
36	18.4	7.8	50	2	BD223995	BD223995 Near infr
37	18.4	7.8	50	2	AR200395	AR200395 Sequence
38	18.4	7.8	50	2	AR682631	AR682631 Sequence
39	18.2	7.7	39	2	CQ970252	CQ970252 Sequence
40	18.2	7.7	41	2	AX516265	AX516265 Sequence
41	18.2	7.7	41	2	AX518600	AX518600 Sequence
42	18.2	7.7	44	2	AR210406	AR210406 Sequence
43	18.2	7.7	44	2	I90213	I90213 Sequence 39
44	18.2	7.7	47	2	BD204757	BD204757 Method of
45	18.2	7.7	47	2	AR290979	AR290979 Sequence

ALIGNMENTS

RESULT 1
BX545753
LOCUS
DEFINITION
Arabidopsis thaliana transposon insertion STS SM_3.36298, sequence tagged site.

ACCESSION
BX545753
VERSION
BX545753.1 GI:32168986
KEYWORDS
STS; STS, sequence tagged site.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana

REFERENCE
1
Clarke, J.H., Bowles, B., Carter, J., Hart, D., McCullagh, B., Walsh, S., Langham, S., Legry, C., Jones, J.D.G. and Bevan, M.

AUTHORS
Clarke, J.H.

REFERENCE
2 (bases 1 to 45)

TITLE
Direct Submision

JOURNAL
Submitted (23-JUN-2003) Clarke J.H., John Innes Centre, Colney lane, Norwich, NR4 7UJ, UK

COMMENT
AT denotes an activation tag dissociation transposon within a single line, ET an enhancer trap dissociation transposon, GT a gene trap dissociation transposon, MT a mis-expression enhancer trap dissociation transposon, SM a defective suppressor mutator transposon. _3 denotes a sequence derived from the 3' end of the transposon. _5 denotes a sequence derived from the 5' end of the transposon. BBSNC GARNET, ARIS project

On-line seed stock requests: <http://nasc.nott.ac.uk/> NASC stock code: NI23009.
Location/Qualifiers
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/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/variety="Columbia-0 NASC stock code NI092"
/db_xref="taxon:3702"
/clone="AC007583"
/note="Derived from superpool 24.2 NASC code N41115"

FEATURES

source

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/standard_name="SM_3.36298"

ORIGIN

Query Match 9.6%; Score 22.6; DB 7; Length 45;
Best Local Similarity 75.7%; Pred. No. 2e+05;
Matches 28; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 136 ACACCTGCTCCCTCTCTCTCTGCGCATGATTTTAA 172
1 ATATCTTCTTCCCTCTCTCTCTGCGCATGATTTTCA 37

RESULT 2
AX516672 41 bp DNA linear PAT 05-OCT-2002

LOCUS AX516672
DEFINITION Sequence 2870 from Patent WO02052044.
ACCESSION AX516672
VERSION AX516672.1 GI:23564627

KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 2870 04-JUL-2002;
Riken (JP)

FEATURES
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Location/Qualifiers

/organism="Homo sapiens"
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ORIGIN

Query Match 9.2%; Score 21.6; DB 2; Length 41;
Best Local Similarity 71.1%; Pred. No. 4e+05;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 141 TGCTCCCTCTCTCTCTGCGCATGATTTTAAATTCC 178
2 TGCTCTTCTTCACTCTCCRCATGATTTGAGGCCCC 39

RESULT 3
AX518841 41 bp DNA linear PAT 05-OCT-2002

LOCUS AX518841
DEFINITION Sequence 5039 from Patent WO02052044.
ACCESSION AX518841
VERSION AX518841.1 GI:23568709

KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS Nakamura,Y., Sekine,A., Iida,A. and Saito,S.
TITLE Detection of genetic polymorphisms
JOURNAL Patent: WO 02052044-A 5039 04-JUL-2002;
Riken (JP)

FEATURES
source 1..41
Location/Qualifiers

/organism="Homo sapiens"
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ORIGIN

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Best Local Similarity 71.1%; Pred. No. 4e+05;
Matches 27; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

Qy 141 TGCTCCCTCTCTCTGCGCATGATTTTAAATTCC 178

Db 2 TGCTCTTCTTCATCTTCRCATGATTTGAGGCCCC 39

RESULT 4
BD190591/c 49 bp DNA linear PAT 17-JUL-2003

LOCUS BD190591/c
DEFINITION Bioreactive alleosteric polynucleotide.
ACCESSION BD190591
VERSION BD190591.1 GI:33000330

KEYWORDS
SOURCE Rattus

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae.

REFERENCE
AUTHORS Braker,R.R.
TITLE Bioreactive alleosteric polynucleotide
JOURNAL Patent: JP 2002514913-A 9 21-MAY-2002;
ALLE UNIVERSITY

COMMENT
PN JP 2002514913-A/9
PD 21-MAY-2002
PF 18-DEC-1997 JP 1998528049
PR 19-DEC-1996 US 60/033684, 08-AUG-1997 US 60/055039 PI

RONALD R BRAKER
PC C12N15/09, C12M1/00, C12Q1/68, C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key

FEATURES
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Location/Qualifiers

/organism="Rattus"
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ORIGIN

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Best Local Similarity 76.5%; Pred. No. 5.1e+05;
Matches 26; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 100 CCCCTCTCATCTCTCTGCTCCCACTCTTGATG 133
35 CCGCTGTCACTCTCCAGCTCCTACCTTGCGCTG 2

RESULT 5
AR405844/c 49 bp DNA linear PAT 18-DEC-2003

LOCUS AR405844/c
DEFINITION Sequence 9 from patent US 6630306.
ACCESSION AR405844
VERSION AR405844.1 GI:40154863

KEYWORDS
SOURCE Unknown.

ORGANISM
Unclassified.

REFERENCE
AUTHORS Breaker,R.R.
TITLE Bioreactive alleosteric polynucleotides
JOURNAL Patent: US 6630306-A 9 07-OCT-2003;
Yale University; New Haven, CT

FEATURES
source 1..49
Location/Qualifiers

/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 9.0%; Score 21.2; DB 2; Length 49;
Best Local Similarity 76.5%; Pred. No. 5.1e+05;
Matches 26; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 100 CCCCTCTCATCTCTGCTCCCACTCTTGATG 133

Db 35 CCGCTGTCTCATCTCCAGCTCTACCTTGCTG 2

RESULT 6
LOCUS 141116 43 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 19 from patent US 5624803.
ACCESSION 141116
VERSION 141116.1 GI:2081706
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 43)
AUTHORS Moonberg,S.B. and Hunt,C.Anthony.
TITLE In vivo oligonucleotide generator, and methods of testing the binding affinity of triplex forming oligonucleotides derived therefrom

JOURNAL
FEATURES Patent: US 5624803-A 19 29-APR-1997;
Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 8.8%; Score 20.8; DB 2; Length 43;
Best Local Similarity 78.1%; Pred. No. 6.9e+05;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 137 CACCTGCTCCCTCTCTCTTGCATGATTT 168
Db 10 CTCCTCTCCACTCTCTCTCTCTGATTT 41

RESULT 7
LOCUS 141117 43 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 20 from patent US 5624803.
ACCESSION 141117
VERSION 141117.1 GI:2081707
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 43)
AUTHORS Noonberg,S.B. and Hunt,C.Anthony.
TITLE In vivo oligonucleotide generator, and methods of testing the binding affinity of triplex forming oligonucleotides derived therefrom

JOURNAL
FEATURES Patent: US 5624803-A 20 29-APR-1997;
Location/Qualifiers
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/organism="unknown"
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ORIGIN
Query Match 8.8%; Score 20.8; DB 2; Length 43;
Best Local Similarity 78.1%; Pred. No. 6.9e+05;
Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 137 CACCTGCTCCCTCTCTCTTGCATGATTT 168
Db 34 CTCCTCTCCACTCTCTCTCTCTGATTT 3

RESULT 8
LOCUS CQ004290 50 bp DNA linear PAT 16-JAN-2004
DEFINITION Sequence 2330 from Patent WO0147944.
ACCESSION CQ004290
VERSION CQ004290.1 GI:41010922
KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Shimkete,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0147944-A 2930 05-JUL-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
misc_feature 25..26
/note="Nucleotide deleted between bases 25 and 26
Accession number cg43976335"

ORIGIN
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Best Local Similarity 69.2%; Pred. No. 1.3e+06;
Matches 27; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 88 GAAGAGCTGGCCCTCTCATTTCTGCTCCACATC 126
Db 12 GAAGGCTATGCTCTCCACTCCCTCTCTACCACTC 50

RESULT 9
LOCUS AR681155 50 bp DNA linear PAT 12-SEP-2005
DEFINITION Sequence 584 from patent US 6905827.
ACCESSION AR681155
VERSION AR681155.1 GI:74462925
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 50)
AUTHORS Wohlgemuth,J., Fry,K., Woodward,R. and Ly,N.
TITLE Methods and compositions for diagnosing or monitoring auto immune and chronic inflammatory diseases
JOURNAL Patent: US 6905827-A 584 14-JUN-2005;
Expression Diagnostics, Inc.; So. San Francisco, CA
FEATURES Location/Qualifiers
1..50
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 8.3%; Score 19.6; DB 2; Length 50;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 28; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 71 GTGAGAGCTGTGTTTGAAGAAGCTGGCCCTCTCATTC 112
Db 6 GTGAGCCCTGTGTTTAAATATCTGTTCACATGTCATTC 47

RESULT 10
LOCUS AR147108 45 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 210 from patent US 6221361.
ACCESSION AR147108
VERSION AR147108.1 GI:15110911
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 45)
AUTHORS Cochran,M.D. and Junker,D.E.
TITLE Recombinant swinepox virus

JOURNAL Patent: US 6221361-A 210 24-APR-2001;
FEATURES Location/Qualifiers

source

1..45

/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 8.2%; Score 19.4; DB 2; Length 45;
Best Local Similarity 70.3%; Pred. No. 1.8e+06;
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 199 ATGCTAACGCCATGCTTCTTGTCTGCAAACT 235

DB 41 ATGATTACGCCAAGCTTCTAGTACAGTATTACGACT 5

RESULT 11
LOCUS AR158296 45 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 210 from patent US 6251403.
ACCESSION AR158296
VERSION AR158296.1 GI:16220314
KEYWORDS

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE 1 (bases 1 to 45)
AUTHORS Cochran,M.D. and Junker,D.E.

TITLE Recombinant swinepox virus

JOURNAL Patent: US 6251403-A 210 26-JUN-2001;
FEATURES Location/Qualifiers

source

1..45

/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 8.2%; Score 19.4; DB 2; Length 45;
Best Local Similarity 70.3%; Pred. No. 1.8e+06;
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 199 ATGCTAACGCCATGCTTCTTGTCTGCAAACT 235

DB 41 ATGATTACGCCAAGCTTCTAGTACAGTATTACGACT 5

RESULT 12
LOCUS AR267871 45 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 210 from patent US 6497882.
ACCESSION AR267871
VERSION AR267871.1 GI:29697996
KEYWORDS

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE 1 (bases 1 to 45)
AUTHORS Cochran,M.D. and Junker,D.E.

TITLE Recombinant swinepox virus

JOURNAL Patent: US 6497882-A 210 24-DEC-2002;
FEATURES Location/Qualifiers

source

1..45

/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 8.2%; Score 19.4; DB 2; Length 45;
Best Local Similarity 70.3%; Pred. No. 1.8e+06;
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 199 ATGCTAACGCCATGCTTCTTGTCTGCAAACT 235

DB 41 ATGATTACGCCAAGCTTCTAGTACAGTATTACGACT 5

RESULT 13
LOCUS AR365906 45 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 210 from patent US 6328975.
ACCESSION AR365906
VERSION AR365906.1 GI:34598093
KEYWORDS

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE 1 (bases 1 to 45)
AUTHORS Cochran,M.D. and Junker,D.E.

TITLE Recombinant swinepox virus

JOURNAL Patent: US 6328975-A 210 11-DEC-2001;
FEATURES Location/Qualifiers

source

1..45

/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 8.2%; Score 19.4; DB 2; Length 45;
Best Local Similarity 70.3%; Pred. No. 1.8e+06;
Matches 26; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 199 ATGCTAACGCCATGCTTCTTGTCTGCAAACT 235

DB 41 ATGATTACGCCAAGCTTCTAGTACAGTATTACGACT 5

RESULT 14
LOCUS AR684817 50 bp DNA linear PAT 12-SEP-2005
DEFINITION Sequence 4246 from patent US 6905827.
ACCESSION AR684817
VERSION AR684817.1 GI:74466587
KEYWORDS

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE 1 (bases 1 to 50)
AUTHORS Wolgemuth,J., Fry,K., Woodward,R. and Ly,N.

TITLE Methods and compositions for diagnosing or monitoring auto immune

JOURNAL and chronic inflammatory diseases

Patent: US 6905827-A 4246 14-JUN-2005;
FEATURES Expression Diagnostics, Inc.; So. San Francisco, CA

Location/Qualifiers

source

1..50

/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 8.2%; Score 19.4; DB 2; Length 50;
Best Local Similarity 79.3%; Pred. No. 1.8e+06;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 104 CTCTCATCTCTCTGCTCCCATCTTTCGAT 132

DB 22 CCTCATCTCTCTGCTCACTCTCTTCAT 50

RESULT 15
LOCUS AR684983 50 bp DNA linear PAT 12-SEP-2005
DEFINITION Sequence 4412 from patent US 6905827.
ACCESSION AR684983
VERSION AR684983.1 GI:74466753
KEYWORDS

SOURCE

Unknown.

ORGANISM

Unclassified.

source

Unknown.

REFERENCE 1 (bases 1 to 50)
 AUTHORS Wohlgemuth, J., Fry, K., Woodward, R. and Ly, N.
 TITLE Methods and compositions for diagnosing or monitoring auto immune
 and chronic inflammatory diseases
 JOURNAL Patent: US 6905827-A 4412 14-JUN-2005;
 Expression Diagnostics, Inc.; So. San Francisco, CA
 FEATURES
 source 1. .50
 Location/Qualifiers
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Query Match 8.2%; Score 19.4; DB 2; Length 50;
 Best Local Similarity 79.3%; Pred. No. 1.8e+06;
 Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 110 TTCTCTGCTCCCACTTGCATGAGACA 138
 |||||
 Db 13 TTATCTGCTTCCACTATGACATGAATCA 41

Search completed: October 1, 2006, 01:33:51
 Job time : 1977.39 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using bw model

Run on: October 2, 2006, 15:36:33 ; Search time 0.001 Seconds
(without alignments)
696.476 Million cell updates/sec

Title: US-10-642-946-6_1967-2208

Perfect score: 242

Sequence: 1 ttctccagcagcagcagcga.....ccaactaaactgattccac 242

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 79 seqs, 1439 residues

Total number of hits satisfying chosen parameters: 158

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 79 summaries

Database : 1891.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18.2	7.5	25	1	US-09-396-196G-18892
2	15.8	6.5	21	1	US-09-657-472-768
3	15.6	6.4	22	1	US-10-085-612A-23
4	15.2	6.3	20	1	US-09-216-393B-262
5	15.2	6.3	21	1	US-09-526-193A-240
6	15	6.2	18	1	US-08-846-020A-32
7	15	6.2	18	1	US-09-617-871-32
8	15	6.2	21	1	US-09-657-472-1850
9	14.2	5.9	20	1	US-09-021-701-404
10	14.2	5.9	20	1	US-09-021-701-405
11	14.2	5.9	20	1	US-09-487-368A-97
12	14.2	5.9	20	1	US-09-628-644A-97
13	14.2	5.9	20	1	US-09-628-644A-97
14	14.2	5.9	20	1	US-09-198-452A-3809
15	14.2	5.9	20	1	US-09-198-452A-6637
16	14.2	5.9	20	1	US-09-495-714C-138
17	14.2	5.9	20	1	US-09-601-844B-23
18	14.2	5.9	20	1	US-09-726-345-2
19	14.2	5.9	20	1	US-10-209-405-27
20	14.2	5.9	20	1	US-10-209-405-27
21	13.8	5.7	19	1	US-09-422-978-6418
22	13.4	5.5	17	1	US-10-156-306B-6888
23	13.4	5.5	17	1	US-10-156-306B-6888
24	13.4	5.5	18	1	US-08-632-673B-9
25	13.4	5.5	18	1	US-09-357-072-17
26	13.4	5.5	18	1	US-08-652-265-17
27	13.4	5.5	18	1	US-08-834-497A-17
28	13.4	5.5	18	1	US-09-503-444A-17
29	13.4	5.5	18	1	US-09-341-700A-294
30	13.4	5.5	19	1	US-08-546-130A-24
31	13.4	5.5	19	1	US-08-680-395-32
32	13.4	5.5	19	1	US-09-066-641-31
33	13.4	5.5	19	1	US-08-892-695-45

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

34	13.2	5.5	18	1	US-08-572-126-3	Sequence 3, Appl
35	13.2	5.5	18	1	US-09-003-199-17	Sequence 17, Appl
36	13.2	5.5	18	1	US-09-003-199-19	Sequence 19, Appl
37	13.2	5.5	18	1	US-08-757-023A-3	Sequence 3, Appl
38	13.2	5.5	18	1	US-08-651-155B-1	Sequence 1, Appl
39	13.2	5.5	18	1	US-09-321-797-3	Sequence 3, Appl
40	13.2	5.5	18	1	US-10-006-937-7	Sequence 7, Appl
41	13.2	5.5	18	1	US-09-194-036B-1	Sequence 1, Appl
42	13	5.4	17	1	US-09-866-108A-9217	Sequence 9217, Ap
43	13	5.4	17	1	US-09-866-108A-9218	Sequence 9218, Ap
44	13	5.4	17	1	US-09-866-108A-9219	Sequence 9219, Ap
45	13	5.4	17	1	US-09-866-108A-9220	Sequence 9220, Ap
46	13	5.4	17	1	US-09-866-108A-9221	Sequence 9221, Ap
47	12.8	5.3	17	1	US-08-584-040-5754	Sequence 5754, Ap
48	12.8	5.3	17	1	US-09-474-432B-580	Sequence 580, Ap
49	12.8	5.3	17	1	US-09-371-772B-2633	Sequence 2633, Ap
50	12.8	5.3	17	1	US-09-476-387-579	Sequence 579, Ap
51	12.8	5.3	17	1	US-09-866-108A-119	Sequence 119, Ap
52	12.8	5.3	17	1	US-09-866-108A-120	Sequence 120, Ap
53	12.8	5.3	17	1	US-09-866-108A-1319	Sequence 1319, Ap
54	12.8	5.3	17	1	US-09-866-108A-1320	Sequence 1320, Ap
55	12.8	5.3	17	1	US-09-866-108A-5889	Sequence 5889, Ap
56	12.8	5.3	17	1	US-09-866-108A-5890	Sequence 5890, Ap
57	12.8	5.3	17	1	US-09-866-108A-7503	Sequence 7503, Ap
58	12.8	5.3	17	1	US-09-866-108A-7504	Sequence 7504, Ap
59	12.8	5.3	17	1	US-09-685-664B-2633	Sequence 2633, Ap
60	12.8	5.3	17	1	US-10-156-306B-4949	Sequence 4949, Ap
61	12.8	5.3	17	1	US-10-138-674B-2633	Sequence 2633, Ap
62	12.8	5.3	18	1	US-09-344-520-29	Sequence 127, Appl
63	12.8	5.3	18	1	US-09-280-409-127	Sequence 42, Appl
64	12.8	5.3	18	1	US-09-474-922A-42	Sequence 33, Appl
65	12.8	5.3	18	1	US-09-475-947A-333	Sequence 406, Appl
66	12.8	5.3	18	1	US-09-544-388B-406	Sequence 406, Appl
67	12.8	5.3	18	1	US-09-543-771B-406	Sequence 691, Appl
68	12.4	5.1	17	1	US-08-758-306-691	Sequence 1715, Ap
69	12.4	5.1	17	1	US-08-292-620A-1715	Sequence 1918, Ap
70	12.4	5.1	17	1	US-08-292-620A-1918	Sequence 1918, Ap
71	12.4	5.1	17	1	US-08-292-620A-1918	Sequence 1918, Ap
72	12.4	5.1	17	1	US-09-071-845-1715	Sequence 1918, Ap
73	12.4	5.1	17	1	US-09-071-845-1918	Sequence 1918, Ap
74	12.4	5.1	17	1	US-09-071-845-1952	Sequence 49, Appl
75	12.4	5.1	17	1	US-08-834-497A-49	Sequence 50, Appl
76	12.4	5.1	17	1	US-08-834-497A-50	Sequence 5891, Ap
77	12.4	5.1	17	1	US-08-866-108A-5891	Sequence 5892, Ap
78	12.4	5.1	17	1	US-08-866-108A-5892	Sequence 5820, Ap
79	12.4	5.1	17	1	US-10-156-306B-5820	

ALIGNMENTS

RESULT 1
US-09-396-196G-18892
Sequence 18892, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mitmann
APPLICANT: David Mack
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09396, 196G
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100, 678
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 18892
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-396-196G-18892

Query Match 7.5%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 4.7;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTCTCCAGCAGCAGCTGATTT 23
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Db 3 TTCTCCAGAACAGCTATGATTT 25

RESULT 2

US-09-657-472-768/c
Sequence 768, Application US/09657472
Patent No. 6727063
GENERAL INFORMATION:
APPLICANT: Lander, Eric S.
APPLICANT: Cargill, Michele
APPLICANT: Ireland, James S.
APPLICANT: Bolik, Stacey
APPLICANT: Daley, George O.
APPLICANT: McCarthy, Jeanette J.
TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
FILE REFERENCE: 2825.1027-001
CURRENT FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: US 60/153,357
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 60/220,947
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: US 60/225,724
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2551
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 768
LENGTH: 21
TYPE: DNA
ORGANISM: Homo sapiens
US-09-657-472-768

Query Match 6.5%; Score 15.8; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 10;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 CTCGACGACGACTGATTT 23
|||
Db 21 CTCGACGACGACTGCTAT 1

RESULT 3

US-10-085-612A-23
Sequence 23, Application US/10085612A
Patent No. 6929812
GENERAL INFORMATION:
APPLICANT: Guida, Marco
APPLICANT: Hall, Jeff
APPLICANT: Petros, William
APPLICANT: Colvin, Oliver
APPLICANT: Vredenburgh, James
APPLICANT: Marks, Jeffrey
TITLE OF INVENTION: METHODS FOR EVALUATING THE ABILITY TO METABOLIZE PHARMACEUTICALS
FILE REFERENCE: DNA-5-C1
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: US/10/085,612A
PRIOR FILING DATE: 1998-08-31/144,367
PRIOR APPLICATION NUMBER: 60/271,630
PRIOR FILING DATE: 2001-02-26
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.2
SEQ ID NO 23
LENGTH: 22
TYPE: DNA
ORGANISM: Homo sapiens

US-10-085-612A-23

Query Match 6.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 56 CTGCTGCCTCAGCTGCTTTCC 77
|||
Db 1 CTCGAGCCCACTCTTCTCC 22

RESULT 4

US-09-216-393B-262
Sequence 262, Application US/09216393B
Patent No. 6514694
GENERAL INFORMATION:
APPLICANT: Milhausen, Michael James
TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF
FILE REFERENCE: TX-1-C2
CURRENT FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: US/09/216,393B
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 366
SOFTWARE: PatentIn version 3.1
SEQ ID NO 262
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic Primer
US-09-216-393B-262

Query Match 6.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 12;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 189 TGTCTGTAGGTTGTTAG 208
|||
Db 1 TGGCTGTTGGGTTGTTG 20

RESULT 5

US-09-526-193A-240
Sequence 240, Application US/09526193A
Patent No. 6617122
GENERAL INFORMATION:
APPLICANT: Hayden, Michael R.
APPLICANT: Brooks-Wilson, Angela R.
APPLICANT: Pimstone, Simon N.
TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING
FILE REFERENCE: 50110/002005
CURRENT FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: 60/124,702
PRIOR FILING DATE: 1999-03-15
PRIOR APPLICATION NUMBER: 60/138,048
PRIOR FILING DATE: 1999-06-08
PRIOR APPLICATION NUMBER: 60/139,600
PRIOR FILING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: 60/151,977
PRIOR FILING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 287
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 240
LENGTH: 21
TYPE: DNA
ORGANISM: Homo sapiens
US-09-526-193A-240

Query Match 6.3%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 13;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 58 GGTGCTCAGCGCTTTCC 77
|||
Db 1 GAGCTCAGCGCTTTCC 20

RESULT 6

US-08-846-020A-32
; Sequence 32, Application US/08846020A
; Patent No. 6090547

; GENERAL INFORMATION:
; APPLICANT: Drazen M.D., Jeffrey M.
; APPLICANT: In M.D., Kwang-Ho
; APPLICANT: Asano M.D., Koichiro
; APPLICANT: Beier, David
; APPLICANT: Grobholz, James
; TITLE OF INVENTION: 5-Lipoxygenase Gene Sequence
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHOATE, HALL & STEWART
; STREET: 53 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2891

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,020A
; FILING DATE:
; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:
; NAME: Jarrell Ph.D., Brenda H.
; REGISTRATION NUMBER: 39,223
; REFERENCE/DOCKET NUMBER: 0092662-0012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-5000
; TELEFAX: (617) 248 4000

; INFORMATION FOR SEQ ID NO: 32:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer"
; IMMEDIATE SOURCE:
; CLONE: Exon 9 sense primer
; US-08-846-020A-32

Query Match 6.2%; Score 15; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 12;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 47 CCTCCCGAGCTGCTG 61
|||
Db 2 CCTCCCGAGCTGCTG 16

RESULT 7

US-09-617-871-32
; Sequence 32, Application US/09617871
; Patent No. 6355434

; GENERAL INFORMATION:
; APPLICANT: Drazen M.D., Jeffrey M.
; APPLICANT: In M.D., Kwang-Ho
; APPLICANT: Asano M.D., Koichiro
; APPLICANT: Beier, David

; APPLICANT: Grobholz, James
; TITLE OF INVENTION: 5-Lipoxygenase Gene Sequence
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHOATE, HALL & STEWART
; STREET: 53 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2891

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/617,871
; FILING DATE:
; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/846,020
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jarrell Ph.D., Brenda H.
; REGISTRATION NUMBER: 39,223
; REFERENCE/DOCKET NUMBER: 0092662-0012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-5000
; TELEFAX: (617) 248 4000
; INFORMATION FOR SEQ ID NO: 32:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer"
; IMMEDIATE SOURCE:
; CLONE: Exon 9 sense primer
; US-09-617-871-32

Query Match 6.2%; Score 15; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 12;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 47 CCTCCCGAGCTGCTG 61
|||
Db 2 CCTCCCGAGCTGCTG 16

RESULT 8

US-09-657-472-1850/C
; Sequence 1850, Application US/09657472
; Patent No. 6727063

; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Bolik, Stacey
; APPLICANT: Daley, George O.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
; FILE REFERENCE: 2825.1027-001
; CURRENT APPLICATION NUMBER: US/09/657,472
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/153,357
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 60/220,947
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: US 60/225,724
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2551

SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1850
LENGTH: 21
TYPE: DNA
ORGANISM: Homo sapiens
US-09-657-472-1850

Query Match 6.2%; Score 15; DB 1; Length 21;
Best Local Similarity 88.2%; Pred. No. 14;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 53 CAGCTGCTGCTCCTTGA 69
DB 21 TCCTTTCATCTCTTGA 20

RESULT 9
US-09-021-701-404
Sequence 404, Application US/09021701
Patent No. 6251588

GENERAL INFORMATION:
APPLICANT: Shannon, Karen W.
APPLICANT: Wolber, Paul K.
APPLICANT: Delenstear, Glenda C.
APPLICANT: Webb, Peter G.
APPLICANT: Kincaid, Robert H.
TITLE OF INVENTION: Methods for evaluating oligonucleotide
TITLE OF INVENTION: probe sequences
NUMBER OF SEQUENCES: 1165
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard Company M/S 20
STREET: 3000 Hanover Street
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/021,701
FILING DATE: 10-FEB-1998

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Choi, Wendy A.

REGISTRATION NUMBER: 36,697
REFERENCE/DOCKET NUMBER: 10971464-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-236-2386
TELEFAX: 650-852-8063

INFORMATION FOR SEQ ID NO: 404:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-021-701-404

Query Match 5.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 18;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 124 TCCTTTCATCTCTTGA 142
DB 2 TCCTTTCATCTCTTGA 20

RESULT 10

US-09-021-701-405
Sequence 405, Application US/09021701
Patent No. 6251588

GENERAL INFORMATION:
APPLICANT: Shannon, Karen W.
APPLICANT: Wolber, Paul K.
APPLICANT: Delenstear, Glenda C.
APPLICANT: Webb, Peter G.
APPLICANT: Kincaid, Robert H.
TITLE OF INVENTION: Methods for evaluating oligonucleotide
TITLE OF INVENTION: probe sequences
NUMBER OF SEQUENCES: 1165
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard Company M/S 20
STREET: 3000 Hanover Street
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/021,701
FILING DATE: 10-FEB-1998

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Choi, Wendy A.
REGISTRATION NUMBER: 36,697
REFERENCE/DOCKET NUMBER: 10971464-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-236-2386
TELEFAX: 650-852-8063

INFORMATION FOR SEQ ID NO: 405:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-021-701-405

Query Match 5.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 18;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 124 TCCTTTCATCTCTTGA 142
DB 1 TCCTTTCATCTCTTGA 19

RESULT 11
US-09-487-368A-97
Sequence 97, Application US/09487368A
Patent No. 6261840

GENERAL INFORMATION:
APPLICANT: Lex M. Cowseart
APPLICANT: Jacqueline Wyatt

TITLE OF INVENTION: ANTISENSE MODULATION OF PTPLB EXPRESSION
FILE REFERENCE: RTS-0093
CURRENT APPLICATION NUMBER: US/09/487,368A
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 240

SEQ ID NO 97
LENGTH: 20
TYPE: DNA

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide

US-09-487-368A-97

Query Match

Best Local Similarity 5.9%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY

44 CCACCTCCCGAGCTGCTGC 62
1 CAACCTCCCGAGCTGCTGC 19

RESULT 12

US-09-629-644A-97

Sequence 97, Application US/09629644A

Patent No. 6492345

GENERAL INFORMATION:

APPLICANT: Lex M. Cowbert

APPLICANT: Jacqueline Wyatt

APPLICANT: Susan M. Freiler

APPLICANT: Brett P. Monia

APPLICANT: Madeline M. Butler

TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION

FILE REFERENCE: ISPH-0478

CURRENT APPLICATION NUMBER: US/09/629,644A

PRIORITY FILING DATE: 2000-07-31

PRIORITY FILING DATE: 2000-01-18

NUMBER OF SEQ ID NOS: 242

SEQ ID NO 97

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

US-09-629-644A-97

Query Match

Best Local Similarity 5.9%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY

44 CCACCTCCCGAGCTGCTGC 62
1 CAACCTCCCGAGCTGCTGC 19

RESULT 13

US-09-629-644A-97

Sequence 97, Application US/09629644A

Patent No. 6602857

GENERAL INFORMATION:

APPLICANT: Lex M. Cowbert

APPLICANT: Jacqueline Wyatt

APPLICANT: Susan M. Freiler

APPLICANT: Brett P. Monia

APPLICANT: Madeline M. Butler

TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION

FILE REFERENCE: ISPH-0478

CURRENT APPLICATION NUMBER: US/09/629,644A

PRIORITY FILING DATE: 2000-07-31

PRIORITY FILING DATE: 2000-01-18

NUMBER OF SEQ ID NOS: 242

SEQ ID NO 97

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

US-09-629-644A-97

Query Match 5.9%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 18;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY

44 CCACCTCCCGAGCTGCTGC 62
1 CAACCTCCCGAGCTGCTGC 19

RESULT 14

US-09-198-452A-3809/C

Sequence 3809, Application US/09198452A

Patent No. 6559294

GENERAL INFORMATION:

APPLICANT: Griffois, R.

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention

TITLE OF INVENTION: and treatment of infection

FILE REFERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A

PRIORITY FILING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 3809

LENGTH: 20

TYPE: DNA

ORGANISM: Chlamydia pneumoniae

US-09-198-452A-3809

Query Match

Best Local Similarity 5.9%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY

122 CCTGTTCCATCTCTTG 140
19 CCTGTTCCATCTCTTG 1

RESULT 15

US-09-198-452A-6637/C

Sequence 6637, Application US/09198452A

Patent No. 6559294

GENERAL INFORMATION:

APPLICANT: Griffois, R.

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention

TITLE OF INVENTION: and treatment of infection

FILE REFERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A

PRIORITY FILING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 6637

LENGTH: 20

TYPE: DNA

ORGANISM: Chlamydia pneumoniae

US-09-198-452A-6637

Query Match

Best Local Similarity 5.9%; Score 14.2; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY

58 GCTGCTCACCTGCTTTC 76
20 GCTGCTCACCTGCTTTC 2

RESULT 16

US-09-495-714C-138/C

Sequence 138, Application US/09495714C

Patent No. 6670465

GENERAL INFORMATION:

APPLICANT: University Technologies International Inc.

TITLE OF INVENTION: RETINAL CALCINUM CHANNEL (ALPHA) 1F-SUBUNIT GENE

FILE REFERENCE: 4549.4 (formerly 45074.6)

CURRENT APPLICATION NUMBER: US/09/495,714C

Query Match 5.9%; Score 14.2; DB 1; Length 20;

```
; CURRENT FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 138
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-495-714C-138
```

```
Query Match          5.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 18;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      7 AGCAGACGACTGATTTG 25
        |||||
Db      19 ACCACATCTCTGATTTG 1
```

```
RESULT 17
US-09-601-844B-23/C
; Sequence 23, Application US/09601844B
; Patent No. 6716621
; GENERAL INFORMATION:
; APPLICANT: Shimizu, No. 6716621yoshi
; APPLICANT: Mizuno, Yoshihumi
; TITLE OF INVENTION: Isolated DNA or Gene Responsible for Parkinson's Disease
; FILE REFERENCE: 0652 210000
; CURRENT APPLICATION NUMBER: US/09/601,844B
; CURRENT FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: PCT/J99/00545
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(10)
; OTHER INFORMATION: Exon 8
; FEATURE:
; NAME/KEY: Intron
; LOCATION: (11)..(20)
; OTHER INFORMATION: Intron
US-09-601-844B-23
```

```
Query Match          5.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 18;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      58 GCTGCTTCACCTGCTTTTC 76
        |||||
Db      20 GCTCCTCCTGCTGCTTTC 2
```

```
RESULT 18
US-09-726-345-2
; Sequence 2, Application US/09726345
; Patent No. 6855521
; GENERAL INFORMATION:
; APPLICANT: Naval Medical Research Center
; TITLE OF INVENTION: Serotype and Dengue Group Specific Fluorescent Probe-Based PCR
; TITLE OF INVENTION: (TagMan) Assays Against the Respective C and NS5 Genomic and 3'
; FILE REFERENCE: NC 82197
; CURRENT APPLICATION NUMBER: US/09/726,345
; CURRENT FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
```

```
; ORGANISM: Dengue virus
US-09-726-345-2
```

```
Query Match          5.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 18;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      28 CACCTGAGCTGAGCTCCA 46
        |||||
Db      1 CACCTGAGCTGAGCTCCA 19
```

```
RESULT 19
US-10-209-405-27/C
; Sequence 27, Application US/10209405
; Patent No. 6906186
; GENERAL INFORMATION:
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freiler
; TITLE OF INVENTION: ANTISENSE MODULATION OF POLO-LIKE KINASE EXPRESSION
; FILE REFERENCE: RTS-0131
; CURRENT APPLICATION NUMBER: US/10/209,405
; CURRENT FILING DATE: 2002-07-30
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-209-405-27
```

```
Query Match          5.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 18;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      148 TCTCAGCTGAGCTGAACA 166
        |||||
Db      20 TCTCCTGAGCTGCACA 2
```

```
RESULT 20
US-10-209-405-96
; Sequence 96, Application US/10209405
; Patent No. 6906186
; GENERAL INFORMATION:
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freiler
; TITLE OF INVENTION: ANTISENSE MODULATION OF POLO-LIKE KINASE EXPRESSION
; FILE REFERENCE: RTS-0131
; CURRENT APPLICATION NUMBER: US/10/209,405
; CURRENT FILING DATE: 2002-07-30
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 96
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-209-405-96
```

```
Query Match          5.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 18;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      148 TCTCAGCTGAGCTGAACA 166
        |||||
Db      1 TCTCCTGAGCTGCACA 19
```

```
RESULT 21
US-09-422-978-6418/C
; Sequence 6418, Application US/09422978
; Patent No. 6537751
```

```

; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Bialistic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6418
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer 99-11313 for SEQ 2484,
US-09-422-978-6418

Query Match          5.7%  Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%  Pred. No. 20;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      165 CAGACGACCTGTTAG 181
DB      17 CATACGACCTGATTAG 1

RESULT 22
US-10-156-306B-6888/C
; Sequence 6888, Application US/10156306B
; Patent No. 7022828
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: MCSW19gen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306B
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8014
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6888
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306B-6888

Query Match          5.5%  Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%  Pred. No. 21;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      38 GGAGCTCCACCTCCC 52
DB      16 GGTCCTCCACCTCCC 2

RESULT 23
US-10-156-306B-6889/C
; Sequence 6889, Application US/10156306B
; Patent No. 7022828
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: MCSW19gen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBHB01-664-A (400/050)
```

```

; CURRENT APPLICATION NUMBER: US/10/156,306B
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8014
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6889
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306B-6889

Query Match          5.5%  Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%  Pred. No. 21;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      38 GGAGCTCCACCTCCC 52
DB      15 GGTCCTCCACCTCCC 1

RESULT 24
US-08-632-673B-9/C
; Sequence 9, Application US/08632673B
; Patent No. 5712098
; GENERAL INFORMATION:
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Gnikte, Andreas
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Ruddy, David
; APPLICANT: Wolff, Roger K.
; APPLICANT: Feder, John N.
; TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS
; TITLE OF INVENTION: DIAGNOSTIC MARKERS AND DIAGNOSTIC METHODS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESSES:
; ADDRESS: TOWNSEND AND TOWNSEND AND CREM LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/632,673B
; FILING DATE: 16-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 017957-000410
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2420
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEetical: NO
; ANTI-SENSE: NO
US-08-632-673B-9

Query Match          5.5%  Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%  Pred. No. 22;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      35 CTGGAGCTCCACCT 49
```



```
Db      17  CTGGGTCTCCACCT 3
RESULT 25
US-09-357-072-17/c
; Sequence 17, Application US/09357072
; Patent No. 6015712
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monla
; APPLICANT: Brenda F. Baker
; APPLICANT: Hong Zhang
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF FADD EXPRESSION
; FILE REFERENCE: RTS-0027
; CURRENT APPLICATION NUMBER: US/09/357,072
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 17
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-357-072-17

Query Match      5.5%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 22;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      162  GACGAGACGACCTG 176
Db      18  GAGCAGACGACCTG 4
RESULT 26
US-08-652-265-17/c
; Sequence 17, Application US/08652265
; Patent No. 6025130
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gairke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Hereditary Hemochromatosis Gene
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,265
; FILING DATE: 23-MAY-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 17957-000500
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 17:
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```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 1
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "N = 5'-phosphorylated cytosine
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 18
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "N = 3'-digoxigenin-conjugated
; OTHER INFORMATION: guanine (G-dig)"
US-08-652-265-17

Query Match      5.5%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 22;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      35  CTGGGAGCTCCACCT 49
Db      17  CTGGGTCTCCACCT 3
RESULT 27
US-08-834-497A-17/c
; Sequence 17, Application US/08834497A
; Patent No. 6140305
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; APPLICANT: Drayna, Dennis T.
; APPLICANT: Feder, John N.
; APPLICANT: Gairke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Penile & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,497A
; FILING DATE: 04-APR-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/652,265
; FILING DATE: 23-MAY-1996
; CLASSIFICATION: 514
; APPLICATION NUMBER: US 08/632,673
; FILING DATE: 16-APR-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,912
; FILING DATE: 04-APR-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
```

REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0056-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: modified_base
LOCATION: 1
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "N = 5'-phosphorylated cytosine
OTHER INFORMATION:
FEATURE:
NAME/KEY: modified_base
LOCATION: 18
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "N = 3'-digoxigenin-conjugated
OTHER INFORMATION: guanine (G-dig)"
US-08-834-497A-17

Query Match 5.5%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 22;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 35 CTGGAGCTCCACCT 49
DB 17 CTGGGTGCTCCACCT 3

RESULT 28
US-09-503-444A-17/C
Sequence 17, Application US/09503444A
Patent No. 6228594
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edwards LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect Version 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,444A
FILING DATE: 14-Feb-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/552,265
FILING DATE: 23-May-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/632,673
FILING DATE: 16-Apr-1996
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/630,912
FILING DATE: 04-Apr-1996
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0088-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: modified_base
LOCATION: 1
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "N = 5'-phosphorylated cytosine
OTHER INFORMATION:
FEATURE:
NAME/KEY: modified_base
LOCATION: 18
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "N = 3'-digoxigenin-conjugated
OTHER INFORMATION: guanine (G-dig)"
US-09-503-444A-17

Query Match 5.5%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 22;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 35 CTGGAGCTCCACCT 49
DB 17 CTGGGTGCTCCACCT 3

RESULT 29
US-09-341-700A-294/C
Sequence 294, Application US/09341700A
Patent No. 6972171
GENERAL INFORMATION:
APPLICANT: Schlingensiepen, Karl-Hermann
APPLICANT: Brysch, Wolfgang
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
FILE REFERENCE: 10496/P63763USO
CURRENT APPLICATION NUMBER: US/09/341,700A
CURRENT FILING DATE: 1999-09-24
PRIOR APPLICATION NUMBER: PCT/EP98/00497
PRIOR FILING DATE: 1998-01-30
PRIOR APPLICATION NUMBER: EP 97 101 531.8
PRIOR FILING DATE: 1997-01-31
NUMBER OF SEQ ID NOS: 1764
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 294
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: antisense oligonucleotide
US-09-341-700A-294

Query Match 5.5%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 22;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 52 CCAGCTGCTGCCTCA 66
DB 15 CCAGCTGCTGCCCA 1

```
RESULT 30
US-08-546-130A-24/C
Sequence 24, Application US/08546130A
Patent No. 5801021
GENERAL INFORMATION:
APPLICANT: Gray, Joe W.
APPLICANT: Collins, Colin
APPLICANT: Pinkel, Daniel
APPLICANT: Kallioniemi, Olli-Pekka
APPLICANT: Tanner, Minna M.
TITLE OF INVENTION: Amplifications of Chromosomal Region
NUMBER OF SEQUENCES: 20q13 as a Prognostic Indicator in Breast Cancer
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/546,130A
FILING DATE: 20-OCT-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-051630US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-546-130A-24

Query Match 5.5%, Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 23;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTCTCCAGCAGACA 15
DB 16 TTCTCCAGCAGACA 2

RESULT 31
US-08-680-395-32/C
Sequence 32, Application US/08680395
Patent No. 5892010
GENERAL INFORMATION:
APPLICANT: Gray, Joe W.
APPLICANT: Collins, Colin
APPLICANT: Hwang, Soo-in
APPLICANT: Godfrey, Tony
APPLICANT: Kowdel, David
APPLICANT: Rommens, Johanna
TITLE OF INVENTION: Genes from the 20q13 Amplicon and Their
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
```

```

CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/680,395
FILING DATE: 15-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Baetian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02307O-068900US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-680-395-32

Query Match 5.5%, Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 23;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTCTCCAGCAGACA 15
DB 16 TTCTCCAGCAGACA 2

RESULT 32
US-09-066-641-31/C
Sequence 31, Application US/0906641
Patent No. 6268184
GENERAL INFORMATION:
APPLICANT: GRAY, JOE W
APPLICANT: COLLINS, COLIN
APPLICANT: PINKEL, DANIEL
APPLICANT: KALLIONIEMI, OLLI-PEKKA
APPLICANT: TANNER, MINNA M
TITLE OF INVENTION: AMPLIFICATIONS OF CHROMOSOMAL REGION 20Q13 AS A
FILE REFERENCE: 2500.136US2 20Q13
CURRENT APPLICATION NUMBER: US/09/066,641
CURRENT FILING DATE: 1998-04-24
EARLIER APPLICATION NUMBER: 08/546,130
EARLIER FILING DATE: 1995-10-20
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 31
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: reverse
OTHER INFORMATION: primer
US-09-066-641-31

Query Match 5.5%, Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 23;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTCTCCAGCAGACA 15
DB 16 TTCTCCAGCAGACA 2
```

```
RESULT 33
US-08-892-695-45/c
; Sequence 45, Application US/08892695A
; Patent No. 6808878
; GENERAL INFORMATION:
; APPLICANT: Gray, Joe W
; APPLICANT: Collins, Collin
; APPLICANT: Hwang, Soo In
; APPLICANT: Godfrey, Tony
; APPLICANT: Kowel, David
; APPLICANT: Rommens, Johanna
; TITLE OF INVENTION: GENES FROM THE 20Q13 AMPLICON AND THEIR USES
; FILE REFERENCE: 2500.124US3
; CURRENT APPLICATION NUMBER: US/08/892,695A
; CURRENT FILING DATE: 1997-07-15
; EARLIER APPLICATION NUMBER: 08/785,532
; EARLIER FILING DATE: 1997-01-17
; EARLIER APPLICATION NUMBER: 08/731,499
; EARLIER FILING DATE: 1996-10-16
; EARLIER APPLICATION NUMBER: 08/660,395
; EARLIER FILING DATE: 1996-07-15
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Backward
; OTHER INFORMATION: Primer
US-08-892-695-45

Query Match          5.5%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 23;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TTCTCCAGCAGCA 15
DB      16 TTCTCCAGCAGCA 2

RESULT 34
US-08-572-126-3
; Sequence 3, Application US/08572126
; Patent No. 5851806
; GENERAL INFORMATION:
; APPLICANT: Kovesdi, Imre
; APPLICANT: Brough, Douglas E.
; APPLICANT: Mcvey, Duncan L.
; APPLICANT: Bruder, Joseph T.
; APPLICANT: Lizanova, Alena
; TITLE OF INVENTION: COMPLEMENTARY ADENO VIRAL VECTOR SYSTEMS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/572,126
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
```

```
APPLICATION NUMBER: US 08/258416
; FILING DATE: 10-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kilya Jr., John
; REGISTRATION NUMBER: 30763
; REFERENCE/DOCKET NUMBER: 74273
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
US-08-572-126-3

Query Match          5.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 24;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      58 GCTGCTCAGCCTGCTTT 75
DB      1 GCCGCTCATCCGCTTT 18

RESULT 35
US-09-003-199-17
; Sequence 17, Application US/09003199
; Patent No. 5985616
; GENERAL INFORMATION:
; APPLICANT: Parker, Eric M
; APPLICANT: Strader, Catherine D
; APPLICANT: Rudinski, Mark S
; TITLE OF INVENTION: CHIMERIC MAMMALIAN NPV Y5 RECEPTORS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: NJ
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Apple Macintosh
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/003,199
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Thampoe, Immac J.
; REGISTRATION NUMBER: 36,322
; REFERENCE/DOCKET NUMBER: C06775
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 298-5061
; TELEFAX: (908) 298-5388
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-003-199-17

Query Match          5.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 24;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

OY 156 GGAGCTGAACAGACGAC 173
|||||
Db 1 GGAGCAAAACGACGAC 18

RESULT 36

US-09-003-199-19
Sequence 19, Application US/09003199
Patent No. 5985616
GENERAL INFORMATION:
APPLICANT: Parker, Eric M
APPLICANT: Strader, Catherine D
APPLICANT: Rudinski, Mark S
TITLE OF INVENTION: CHIMERIC MAMMALIAN NPY Y5 RECEPTORS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STATE: NJ
COUNTRY: USA
ZIP: 07033-0530
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5.3
SOFTWARE: Microsoft Word 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,199
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Thampoe, Immac J.
REGISTRATION NUMBER: 36,322
REFERENCE/DOCKET NUMBER: CU0775
TELEPHONE: (908)298-5061
TELECOMMUNICATION INFORMATION:
TELEFAX: (908)298-5388
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-003-199-19

Query Match 5.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 24;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 156 GGAGCTGAACAGACGAC 173
|||||
Db 1 GGAGCAAAACGACGAC 18

RESULT 37

US-08-757-023A-3
Sequence 3, Application US/08757023A
Patent No. 5994106
GENERAL INFORMATION:
APPLICANT: Kovsedl, Imre
APPLICANT: Brough, Douglas E.
APPLICANT: McVey, Joseph T.
APPLICANT: Bruder, Joseph T.
APPLICANT: Lizanova, Alena
TITLE OF INVENTION: COMPLEMENTARY ADENOVIRAL VECTOR SYSTEMS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydis, Voic & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago

STATE: Illinois
COUNTRY: USA
ZIP: 60601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,023A
FILING DATE: 26-NOV-1996
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: 514
APPLICATION NUMBER: US 08/258416
FILING DATE: 10-JUN-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 74273
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
US-08-757-023A-3

Query Match 5.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 24;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 58 GCTGCTTACCTGCTTT 75
|||||
Db 1 GCCGCTCATCCGCTTT 18

RESULT 38

US-08-651-155B-1
Sequence 1, Application US/08651155B
Patent No. 6365401
GENERAL INFORMATION:
APPLICANT: Mahan Dr., Michael J.
APPLICANT: Conner Mr., Christopher P.
APPLICANT: Hiehof Mr., Douglas M.
TITLE OF INVENTION: METHOD AND PROBES FOR THE IDENTIFICATION
TITLE OF INVENTION: OF MICROBIAL GENES SPECIFICALLY INDUCED DURING HOST
NUMBER OF SEQUENCES: 255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chrisman, Bynum & Johnson, P.C.
STREET: 1900 Fifteenth Street
CITY: Boulder
STATE: CO
COUNTRY: USA
ZIP: 80302
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/651,155B
FILING DATE: 17-MAY-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Peteren Mr., Steven C.
REGISTRATION NUMBER: 36,238
REFERENCE/DOCKET NUMBER: 17060.1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/546-1300
TELEFAX: 303/449-5426
TELEX: ABA1475
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-651-155B-1

Query Match 5.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 24;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 104 CATTGTGCGCCACTAG 121
Db 1 CATTGCGTCCCACTAG 18

RESULT 39
US-09-321-797-3
Sequence 3, Application US/09321797
Patent No. 6482616
GENERAL INFORMATION:
APPLICANT: Koveadl, Imre
Brough, Douglas E.
McVey, Duncan L.
Bruder, Joseph T.
Lizanova, Alena
TITLE OF INVENTION: COMPLEMENTARY ADENOVIRAL VECTOR SYSTEMS
AND CELL LINES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Volt & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/321,797
FILING DATE: 27-May-1999
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/757,023A
FILING DATE: 26-NOV-1996
APPLICATION NUMBER: US 08/258416
FILING DATE: 10-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kilyk Jr., John
REGISTRATION NUMBER: 30763
REFERENCE/DOCKET NUMBER: 74273
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5700
TELEFAX: (312) 616-5700
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (synthetic)
SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-321-797-3

Query Match 5.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 24;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 58 GCTGCTCACCCTGCTTT 75
Db 1 GCCGCTCATCTCGCTTT 18

RESULT 40
US-10-006-937-7
Sequence 7, Application US/1006937
Patent No. 6518047
GENERAL INFORMATION:
APPLICANT: Joniaux, Jean-Luc
APPLICANT: Rauw, Karl
APPLICANT: Thonart, Philippe
APPLICANT: Dauvin, Thierry
TITLE OF INVENTION: ENZYME OR CELL PREPARATION WITH
TITLE OF INVENTION: INDULINASE ACTIVITY
FILE REFERENCE: VANM237.001AUS
CURRENT APPLICATION NUMBER: US/10/006,937
CURRENT FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: EP 00870264.9
PRIOR FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: primer for sequencing
US-10-006-937-7

Query Match 5.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 24;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 TCTCCAGCAGCAGCTG 19
Db 1 TCTCCTGTAAGCACTG 18

RESULT 41
US-09-194-036B-1
Sequence 1, Application US/09194036B
Patent No. 6548246
GENERAL INFORMATION:
APPLICANT: Mahan, Michael J.
Conner, Christopher P.
Hietchoff, Douglas M.
TITLE OF INVENTION: METHOD AND PROBES FOR THE IDENTIFICATION
OF MICROBIAL GENES SPECIFICALLY INDUCED DURING HOST
INFECTION
NUMBER OF SEQUENCES: 255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Mountain View
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/194,036B
FILING DATE: 17-No. 6548246-1998

```
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/08208
; FILING DATE: 1997-05-16
; APPLICATION NUMBER: US 08/651,155
; FILING DATE: 1996-05-17
; ATTORNEY/AGENT INFORMATION:
; NAME: Shantanu Basu
; REGISTRATION NUMBER: 43,318
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5995
; TELEFAX: (650) 494-0792
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: DNA (other)
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-194-0368-1

Query Match          5.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 24;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy          104 CATTGTGCGCCACTAGC 121
Db          1 CATTGGTGCACAGTACG 18

RESULT 42
US-09-866-108A-9217/c
; Sequence 9217, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
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; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9217
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9217

Query Match          5.4%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          31 CTGGCTGGAGCT 43
Db          17 CTGGCTGGAGCT 5

RESULT 43
US-09-866-108A-9218/c
; Sequence 9218, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9218
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9218

Query Match          5.4%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          31 CTGGCTGGAGCT 43
Db          16 CTGGCTGGAGCT 4

RESULT 44
```



```
US-09-866-108A-9219/c
; Sequence 9219, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9219
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9219

Query Match          5.4%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      31 CTGGCTGGGAGCT 43
Db      15 CTGGCTGGGAGCT 3

RESULT 45
US-09-866-108A-9220/c
; Sequence 9220, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
```

```
PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 9220
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-9220

Query Match          5.4%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      31 CTGGCTGGGAGCT 43
Db      14 CTGGCTGGGAGCT 2

RESULT 46
US-09-866-108A-9221/c
; Sequence 9221, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AECOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
```

```

? NUMBER OF SEQ ID NOS: 15755
? SOFTWARE: Acomida Sequence Engineering
? Patent No. 6686188
? SEQ ID NO 9221
? LENGTH: 17
? TYPE: DNA
? ORGANISM: Homo sapiens
? OS-09-866-108A-9221

```

```
Query Match      5.4%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 13; Conservative 0; Mismatches 0; Gaps 0
```

Qy	31	CTGGCTGGAGCT	43
Db	13	CTGGCTGGAGCT	1

RESULT 47
US-08-584

```

Sequence 5754, Application US/08584040
Patent No. 6346398

GENERAL INFORMATION:
APPLICANT: Pavco, Pamela
APPLICANT: McSwigen, James
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OR
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL
GROWTH FACTOR
NUMBER OF SEQUENCES: 8502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Waiburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 5754:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-584-040-5754

Query Match 5.3%, Score 12.8, DB 1, Length 17,
Best Local Similarity 75.0%, Pred. No. 26,
Matches 12, Conservative 2, Indels 0, Gaps 0

```

```
QY      153 CGTGAGCTGAACAGA 168
          ||:|||||:|||||
Db       2  CGUGAUCUGAAAAGA 17
```

RESULT 48
US-09-474-432B-580

```

: Sequence 580, Application US/09474432B
: Patent No. 6528640
:
: GENERAL INFORMATION:
: APPLICANT: Ribozyme Pharmaceuticals, Inc.
: APPLICANT: Belgelman, Leo
: APPLICANT: Burgin, Alex
: APPLICANT: Beaudry, Amber
: APPLICANT: Karpelsky, Alex
: APPLICANT: Adamic, Jasenka
: APPLICANT: Sweedler, David
: APPLICANT: Zinnen, Shawn
: TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleotides
: FILE REFERENCE: MEBH00-831-B (247/276)
: CURRENT APPLICATION NUMBER: US/09/474,432B
: CURRENT FILING DATE: 1999-12-19
: PRIOR APPLICATION NUMBER: US 60/064,866
: PRIOR FILING DATE: 1997-11-05
: PRIOR APPLICATION NUMBER: US 60/084,727
: PRIOR FILING DATE: 1998-04-29
: PRIOR APPLICATION NUMBER: US 09/186,675
: PRIOR FILING DATE: 1998-11-04
: PRIOR APPLICATION NUMBER: US 09/301,511
: PRIOR FILING DATE: 1999-04-28
: NUMBER OF SEQ ID NOS: 1526
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 580
: LENGTH: 17
: TYPE: RNA
: ORGANISM: Homo sapiens
: US-09-474-432B-580

```

Query Match	5.3%	Score 12.8	DB 1	Length 17
Best Local Similarly	68.8%	Pred. No. 26		
Matches 11, Conservative	3	Mismatches 2	Indels 0	Gaps 0

QY 34 GCTGGAGCTCCACT 49
||:|||||:||||:
Db 2 GCUGGGGCUCCUCU 17

RESULT 49
US-09-371-772B-2633

```

: Sequence 2633, Application US/09371772B
: Patent No. 6566127
:
: GENERAL INFORMATION:
:
: APPLICANT: Ribozyme Pharmaceuticals, Inc.
:
: APPLICANT: Pavco, Pam
:
: APPLICANT: McSwiggen, Jim
:
: APPLICANT: Stinchcomb, Dan
:
: APPLICANT: Escobedo, Jaime
:
: TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
:
: TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
:
: FILE REFERENCE: MBHD00, 876-J (237/198)
:
: CURRENT APPLICATION NUMBER: US/09/371, 772B
:
: CURRENT FILING DATE: 1999-08-10
:
: PRIOR APPLICATION NUMBER: US 60/005, 974
:
: PRIOR FILING DATE: 1995-10-26
:
: PRIOR APPLICATION NUMBER: US 08/584, 040
:
: PRIOR FILING DATE: 1996-01-08
:
: NUMBER OF SEQ ID NOS: 14225
:
: SOFTWARE: PatentIn version 3.0
:
: SEQ ID NO 2633
:
: LENGTH: 17
:
: TYPE: RNA
:
: ORGANISM: Mus sp.

```

US-09-371-772B-2633

Query Match 5.3%; Score 12.8; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 26;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 153 CGTGAGCTGACAGCA 168
||:||||:||||:
Db 2 CGUGAGUGGAAACGA 17

RESULT 50

US-09-476-387-579

Sequence 579, Application US/09476387

Patent No. 6617438

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Beigelman, Leo

APPLICANT: Beaudry, Amber

APPLICANT: Karpelesky, Alex

APPLICANT: Adamic, Jasenka Matulic

APPLICANT: Sweedler, Dave

APPLICANT: Zimnen, Shawn

TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleot

FILE REFERENCE: MBH800-831-C (249/073)

CURRENT APPLICATION NUMBER: US/09/476,387

CURRENT FILING DATE: 2001-04-04

PRIOR APPLICATION NUMBER: 09/474,432

PRIOR FILING DATE: 1999-12-29

PRIOR APPLICATION NUMBER: 09/301,511

PRIOR FILING DATE: 1999-04-28

PRIOR APPLICATION NUMBER: 09/186,675

PRIOR FILING DATE: 1998-11-04

PRIOR APPLICATION NUMBER: 60/083,727

PRIOR FILING DATE: 1998-04-29

PRIOR APPLICATION NUMBER: 60/064,866

PRIOR FILING DATE: 1997-11-05

NUMBER OF SEQ ID NOS: 1524

SOFTWARE: PatentIn version 3.0

SEQ ID NO 579

LENGTH: 17

TYPE: RNA

ORGANISM: Homo sapiens

US-09-476-387-579

Query Match 5.3%; Score 12.8; DB 1; Length 17;
Best Local Similarity 68.8%; Pred. No. 26;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 34 GGTGGAGCTCCACT 49
||:||||:||||:
Db 2 GCUGGGGCGCCUCCU 17

RESULT 51

US-09-866-108A-119

Sequence 119, Application US/09866108A

Patent No. 6686188

GENERAL INFORMATION:

APPLICANT: GU, Yizhong

APPLICANT: JI, Yonggang

APPLICANT: PENN, Sharon G.

APPLICANT: HANZEL, David K.

APPLICANT: RANK, David R.

APPLICANT: CHEN, Wensheng

APPLICANT: SHANNON, Mark

TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

FILE REFERENCE: A6OMICA-7

CURRENT APPLICATION NUMBER: US/09/866,108A

CURRENT FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1575
SOFTWARE: A6omica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 119
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108A-119

Query Match 5.3%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 26;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 31 CTGGCTGGAGCTCCA 46
|||:||||:||||:
Db 2 CTGGCAGGAGCTCCA 17

RESULT 52

US-09-866-108A-120

Sequence 120, Application US/09866108A

Patent No. 6686188

GENERAL INFORMATION:

APPLICANT: GU, Yizhong

APPLICANT: JI, Yonggang

APPLICANT: PENN, Sharon G.

APPLICANT: HANZEL, David K.

APPLICANT: RANK, David R.

APPLICANT: CHEN, Wensheng

APPLICANT: SHANNON, Mark

TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE

FILE REFERENCE: A6OMICA-7

CURRENT APPLICATION NUMBER: US/09/866,108A

CURRENT FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

Remaining Prior Application data removed - See File Wrapper or PALM.

```
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 120
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-120
```

```
Query Match      5.3%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 26;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY      31 CTGCGCTGGAGCTTCCA 46
Db      1 CTGCGAGAGAGCTTCCA 16
```

RESULT 53

```
US-09-866-108A-1319/c
; Sequence 1319, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AROMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1319
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-1319
```

```
Query Match      5.3%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 26;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY      63 CTCACCTGCTTTCCA 78
Db      17 CTCACCTGCTTTCCA 2
```

RESULT 54

```
US-09-866-108A-1320/c
; Sequence 1320, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AROMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 1320
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-1320
```

```
Query Match      5.3%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 26;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY      63 CTCACCTGCTTTCCA 78
Db      16 CTCACCTGCTTTCCA 1
```

RESULT 55

```
US-09-866-108A-5889
; Sequence 5889, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AROMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
```

```
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 15755
;; SOFTWARE: Aeomica Sequence Listing Engine
;; Patent No. 6686188
;; SEQ ID NO 5889
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-866-108A-5889
```

```
Query Match      5.3%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 26;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      181 GCCCACCCTGTCTGTT 196
Db      2 GACCACCGTGTCTGTT 17
```

```
RESULT 56
US-09-866-108A-5890
;; Sequence 5890, Application US/09866108A
;; Patent No. 6686188
;; GENERAL INFORMATION:
;; APPLICANT: GU, Yizhong
;; APPLICANT: PENN, Sharon G.
;; APPLICANT: HANZEL, David K.
;; APPLICANT: RANK, David R.
;; APPLICANT: CHEN, Wenheng
;; APPLICANT: SHANNON, Mark
;; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;; FILE REFERENCE: AECOMICA-7
;; CURRENT APPLICATION NUMBER: US/09/866,108A
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
```

```
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 15755
;; SOFTWARE: Aeomica Sequence Listing Engine
;; Patent No. 6686188
;; SEQ ID NO 5890
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-866-108A-5890
```

```
Query Match      5.3%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 26;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      181 GCCCACCCTGTCTGTT 196
Db      1 GACCACCGTGTCTGTT 16
```

```
RESULT 57
US-09-866-108A-7503/C
;; Sequence 7503, Application US/09866108A
;; Patent No. 6686188
;; GENERAL INFORMATION:
;; APPLICANT: GU, Yizhong
;; APPLICANT: PENN, Sharon G.
;; APPLICANT: HANZEL, David K.
;; APPLICANT: RANK, David R.
;; APPLICANT: CHEN, Wenheng
;; APPLICANT: SHANNON, Mark
;; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;; FILE REFERENCE: AECOMICA-7
;; CURRENT APPLICATION NUMBER: US/09/866,108A
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 15755
;; SOFTWARE: Aeomica Sequence Listing Engine
;; Patent No. 6686188
;; SEQ ID NO 7503
;; LENGTH: 17
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-866-108A-7503
```

```
Query Match      5.3%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 26;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      30 CCGGCTGGGAGCTCC 45
Db      17 CCGGCTGTGAGCTCC 2
```

```
RESULT 58
US-09-866-108A-7504/C
; Sequence 7504, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ABOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeonica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7504
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-7504

Query Match          5.3%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 26;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      30 CCTGGCTGGAGCTCC 45
Db      16 CCTGGCTGTCTAGCTCC 1

RESULT 59
US-09-685-664B-2633
; Sequence 2633, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBHB00-876-K (400/021)
; CURRENT APPLICATION NUMBER: US/09/685,664B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
```

```
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: US 09/371,772
; PRIOR FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 8231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2633
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-09-685-664B-2633

Query Match          5.3%; Score 12.8; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 26;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      153 CGTGAGCTTGACAGA 168
Db      2 CGUGAUCUGAAAAGA 17

RESULT 60
US-10-156-306B-4949
; Sequence 4949, Application US/10156306B
; Patent No. 7022828
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MBHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306B
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8014
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4949
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306B-4949

Query Match          5.3%; Score 12.8; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 26;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      64 TCACCTGCTTTTCCAA 79
Db      1 UCACCAAGCUCUCCAA 16

RESULT 61
US-10-138-674B-2633
; Sequence 2633, Application US/10138674B
; Patent No. 7034009
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwigen, James
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674B
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20829
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2633
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-138-674B-2633
```

```
Query Match          5.3%; Score 12.8; DB 1; Length 17;
Best Local Similarity 75.0%; Pred. No. 26;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      153 CGTGAAGCTGAACAGA 168
      |||||
Db      2  CGUGAUCUGAAGAAAGA 17

RESULT 62
US-09-344-520-29/c
; Sequence 29, Application US/09344520
; Patent No. 6037176
; GENERAL INFORMATION:
; APPLICANT: Frank Bennett
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF Integrin beta 3 EXPRESSION
; FILE REFERENCE: RTS-0070
; CURRENT APPLICATION NUMBER: US/09/344,520
; CURRENT FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 29
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-344-520-29

Query Match          5.3%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 28;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      44  CCACCTCCCGACGCTGC 59
      |||||
Db      18  CCACCTGCCAGATGC 3

RESULT 63
US-09-280-409-127/c
; Sequence 127, Application US/09280409
; Patent No. 6107092
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: C. Frank Bennett
; APPLICANT: Bert W. O'Malley
; TITLE OF INVENTION: ANTISENSE MODULATION OF SRA EXPRESSION
; FILE REFERENCE: RTS-0048
; CURRENT APPLICATION NUMBER: US/09/280,409
; CURRENT FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 146
; SEQ ID NO 127
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-280-409-127

Query Match          5.3%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 28;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      36  TGGGAGCTCCACCTCC 51
      |||||
Db      18  TGGGAGCTCCACCTCC 3

RESULT 64
US-09-474-922A-42/c
; Sequence 42, Application US/09474922A
; Patent No. 6187586

GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; APPLICANT: Richard A. Roth
; TITLE OF INVENTION: ANTISENSE MODULATION OF Akt-3 EXPRESSION
; FILE REFERENCE: RTS-0036
; CURRENT APPLICATION NUMBER: US/09/474,922A
; CURRENT FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 42
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-474-922A-42

Query Match          5.3%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 28;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      204 TCTAGGCTGTATCAGA 219
      |||||
Db      17  TCCAGGCTGTATCAGA 2

RESULT 65
US-09-475-947A-333
; Sequence 333, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTS0667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 333
; LENGTH: 18
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-333

Query Match          5.3%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 28;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      50  CCCGAGCTGCTGCTC 65
      |||||
Db      3  CCCGAGCTGCTGCTC 18

RESULT 66
US-09-544-398B-406/c
; Sequence 406, Application US/09544398B
; Patent No. 6770461
; GENERAL INFORMATION:
; APPLICANT: Camilli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-013
; CURRENT APPLICATION NUMBER: US/09/544,398B
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
```


; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 406
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-544-398B-406

Query Match 5.3%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 28;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TTCTCAGACAGCAGC 16
Db 16 TTCCCACACAGCAGC 1

RESULT 67
US-09-543-771B-406/c
; Sequence 406, Application US/09543771B
; Patent No. 6780609
; GENERAL INFORMATION:
; APPLICANT: Carulli, John P.
; APPLICANT: Little, Randall D.
; APPLICANT: Recker, Robert R.
; APPLICANT: Johnson, Mark L.
; TITLE OF INVENTION: High bone mass gene of 11q13.3
; FILE REFERENCE: 032796-014
; CURRENT APPLICATION NUMBER: US/09/543, 771B
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 641
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 406
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-543-771B-406

Query Match 5.3%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 28;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 TTCTCAGACAGCAGC 16
Db 16 TTCCCACACAGCAGC 1

RESULT 68
US-08-758-306-691/c
; Sequence 691, Application US/08758306
; Patent No. 5807743
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: McSwigen, James A.
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE
; TITLE OF INVENTION: TREATMENT OF DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH
; TITLE OF INVENTION: INTERLEUKIN-2 RECEPTOR
; TITLE OF INVENTION: GAMMA-CHAIN EXPRESSION
; NUMBER OF SEQUENCES: 1379
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California

; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/758,306
; FILING DATE: December 3, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wartburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 212/132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 691:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-758-306-691

Query Match 5.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 133 TCTCTTGAGAGCAGC 146
Db 17 TCTCTTGAGAGCAGC 4

RESULT 69
US-08-292-620A-1715
; Sequence 1715, Application US/08292620A
; Patent No. 5837542
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwigen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620A
; FILING DATE: August 17, 1994

CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1715:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-1715

Query Match 5.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 78.6%; Pred. No. 30;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 44 CCACCTCCCGACT 57
DB 3 CCACCTCCCGACT 16

RESULT 70
US-08-292-620A-1918
Sequence 1918, Application US/08292620A
Patent No. 5837542
GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849

FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1918:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-292-620A-1918

Query Match 5.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 78.6%; Pred. No. 30;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 44 CCACCTCCCGACT 57
DB 3 CCACCTCCCGACT 16

RESULT 71
US-08-292-620A-1952
Sequence 1952, Application US/08292620A
Patent No. 5837542
GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwiggen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620A
FILING DATE: August 17, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600

```

; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1952:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-292-620A-1952

Query Match          5.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 78.6%; Pred. No. 30;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy      44 CCACCTCCCGAGCT 57
Db      3 CCACCTCCCGAGCT 16

RESULT 72
; Sequence 1715, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1715:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

```

```

; TOPOLOGY: linear
;
US-09-071-845-1715

Query Match          5.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 78.6%; Pred. No. 30;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy      44 CCACCTCCCGAGCT 57
Db      3 CCACCTCCCGAGCT 16

RESULT 73
; Sequence 1918, Application US/09071845
; Patent No. 6132967
; GENERAL INFORMATION:
; APPLICANT: Susan Grimm
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James McSwiggen
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF
; TITLE OF INVENTION: INTRACELLULAR ADHESION
; TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
; NUMBER OF SEQUENCES: 2390
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,845
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,620
; FILING DATE: August 17, 1994
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/149
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1918:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-071-845-1918

Query Match          5.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 78.6%; Pred. No. 30;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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OY 44 CCACCTCCCGACT 57
Db 3 CCACCTCCCGACT 16

RESULT 74

US-09-071-845-1952
Sequence 1952, Application US/09071845
Patent No. 6132967
GENERAL INFORMATION:
APPLICANT: Susan Grimm
APPLICANT: Dan T. Stinchcomb
APPLICANT: James McSwigen
APPLICANT: Sean Sullivan
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: RIBOZYME TREATMENT OF
TITLE OF INVENTION: DISEASES OR CONDITIONS
TITLE OF INVENTION: RELATED TO LEVELS OF
TITLE OF INVENTION: INTRACELLULAR ADHESION
TITLE OF INVENTION: MOLECULE-1 (I-CAM-1)
NUMBER OF SEQUENCES: 2390
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,845
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/292,620
FILING DATE: August 17, 1994
APPLICATION NUMBER: 08/008,895
FILING DATE: January 19, 1993
APPLICATION NUMBER: 07/989,849
FILING DATE: December 7, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Wardburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/149
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1952:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-071-845-1952

Query Match 5.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 78.6%; Pred. No. 30;
Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 44 CCACCTCCCGACT 57
Db 3 CCACCTCCCGACT 16

RESULT 75

US-08-834-497A-49

Sequence 49, Application US/08834497A
Patent No. 6140305
GENERAL INFORMATION:

APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.
APPLICANT: Feder, John N.
APPLICANT: Gritke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,497A
FILING DATE: 04-APR-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
CLASSIFICATION: 514
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0056-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-834-497A-49

Query Match 5.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 36 TGGAGCTCCGACT 49
Db 1 TGGAGCTCCGACT 14

RESULT 76

US-08-834-497A-50
Sequence 50, Application US/08834497A
Patent No. 6140305
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
APPLICANT: Drayna, Dennis T.

```

; APPLICANT: Feder, John N.
; APPLICANT: Guirke, Andreas
; APPLICANT: Ruddy, David
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolf, Roger K.
; TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,497A
; FILING DATE: 04-APR-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/652,265
; FILING DATE: 23-MAY-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/632,673
; FILING DATE: 16-APR-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,912
; FILING DATE: 04-APR-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0056-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-834-497A-50

Query Match 5.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 TGGAGCTCCACCT 49
Db 1 TGGGTGCTCCACT 14

RESULT 77
US-09-866-108A-5891
; Sequence 5891, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
```

```

; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 5891
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-866-108A-5891

Query Match 5.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 183 CCACCGTGTCTGT 196
Db 2 CCACCGTGTCTGT 15

RESULT 78
US-09-866-108A-5892
; Sequence 5892, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
```

; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Acemica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 5892
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-5892

Query Match 5.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 183 CCACCGTCTCTGTT 196
Db 1 CCACCGTCTGTT 14

RESULT 79
US-10-156-306B-5820/C
; Sequence 5820, Application US/10156306B
; Patent No. 7022828
; GENERAL INFORMATION:

; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306B
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8014
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5820
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306B-5820

Query Match 5.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 39 GAGCTCCACCTCCC 52
Db 17 GTGCTCCACCTCCC 4

Search completed: October 2, 2006, 15:36:33
Job time : 0.001 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 2, 2006, 15:44:33 ; Search time 0.001 Seconds
(without alignments)
585.156 Million cell updates/sec

Title: US-10-642-946-6_1967-2208

Perfect score: 242
Sequence: 1 ttcccgcagcacagcaccgga.....ccaactaaactgattccac 242

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 58 seqs, 1209 residues

Total number of hits satisfying chosen parameters: 116

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 58 summaries

Database : ngsdb1.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18.6	7.7	25	1	127B probe for det
2	18.4	7.6	24	1	Parkinson syndrome
3	18.2	7.5	26	1	Microorganism tran
4	17.2	7.1	24	1	REC-1 primer used
5	16.4	6.8	19	1	Microsatellite mar
6	16.2	6.7	21	1	Human gene single
7	16.2	6.7	22	1	Human G-protein co
8	16.2	6.7	22	1	Human GPCR9 revers
9	16.2	6.7	22	1	PCR related rever
10	16.2	6.7	22	1	NOV85 PCR primer,
11	16.2	6.7	22	1	DNA detection exte
12	16.2	6.7	23	1	DNA target sequenc
13	15.8	6.5	19	1	Intestinal epithel
14	15.8	6.5	21	1	ENPP3 target oligo
15	15.8	6.5	21	1	ENPP3 siRNA antisense
16	15.8	6.5	21	1	ENPP3 siRNA antisense
17	15.8	6.5	21	1	ENPP3 target oligo
18	15.6	6.4	22	1	Human promoter -14
19	15.6	6.4	22	1	Expression system
20	15.4	6.3	18	1	Human SRC-3 antisense
21	15.4	6.3	20	1	Primer for RT-PCR
22	15.2	6.3	20	1	T. gondii immunoge
23	15.2	6.3	20	1	T. gondii immunoge
24	15.2	6.3	20	1	Chimeric phosphoro
25	15.2	6.3	21	1	Human ABC1 gene in
26	15.2	6.3	21	1	NF-kappa-B inhibit
27	15.2	6.3	21	1	Human MAP kinase 8
28	15.2	6.3	21	1	ADPW72412
29	15.2	6.3	21	1	ADPW72414
30	15.2	6.3	21	1	AAVC03076
31	15.2	6.3	21	1	AAVC03076
32	15.2	6.3	18	1	ADJ95475
33	14.8	6.1	18	1	AEI10387

N. Gmelig

ALIGNMENTS

RESULT 1	34	14.8	6.1	20	1	ADG31596	PCR primer used to
AEB90482	35	14.8	6.1	20	1	ADP78946	Chimeric phosphoro
ID AEB90482 standard; DNA; 25 BP.	36	14.8	6.1	20	1	ADP78939	Chimeric phosphoro
AC AEB90482;	37	14.8	6.1	20	1	ADP81801	Human MD-1 RP105-a
XX	38	14.8	6.1	20	1	ADP81821	Human MD-1 RP105-a
XX	39	14.8	6.1	20	1	ADP70686	Solanum glycosylas
XX	40	14.8	6.1	20	1	ADZ47085	Human phosphodiast
XX	41	14.8	6.1	20	1	ADZ47045	Human phosphodiast
XX	42	14.8	6.1	20	1	ADZ47045	Human phosphodiast
XX	43	14.8	6.1	21	1	AAV25273	Skin permeabilizat
XX	44	14.8	6.1	21	1	AAV77769	Primer F2 for H. py
XX	45	14.8	6.1	21	1	ADH77769	Human Alstrom's sy
XX	46	14.8	6.1	21	1	ADH77769	Human Alstrom's sy
XX	47	14.8	6.1	21	1	ADH77769	Human Alstrom's sy
XX	48	14.8	6.1	21	1	ADH77769	Human Alstrom's sy
XX	49	14.8	6.1	21	1	ADH77769	Human Alstrom's sy
XX	50	14.8	6.1	21	1	ADH77769	Human Alstrom's sy
XX	51	14.8	6.1	21	1	ADH77769	Human Alstrom's sy
XX	52	14.8	6.1	21	1	ADH77769	Human Alstrom's sy
XX	53	14.8	6.1	21	1	ADH77769	Human Alstrom's sy
XX	54	14.8	6.1	21	1	ADH77769	Human Alstrom's sy
XX	55	14.4	6.0	20	1	AAA66531	Dog genomic marker
XX	56	14.4	6.0	20	1	AAA66531	Dog genomic marker
XX	57	14.4	6.0	20	1	ADP10727	Set 1 left PCR pri
XX	58	14.4	6.0	20	1	ADX81409	Melanoma associate

The present invention relates to degenerative joint diseases, such as osteoarthritis and new compositions, devices and methods based on unique profiles of gene expression associated with osteoarthritis. Specifically claimed is a combination (A) comprising polynucleotide molecules (I), where (I) are differentially expressed in an osteoarthritic or in a pre-osteoarthritic subject compared to expression in subjects which are not osteoarthritic or pre-osteoarthritic. Also given is a method of detecting (M) differential expression of nucleic acids in a sample; detecting (M2)

CC differential expression of polypeptides; measuring (M3) the effect of a
 CC test compound on the expression of one or more genes differentially
 CC expressed in osteoarthritis; diagnosing or prognosticating (M4)
 CC osteoarthritis by measuring the production of transcription or
 CC translation products of one or more genes comprising any of SEQ ID NOs 1-
 CC 1558 in a sample from the subject; a kit for detecting osteoarthritis by
 CC oligonucleotides of at least 10 consecutive bases comprising any of SEQ
 CC ID NOs 1-1558 or their fragments; and modulating (M5) osteoarthritis-
 CC arthritis associated gene expression in a cell by administering a
 CC compound that affects the expression of at least one gene comprising a
 CC sequence selected from SEQ ID NOs 1-1558. In M5 the compound is a vitamin
 CC (preferably 1 alpha,25-dihydroxy vitamin D3 or 24R,25-dihydroxyvitamin
 CC D3), mineral, nutraceutical, small molecule pharmaceutical, protein,
 CC polypeptide, nucleic acid, fatty acid (preferably eicosapentaenoic acid
 CC or arachidonic acid) or polysaccharide (glucosamine or chondroitin
 CC sulfate). The present sequence is 127B probe for detection of an
 CC osteoarthritis-related gene.

CC
 XX Sequence 25 BP; 3 A; 13 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 7.7%; Score 18.6; DB 1; Length 25;

Best Local Similarity 84.0%; Pred. No. 7.3;

Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 43 TCACCTCCCGAGCTGCTGCTCAC 67
 DB 1 TCTATCTCCCGAGCTGCTGCTCAC 25

RESULT 2
 ABL40677
 ID ABL40677 standard; DNA; 24 BP.

XX ABL40677;

XX 17-JUN-2002 (first entry)

XX Parkinson syndrome associated protein 13.31 cDNA RT-PCR primer 1.

XX Parkinson syndrome associated protein 13.31 human; anti-Parkinson;
 KM cerebral cortex function disorder; gene therapy; RT-PCR; primer; ss.

XX Homo sapiens.

XX CNJ328042-A.

XX 26-DEC-2001.

XX 14-JUN-2000; 2000CN-00116476.

XX 14-JUN-2000; 2000CN-00116476.

XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.

XX Mao Y; Xie Y;

XX WPI; 2002-242316/30.

XX Polypeptide-human Parkinson syndrome associated protein 13.31 and
 PT polynucleotide encoding it.

XX Example 2; Page 18 (Disclosure); 34pp; Chinese.

XX The invention relates to a novel human Parkinson syndrome associated
 CC protein 13.31. The protein can be expressed by standard DNA
 CC recombination. The Parkinson syndrome associated protein 13.31 and
 CC encoding polynucleotides are useful for treating diseases such as
 CC cerebral cortex function disorder. The present sequence represents the
 CC human Parkinson syndrome associated protein 13.31 cDNA isolating RT-PCR
 CC primer

XX Sequence 24 BP; 3 A; 11 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 7.6%; Score 18.4; DB 1; Length 24;
 Best Local Similarity 95.0%; Pred. No. 8;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 44 CCACCTCCCGAGCTGCTGCC 63
 DB 5 CCACCTCCCGAGCTGCTGCC 24

RESULT 3

ADO23704
 ID ADO23704 standard; DNA; 26 BP.

XX ADO23704;

XX 15-JUL-2004 (first entry)

XX Microorganism transformation/DNA preparation-related PCR primer - SEQ 49.

XX microorganism transformation; DNA fragment preparation; PCR; primer; ss.

XX Unidentified.

XX JP2004129654-A.

XX 30-APR-2004.

XX 10-SEP-2003; 2003JP-00317927.

XX 19-SEP-2002; 2002JP-00273747.

XX (MITU) MITSUBISHI CHEM CORP.

XX WPI; 2004-433769/41.

XX Preparing DNA fragment from microorganism transformation, by preparing
 PT DNA units which have structure for connecting DNA fragment for homologous
 PT recombination, connecting DNA units with DNA fragment, and producing DNA
 PT fragment.

XX Example 2; SEQ ID NO 49; 27pp; Japanese.

XX The invention relates to a novel method for preparing a DNA fragment from
 CC a microorganism transformation. The method comprises preparing DNA units
 CC which have a structure enabling them to connect DNA fragments for
 CC homologous recombination, connecting these DNA units with a DNA fragment
 CC and producing a DNA fragment. The current sequence is that of a PCR
 CC primer of the invention which is related to microorganism
 CC transformation/DNA fragment preparation.

XX Sequence 26 BP; 5 A; 9 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 7.5%; Score 18.2; DB 1; Length 26;

Best Local Similarity 87.0%; Pred. No. 7.8; 3; Indels 0; Gaps 0;

QY 129 TCACCTCTTGGAGCAGCTCTC 151
 DB 4 TCACCTCTTGGAGCAGCTCTC 26

RESULT 4

AD31117/c
 ID AD31117 standard; DNA; 24 BP.

XX AD31117;

XX 21-AUG-2002 (first entry)

XX RFC-1 primer used in production of heterozygous mutant RFC mouse.

XX Reduced folate carrier; rfc; genetic modification; animal model; cancer;
 KM neural tube defect; Parkinson's disease; Alzheimer's disease;

XX	cardiovascular disease; stroke; cleft palate; mouse; PCR primer; ss.
XX	
OS	Mus musculus.
XX	
PN	WO200224868-A2.
XX	
PD	28-MAR-2002.
XX	
PF	24-SEP-2001; 2001WO-US029966.
XX	
PR	22-SEP-2000; 2000US-0234853P.
XX	
PA	(ROOS-) ROOSEVELT INST ELEANOR.
XX	(OKLA-) OKLAHOMA MEDICAL RES FOUND.
PA	(UTWO-) UNIV WESTERN ONTARIO.
XX	
PI	Patereson D, Brennan MB, Hochgeschwender U, Flintoff WP;
PI	Sadlish H, Underhill TM, Williams FMR;
XX	
DR	WPI; 2002-416280/44.
XX	
PT	Novel genetically modified non-human animal useful as model for defective
PT	folate transport comprises genetic modification resulting in decreased
PT	expression and/or biological activity of endogenous reduced folate
PT	carrier gene.
XX	
PS	Example 1; Page 32; 69pp; English.
XX	
CC	The invention relates to genetically modified non-human animal comprising
CC	modification in at least one allele of endogenous reduced folate carrier
CC	(rfc) gene in the animal, where genetic modification results in reduction
CC	in endogenous RFC expression or biological activity in animal. The non-
CC	human animal optionally is further modified by introduction into genome,
CC	a nucleic acid sequence encoding biologically active human RFC. The
CC	modified animal of the invention is useful for evaluating anti-folate
CC	compounds for treating cancer, for studying the molecular and biochemical
CC	events associated with folate transport and for identifying compounds
CC	useful for treating conditions associated with defective folate
CC	transport. Furthermore, a compound which binds to RFC with a higher
CC	affinity than the affinity of folate for human RFC may be useful for
CC	treating a neural tube defect, Parkinson's disease, Alzheimer's disease,
CC	cardiovascular disease, stroke, cleft palate. In the genetically modified
CC	animal, expression level of human rfc can be varied, as desired, to
CC	provide a model system for testing various compounds. The present
CC	sequence is a PCR primer used in production of heterozygous mutant RFC
CC	mouse
XX	
SO	Sequence 24 BP; 5 A; 7 C; 6 G; 6 T; 0 U; 0 Other;
XX	
Query Match	7.1%; Score 17.2; DB 1; Length 24;
Best Local Similarity	86.4%; Pred. No. 11;
Matches 19; Conservative	0; Mismatches 3; Indels 0; Gaps 0
Oy	14 CACTGGATTGGTCACCTGGC 35
DB	23 CAATGGATGCTGTCACCTGGC 2
XX	
RESULT 5	
ID	ADR46326
XX	ADR46326 standard; DNA; 19 BP.
XX	
AC	ADR46326;
XX	
DT	18-NOV-2004 (first entry)
DE	Microsatellite marker PCR primer 19-R.
XX	
XX	Microsatellite marker; Bex4; ovarian cancer; cytostatic; human;
KW	gene therapy; tumour suppressor protein; PCR; primer; ss.
XX	
CS	Homo sapiens.
XX	

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PN MO2004072269-A2.
XX
XX 26-AUG-2004.
XX
XX 12-FEB-2004; 2004MO-US004413.
XX
XX 12-FEB-2003; 2003US-0446877P.
XX
XX (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
XX
XX Shridhar V, Chien J;
XX
XX WPI; 2004-625868/60.
XX
XX New vector comprising an isolated nucleic acid encoding a Bex4
XX polypeptide, useful for treating cancer, e.g. ovarian, cervical, brain,
XX breast, prostate or liver cancer.
XX
XX Example 1; SEQ ID NO 39; 47pp; English.
XX
XX The present sequence is that of PCR primer 19-R for a microsatellite
XX marker within BAC CTR-B-470f8 on 19q14.3. PCR was performed on genomic
XX DNA from 15 early-stage and 18 late-stage ovarian tumours of different
XX histologies. LOH analysis was performed to identify potential candidate
XX tumour suppressor genes involved in ovarian carcinogenesis. The invention
XX is based on the discovery that Bex4 (or proapoptotic protein on
XX chromosome X (PAPX)) ADR46296 is down-regulated in cancer cells. Claimed
XX methods for killing a tumour cell comprise administering to the tumour
XX cell a nucleic acid that encodes a Bex4 polypeptide, a vector comprising
XX the nucleic acid, or a Bex4 polypeptide. The tumour cell is selected from
XX an ovarian, cervical, brain, breast, prostate and hepatic tumour cell.
XX Detection of a lower than normal level of Bex4 polypeptide in cells in a
XX sample indicates a predisposition of an individual to develop cancer. A
XX claimed method for detecting cancer recurrence in an individual diagnosed
XX with and treated for cancer comprises measuring the level of bex4 gene
XX methylation. The presence of hypermethylation indicates recurrence. The
XX cancer is ovarian, breast, prostate, cervical, brain or liver cancer.
XX
XX Sequence 19 BP; 2 A; 8 C; 4 G; 5 T; 0 U; 0 Other;
XX
XX
XX Query Match 6.8%; Score 16.4; DB 1; Length 19;
XX Best Local Similarity 94.4%; Pred. No. 17;
XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0.
XX
XX QY 52 CCAGCTGCTGCCTCACCT 69
XX ||||||| |||||
XX 1 CCAGCTGCTGCCTCACCT 18
XX
XX DB
XX
XX RESULT 6
XX ID AAF96003/C
XX AC AAF96003 standard; DNA; 21 BP.
XX
XX AAFA96003;
XX
XX 18-NOV-2004 (revised)
XX DT 06-JUN-2001 (first entry)
XX
XX DE Human gene single nucleotide polymorphism #764.
XX
XX XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
XX polymorphism; vascular disease; coronary artery disease; forensics;
XX myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
XX pulmonary embolism; paternity test; ds.
XX
XX OS Homo sapiens.
XX OS Unidentified.
XX
XX Key Location/Qualifiers
XX FT 11
XX FT /*tag= a
XX FT /standard_name= "Single nucleotide polymorphism"
XX

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PN WO200118250-A2.
XX
PD 15-MAR-2001.
XX
PF 07-SEP-2000; 2000WO-US024503.
XX
PR 10-SEP-1999; 99US-0153357P.
PR 26-JUL-2000; 2000US-0220947P.
PR 16-AUG-2000; 2000US-0225724P.
XX
PA (WHEED ) WHITEHEAD INST BIOMEDICAL RES.
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, McCarthy JJ,
DR WPI; 2001-226749/23.
XX
XX
XX Nucleic acids comprising single nucleotide polymorphisms, useful in
PT applications such as forensics, paternity testing, medicine, genetic
PT analysis and phenotype correlations to diseases such as diabetes and
PT atherosclerosis.
XX
PS Example; Page 101; 242pp; English.
XX
CC The present invention provides a method of diagnosing a vascular disease
CC in an individual, involving determining the sequence at various
CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC genes. The sequences at a number of polymorphic sites are also provided
CC in the specification. In particular, the method can be used in the
CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC useful in forensics, paternity testing, genetic analysis and phenotype
CC correlations to diseases. The present sequence is an example of one of
CC the human gene SNPs shown in the specification
CC
CC Revised record issued on 18-NOV-2004 : The variantion feature was
CC incorrectly given a capital V
XX
SQ Sequence 21 BP; 5 A; 4 C; 8 G; 4 T; 0 U; 0 Other;
Query Match 6.7%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 3 CTCGACGACGACTGATTT 23
DB 21 CTCGACGACGACTGCTAT 1
RESULT 7
ID ABB59191 standard; DNA; 22 BP.
XX
AC ABB59191;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human G-protein coupled receptor, reverse primer #113.
XX
KW Human; G-protein coupled receptor; GPCR; cardiomyopathy; atherosclerosis;
KW diabetes; cell signal processing; metabolic pathway modulation; cancer;
KW adenocarcinoma; lymphoma; prostate cancer; uterus cancer; asthma;
KW immune response; neurodegenerative disorder; inflammatory disorder;
KW Crohn's disease; multiple sclerosis; Albright hereditary osteodystrophy;
KW primer; PCR; ss.
XX
OS Homo sapiens.
XX
PN WO200259313-A2.
XX
PD 01-AUG-2002.

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PF 18-DEC-2001; 2001WO-US049394.
XX
PR 18-DEC-2000; 2000US-0256635P.
PR 21-DEC-2000; 2000US-0257876P.
PR 04-JAN-2001; 2001US-0259743P.
PR 10-JAN-2001; 2001US-0260718P.
PR 12-JAN-2001; 2001US-0261498P.
PR 24-JAN-2001; 2001US-0263689P.
PR 08-FEB-2001; 2001US-0267464P.
PR 22-FEB-2001; 2001US-0271021P.
PR 14-MAR-2001; 2001US-0275946P.
PR 23-MAR-2001; 2001US-0278150P.
PR 18-APR-2001; 2001US-0284591P.
PR 23-APR-2001; 2001US-0285718P.
PR 19-JUN-2001; 2001US-0299327P.
PR 16-AUG-2001; 2001US-0312902P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Li L, Ballinger RA, Padigaru M, Kekuda R, Colman SD, Spytek KA;
PI Casman SJ, Vernet CM, Shenoy SG, Guise V, Malvankar UM, Edinger S;
PI Gerlach V, Smitheon G, Stone DJ, Sctore P, MacDougall JR, Gunther E;
PI Peyman JA, Ellerman K, Gangolli EA, Millet I;
XX
DR WPI; 2002-599789/64.
XX
XX New G protein coupled receptor polypeptides and polynucleotides, useful
PT in gene therapy, particularly for treating or preventing cardiomyopathy,
PT atherosclerosis, diabetes, multiple sclerosis, Crohn's disease or cancer
PT in humans.
XX
PS Claim 9; Page 586; 685pp; English.
XX
CC The invention relates to novel isolated G-protein coupled receptor (GPCR)
CC polypeptides and polynucleotides. The GPCR polypeptide, GPCR nucleic acid
CC and antibody are useful for treating, preventing or alleviating a GPCR-
CC associated disorder or a pathological state in a subject, particularly a
CC human. In particular, the disorder is cardiomyopathy, atherosclerosis,
CC diabetes, or a disorder related to cell signal processing and metabolic
CC pathway modulation. The GPCR polypeptide and nucleic acid are also useful
CC for diagnosing the presence of or predisposition to a disease associated
CC with altered levels of GPCR, particularly cancer. The GPCR nucleic acid
CC and polypeptide are especially useful in therapeutic or prophylactic
CC applications for disorders associated with aberrant GPCR expression or
CC activity. The DNA encoding the protein is useful in gene therapy for
CC treating the above conditions. Furthermore, the nucleic acids and
CC polypeptides are useful in treating adenocarcinoma, lymphoma, prostate
CC cancer, uterus cancer, immune response, neurodegenerative disorders,
CC asthma, inflammatory disorders, Crohn's disease, multiple sclerosis or
CC Albritght hereditary osteodystrophy. These are also useful in developing a
CC powerful assay system for functional analysis of various human disorders,
CC as well as in diagnostic applications. ABB58747-ABB59231 represent human
CC GPCR coding sequences, primers and probes of the invention
XX
XX
SQ Sequence 22 BP; 3 A; 9 C; 2 G; 8 T; 0 U; 0 Other;
Query Match 6.7%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 133 TCTCTTTGAGCACCCTCTCAC 153
DB 2 TCTCTTTAGAGCCCTTTTAC 22
RESULT 8
ID ABB89181 standard; DNA; 22 BP.
XX
AC ABB89181;
XX
DT 28-AUG-2002 (first entry)
XX

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DE Human GPCR9 reverse PCR primer SEQ ID NO:121.
 XX
 KW Human; GPCR; GPCRX; G protein-coupled receptor; antiatherosclerotic;
 KW anorectic; antibacterial; fungicide; protozoacide; virocid; analgesic;
 KW cyrostatic; immunomodulator; metabolic; antiasthmatic; antiparkinsonian;
 KW hypertensive; hypotensive; osteopathic; antiinflammatory; anti-HIV;
 KW antifertility; neuroprotective; antiangiinal; cardiant; antileiser;
 KW antiallergic; nootropic; tranquilliser; neuroleptic; antidepressant;
 KW antitumoric; anticonvulsant; haemostatic; immunosuppressive; hepatotropic;
 KW cerebroprotective; dermatological; antiaddictive; gynaecological; cancer;
 KW nephrotropic; gene therapy; vaccine; developmental disease; diabetes;
 KW cardiomyopathy; atherosclerosis; neurodegenerative disorder;
 KW autoimmune disorder; infectious disease; PCR primer; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200226985-A2.
 XX
 PD 04-APR-2002.
 XX
 PF 28-SEP-2001; 2001WO-US030552.
 XX
 XX 28-SEP-2000; 2000US-0236284P.
 PR 28-SEP-2000; 2000US-0236286P.
 PR 03-OCT-2000; 2000US-0237581P.
 PR 06-OCT-2000; 2000US-0238735P.
 PR 16-OCT-2000; 2000US-0240736P.
 PR 05-JAN-2001; 2001US-0260013P.
 PR 08-JAN-2001; 2001US-0260338P.
 PR 17-JAN-2001; 2001US-0262156P.
 PR 18-JAN-2001; 2001US-0262498P.
 PR 19-JAN-2001; 2001US-0263133P.
 PR 24-JAN-2001; 2001US-0263691P.
 PR 02-FEB-2001; 2001US-0266109P.
 PR 26-FEB-2001; 2001US-0271634P.
 PR 27-SEP-2001; 2001US-00965422.
 XX
 XX (CURA-) CURAGEN CORP.
 PA
 PI Spytek KA, Casman S, Padigaru M, Dickson K, Vernet C;
 PI Spaderna SK, Shenoy S, Gerlach V, Ellerman K, Edinger S;
 PI Macdougall JR, Smithson G, Li L, Malanker UM, Taylor S, Gunther E;
 PI Tchernev VT;
 PI
 XX Tchernev VT;
 DR WPI; 2002-499868/53.
 XX
 PS Example 1; Page 198; 213pp; English.
 XX
 CC ABN89112 to ABN89130 encoding the human G protein-coupled receptor
 CC (GPCRX) proteins given in AB891440 to AB891458. GPCRX proteins can have
 CC antiatherosclerotic, anorectic, antibacterial, fungicide, protozoacide,
 CC virocid, analgesic, cyrostatic, immunomodulator, metabolic, hypotensive,
 CC antiasthmatic, antiparkinsonian, hypertensive, osteopathic, hypotensive,
 CC antiinflammatory, antifertility, neuroprotective, antiangiinal,
 CC cardiant, antileiser, antiallergic, nootropic, tranquilliser, neuroleptic,
 CC antidepressant, antitumoric, anticonvulsant, haemostatic, hepatotropic,
 CC immunosuppressive, cerebroprotective, dermatological, antiaddictive,
 CC nephrotropic and gynaecological activities, and can be used in vaccines
 CC and gene therapy. GPCRX proteins and polynucleotides can be used for
 CC treating or preventing a GPCRX-associated disorder such as
 CC cardiomyopathy, atherosclerosis, a disorder related to cell signal
 CC processing and metabolic pathway modulation, in a human. GPCRX proteins
 CC and polynucleotides can also be used in the manufacture of a medicament
 CC for preventing or treating disorders or syndromes including developmental
 CC diseases, cardiomyopathy, atherosclerosis, cancer, neurodegenerative
 CC disorders, autoimmune disorders, infectious diseases and diabetes.
 CC ABN89131 to ABN89187 represent PCR primers and probes used in the

CC exemplification of the present invention
 XX
 SQ Sequence 22 BP; 3 A; 9 C; 2 G; 8 T; 0 U; 0 Other;
 Query Match 6.7%; Score 16.2; DB 1; Length 22;
 Best Local Similarity 85.7%; Pred. No. 16;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 133 TCTCTTTGAGACCTCTTCAC 153
 Db 2 TCTCTTTAGAGCCCTTTTCAC 22
 RESULT 9
 ABT05734
 ID ABT05734 standard; DNA; 22 BP.
 XX
 AC ABT05734;
 XX
 DT 16-OCT-2002 (first entry)
 XX
 DE GPCR related reverse PCR primer SEQ ID No 187.
 XX
 XX Antidiabetic; cyrostatic; anorectic; nootropic; neuroprotective; GPCRX;
 KW antiparkinsonian; cardiant; antiarteriosclerotic; immunosuppressive;
 KW hypotensive; haemostatic; antifertility; antiasthmatic; antiinflammatory;
 KW anti-HIV; G-protein coupled receptor X; cardiomyopathy; atherosclerosis;
 KW diabetes; metabolic disorder; diabetes; obesity; infectious disease;
 KW anorexia; neurodegenerative disorder; Alzheimer's disease; dyslipidaemia;
 KW Parkinson's disorder; immune disorder; haematopoietic disorder; obesity;
 KW congenital syndrome X; wasting disorder; cancer; hypertension; neoplasm;
 KW congenital heart defect; aortic stenosis; subaortic stenosis; lymphoma;
 KW transplantation; adrenoleukodystrophy; congenital adrenal hyperplasia;
 KW prostate cancer; adenocarcinoma; uterus cancer; fertility; haemophilia;
 KW hypercoagulation; idiopathic thrombocytopenic purpura; immunodeficiency;
 KW graft versus host disease; AIDS; bronchial asthma; Crohn's disease;
 KW multiple sclerosis; chromosomal mapping; tissue typing; forensic biology;
 KW gene therapy; transgenic animal; PCR; primer; ss.
 KW
 XX Undentified.
 OS
 XX
 PN WO200246229-A2.
 XX
 PD 13-JUN-2002.
 XX
 PF 05-DEC-2001; 2001WO-US046530.
 XX
 PR 05-DEC-2000; 2000US-0251459P.
 PR 29-DEC-2000; 2000US-0259007P.
 PR 04-DEC-2001; 2001US-00005041.
 XX
 XX (CURA-) CURAGEN CORP.
 PA
 PI Casman SJ, Padigaru M, Burgess CE, Shinkete RA, Spytek KA;
 PI Gilbert JH, Mayotte JE, Baumgartner JC, Mishra V, Vernet CM;
 PI Dickinson KS, Ballinger RA, Wolenc AR;
 PI
 XX WPI; 2002-537559/57.
 XX
 PT Novel isolated G-protein coupled receptor polypeptide, designated NOVX,
 PT useful for treating or preventing in human receptor-associated disorders
 PT e.g. cardiomyopathy, atherosclerosis or diabetes.
 PT
 PS Example 2; Page 226; 264pp; English.
 XX
 CC The invention relates to a novel isolated G-protein coupled receptor X
 CC (GPCRX) polypeptide. The isolated protein, its encoding polynucleotide
 CC and the antibody of the isolated protein is useful for treating or
 CC preventing a GPCRX-associated disorder in a subject, preferably human,
 CC where the disorder is cardiomyopathy, atherosclerosis or diabetes. The
 CC isolated protein, its encoding polynucleotide and the antibody of the
 CC isolated protein is useful for treating or preventing metabolic
 CC disorders, diabetes, obesity, infectious disease, anorexia,

CC neurodegenerative disorder, Alzheimer's disease, Parkinson's disorder,
 CC immune disorders, haemopoietic disorders, and various dyslipidaemias,
 CC metabolic disturbances associated with obesity, the metabolic syndrome X,
 CC wasting disorders associated with chronic diseases, and cancer. The
 CC disorders also include cardiomyopathy, atherosclerosis, hypertension,
 CC congenital heart defects, aortic stenosis, subaortic stenosis,
 CC transplantation, adrenoleukodystrophy, congenital adrenal hyperplasia,
 CC prostate cancer, neoplasm, adenocarcinoma, lymphoma, uterus cancer,
 CC fertility, haemophilia, hypercoagulation, idiopathic thrombocytopenic
 CC purpura, immunodeficiencies, graft versus host disease, AIDS, bronchial
 CC asthma, Crohn's disease, and multiple sclerosis. The isolated protein,
 CC its encoding polynucleotide and the antibody of the isolated protein is
 CC useful in screening assays, detection assays (e.g., chromosomal mapping,
 CC tissue typing, forensic biology). The isolated polynucleotide is useful
 CC in gene therapy, to express the isolated protein, to detect GPCR mRNA or
 CC a genetic lesion in a GPCR gene, and to modulate GPCR activity. The
 CC cell of the invention is useful for producing non-human transgenic
 CC animals. This polynucleotide sequence represents a reverse PCR primer of
 CC a GPCR protein of the invention
 CC
 SQ Sequence 22 BP, 3 A; 9 C; 2 G; 8 T; 0 U; 0 Other;

Query Match 6.7%; Score 16.2; DB 1; Length 22;
 Best Local Similarity 85.7%; Pred. No. 16;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 133 TCTCTTGAGACCTCTCAG 153
 Db 2 TCTCTTGAGACCTCTTCC 22

RESULT 10
 ID ADH49242
 ADH49242 standard; DNA; 22 BP.

AC ADH49242;
 DT 25-MAR-2004 (first entry)
 DE NOV85 PCR primer, SEQ ID 526.

XX Human, NOVA; atherosclerosis; hypertension; obesity; cancer; cytostatic;
 KW hypotensive; antiarteriosclerotic; anorectic; gene therapy; NOV85; PCR;
 KM primer; ss.

XX Homo sapiens.

XX WO200268652-A2.

XX 06-SEP-2002.

XX 26-FEB-2002; 2002WO-US005910.

XX 26-FEB-2001; 2001US-0271646P.
 PR 27-FEB-2001; 2001US-0271840P.
 PR 28-FEB-2001; 2001US-0272404P.
 PR 28-FEB-2001; 2001US-0272405P.
 PR 28-FEB-2001; 2001US-0272410P.
 PR 28-FEB-2001; 2001US-0272414P.
 PR 02-MAR-2001; 2001US-0272787P.
 PR 02-MAR-2001; 2001US-0272922P.
 PR 02-MAR-2001; 2001US-0273048P.
 PR 16-MAR-2001; 2001US-0276401P.
 PR 20-MAR-2001; 2001US-0277324P.
 PR 20-MAR-2001; 2001US-0278609P.
 PR 30-MAR-2001; 2001US-0280039P.
 PR 02-APR-2001; 2001US-0280818P.
 PR 12-APR-2001; 2001US-0283443P.
 PR 23-APR-2001; 2001US-0285754P.
 PR 24-APR-2001; 2001US-0286096P.
 PR 03-MAY-2001; 2001US-0288353P.

PR 17-MAY-2001; 2001US-0291703P.
 PR 31-MAY-2001; 2001US-0294834P.
 PR 20-JUN-2001; 2001US-0296959P.
 PR 21-JUN-2001; 2001US-0299845P.
 PR 05-JUL-2001; 2001US-0303422P.
 PR 13-AUG-2001; 2001US-0311981P.
 PR 16-AUG-2001; 2001US-0312858P.
 PR 17-AUG-2001; 2001US-0313280P.
 PR 29-AUG-2001; 2001US-0315614P.
 PR 17-SEP-2001; 2001US-0322818P.
 PR 25-FEB-2002; 2002US-00322818.

XX (CURA-) CURAGEN CORP.

PI Alsobrook JP, Anderson DM, Ballinger RA, Boldog FL, Burgess CE,
 PI Cesman ST, Ellerman KE, Gangoli EA, Gerlach VL, Gilbert JA,
 PI Gorman L, Guo X, Guev VY, Kekuda R, Li L, Liu X, Malyanar UM,
 PI Miller CE, Miller I, Padigaru M, Patuajan M, Pena CE, Peyman JA,
 PI Rastelli L, Shenoy SG, Shinkets RA, Smithson G, Spytek KA, Stone DJ,
 PI Taupier RJ, Tchernev VT, Vernet CM, Zerhusen BD,
 XX WPI; 2002-698672/75.

XX New NOVX polypeptides or polynucleotides, useful for preventing or
 PT treating disorders or syndromes e.g., atherosclerosis, hypertension,
 PT obesity or cancer.

XX Example 2; Page 882; 923pp; English.

XX The present invention relates to novel human NOVX proteins, where X is
 CC any number from 1 to 91 and their coding sequences (see ADH48717-
 CC ADH48930). The proteins and coding sequences are useful for preventing or
 CC treating disorders or syndromes e.g., atherosclerosis, hypertension,
 CC obesity or cancer. The present sequence was used in an example from the
 CC invention.

XX Sequence 22 BP, 3 A; 9 C; 2 G; 8 T; 0 U; 0 Other;

Query Match 6.7%; Score 16.2; DB 1; Length 22;
 Best Local Similarity 85.7%; Pred. No. 16;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 133 TCTCTTGAGACCTCTCAG 153
 Db 2 TCTCTTGAGACCTCTTCC 22

RESULT 11

ADH84073
 ID ADH84073 standard; DNA; 22 BP.

AC ADH84073;

DT 05-MAY-2005 (first entry)

DE DNA detection extension primer #48.

XX Analysis; mass spectroscopy; PCR; primer; ss.

XX Synthetic.

XX WO2005014850-A2.

XX 17-FEB-2005.

XX 06-AUG-2004; 2004WO-US025526.

XX 06-AUG-2003; 2003US-0493238P.

XX 07-MAY-2004; 2004US-0568958P.

XX (UTMA-) UNIV MASSACHUSETTS.

XX Gims EI, Galdzicka M;

XX WPI; 2005-195764/20.
DR Clinical assay system for assaying sample, has central controller, sample
XX transfer module, nucleic acid extraction and measurement module,
PT thermocycling module, primer extension module, mass spectrometry module
PT analyzing sample.
XX
XX Claim 6; SEQ ID NO 144; 207bp; English.
XX
XX The invention relates to a system for performing an assay on a biological
CC sample, comprising a central controller programmed to exchange
CC information about the biological sample with an outside system or
CC database and exchange information about the biological sample with one or
CC more modules of the system, a sample transfer module for transferring a
CC portion of the sample to a first container, a nucleic acid extraction
CC module for extracting nucleic acids from cells within the portion and for
CC transferring the portion from the first container to a second container,
CC a nucleic acid measurement module for measuring the concentration of
CC nucleic acids in the portion, a PCR preparation module for adding PCR
CC reaction materials to the portion, a thermocycling module for amplifying
CC a target sequence and extending a primer in the portion, a primer
CC extension preparation module for adding primer extension reaction
CC materials to the portion, a mass spectrometry preparation module for
CC removing a sample of the portion from the second container to a support
CC for analysis by mass spectrometry and a mass spectrometry module for
CC analyzing the sample. The invention also relates to an automated method
CC for detecting mutations in a target gene. The diagnostic assay is an
CC assay for detecting a pathogen in the sample. The pathogen is a virus,
CC bacterium or fungus. The virus is a virus of the family Herpesviridae,
CC preferably Cytomegalovirus (CMV). The system enables high accurate assays
CC on nucleic acid sequences (e.g. clinically relevant nucleic acid
CC sequences) using mass spectrometry. This sequence represents a DNA
CC detection extension primer used in the scope of the invention.
XX
SQ Sequence 22 BP; 5 A; 5 C; 3 G; 9 T; 0 U; 0 Other;
Query Match 6.7%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 126 GTTTCATCTCTTGGAGCAC 146
Db 1 GTTTCATCTATTGGTACAC 21
RESULT 12
ADL24990 standard; DNA; 23 BP.
XX
XX ADL24990;
XX
XX 05-MAY-2005 (first entry)
XX
XX DNA target sequence #56.
XX
XX Analysis; mass spectroscopy; ss.
XX
XX Synthetic.
XX
XX WO2005014850-A2.
XX
XX 17-FEB-2005.
XX
XX 06-AUG-2004; 2004WO-US025526.
XX
XX 06-AUG-2003; 2003US-0493238P.
XX
XX 07-MAY-2004; 2004US-0568958P.
XX
XX (UTMA-) UNIV MASSACHUSETTS.
XX
XX Glime BI, Galdzicka M;
XX

DR WPI; 2005-195764/20.
XX
XX Clinical assay system for assaying sample, has central controller, sample
PT transfer module, nucleic acid extraction and measurement module,
PT thermocycling module, primer extension module, mass spectrometry module
PT analyzing sample.
XX
XX Disclosure; SEQ ID NO 562; 207bp; English.
XX
XX The invention relates to a system for performing an assay on a biological
CC sample, comprising a central controller programmed to exchange
CC information about the biological sample with an outside system or
CC database and exchange information about the biological sample with one or
CC more modules of the system, a sample transfer module for transferring a
CC portion of the sample to a first container, a nucleic acid extraction
CC module for extracting nucleic acids from cells within the portion and for
CC transferring the portion from the first container to a second container,
CC a nucleic acid measurement module for measuring the concentration of
CC nucleic acids in the portion, a PCR preparation module for adding PCR
CC reaction materials to the portion, a thermocycling module for amplifying
CC a target sequence and extending a primer in the portion, a primer
CC extension preparation module for adding primer extension reaction
CC materials to the portion, a mass spectrometry preparation module for
CC removing a sample of the portion from the second container to a support
CC for analysis by mass spectrometry and a mass spectrometry module for
CC analyzing the sample. The invention also relates to an automated method
CC for detecting mutations in a target gene. The diagnostic assay is an
CC assay for detecting a pathogen in the sample. The pathogen is a virus,
CC bacterium or fungus. The virus is a virus of the family Herpesviridae,
CC preferably Cytomegalovirus (CMV). The system enables high accurate assays
CC on nucleic acid sequences (e.g. clinically relevant nucleic acid
CC sequences) using mass spectrometry. This sequence represents a DNA target
CC sequence used in the scope of the invention.
XX
SQ Sequence 23 BP; 5 A; 6 C; 3 G; 9 T; 0 U; 0 Other;
Query Match 6.7%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 126 GTTTCATCTCTTGGAGCAC 146
Db 1 GTTTCATCTATTGGTACAC 21
RESULT 13
ADL24990/C
ID ADL24990 standard; DNA; 19 BP.
XX
XX ADL24990;
XX
XX 20-MAY-2004 (first entry)
XX
XX Intestinal epithelium/geyer's patch M cell-associated PCR primer #135.
XX
XX Intestinal epithelium cell development; peyer's patch M cell development;
XX inflammatory bowel disease; glutenenteropathy; infectious disease;
XX autoimmune disease; haemolytic anaemia; rheumatoid arthritis; dermatitis;
XX Grave's disease; multiple sclerosis; allergy; asthma; diabetic mellitus;
XX immune system disorder; hypersensitivity; anaphylaxis;
XX blood group incompatibility; ss; human; PCR; primer.
XX
XX Homo sapiens.
XX
XX OS
XX PN WO200280852-A2.
XX
XX 17-OCT-2002.
XX
XX 04-APR-2002; 2002WO-US010873.
XX
XX 04-APR-2001; 2001US-0281416P.
XX
XX (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
PA

XX Brayden DJ, Byrne D, O'mahony DJ, Evans CF, Mah SP, Lo DD;
XX WPI; 2003-075470/07.
XX Novel isolated or purified polypeptide encoded by genes associated with
XX intestinal epithelium or M cell development, differentiation or function,
XX useful for treating autoimmune diseases and infectious diseases.
XX
XX Disclosure: SEQ ID NO 500; 152pp; English.
XX
XX The invention comprises DNA sequences which are associated with
XX intestinal epithelium and Peyer's patch M cells. The DNA sequences of the
XX invention are useful for assessing, modifying, modulating or regulating
XX intestinal epithelium or M cell development. The DNA sequences of the
XX invention are also useful in the treatment of: inflammatory bowel
XX disease, glutenenteropathy, infectious diseases, autoimmune diseases
XX (e.g. haemolytic anaemia, rheumatoid arthritis, dermatitis, Grave's
XX disease, multiple sclerosis, allergy, asthma and diabetic mellitus),
XX diseases or disorders of the immune system, hypersensitivity,
XX anaphylaxis, and blood group incompatibility. The present DNA sequence
XX represents a PCR primer that was used to amplify an intestinal
XX epithelium/peyer's patch M cell-associated DNA sequence of the invention.
XX
SQ Sequence 19 BP; 6 A; 7 C; 6 G; 0 T; 0 U; 0 Other;
Query Match 6.5%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 20;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 26 GTCACCTGCTGGAGCTC 44
Db 19 GTCCTCTGGCTGGGCTC 1
RESULT 14
ACL46618
ID ACL46618 standard; DNA; 21 BP.
XX
XX ACL46618;
XX
XX 24-MAR-2005 (first entry)
XX
XX ENPP3 target oligonucleotide, SEQ ID 7690.
XX
XX ENPP3 target oligonucleotide, SEQ ID 7690.
XX
XX Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss.
XX
XX Homo sapiens.
XX
XX WO2005001092-A2.
XX
XX 06-JAN-2005.
XX
XX 19-MAY-2004; 2004WO-US015645.
XX
XX 20-MAY-2003; 2003US-0471729P.
XX
XX (AMHP) WYETH.
XX
XX Be X, Wei L, Slonim DK, Howes SH;
XX
XX WPI; 2005-075568/08.
XX
XX Pharmaceutical composition comprising an agent capable of modulating an
XX expression level or protein activity of a gene, e.g. ABC4, or a T cell
XX activated by the polypeptide or antibody, and a carrier, useful for
XX treating cancer.
XX
XX Claim 3; SEQ ID NO 7690; 113pp; English.
XX
XX The present invention relates to a novel pharmaceutical composition
XX comprising: (a) an agent capable of modulating an expression level or
XX protein activity of a cancer-related transmembrane protein (CRTP) or gene
XX

CC ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and
CC (b) a carrier. The pharmaceutical composition may also comprise a
CC polynucleotide capable of inhibiting or decreasing the expression of the
CC CRTP by RNA interference or an antisense mechanism. The CRTPs of the
CC invention are selected from ABC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
CC FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
CC pharmaceutical composition is useful for treating cancer, e.g. colon
CC cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
CC cancer, stomach cancer, and esophageal cancer. The present sequence is a
CC target oligonucleotide from one such CRTP for which short interfering
CC RNAs (siRNA) were produced. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 21 BP; 10 A; 4 C; 4 G; 3 T; 0 U; 0 Other;
Query Match 6.5%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 18;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 163 AACGAAACGACCTGTAAG 181
Db 1 AACGAAACACCTGTAAG 19
RESULT 15
ACL46980/c
ID ACL46980 standard; RNA; 21 BP.
XX
XX ACL46980;
XX
XX 24-MAR-2005 (first entry)
XX
XX ENPP3 siRNA antisense sequence, SEQ ID 8052.
XX
XX Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss;
XX short interfering RNA; gene silencing.
XX
XX Synthetic.
XX
XX WO2005001092-A2.
XX
XX 06-JAN-2005.
XX
XX 19-MAY-2004; 2004WO-US015645.
XX
XX 20-MAY-2003; 2003US-0471729P.
XX
XX (AMHP) WYETH.
XX
XX Be X, Wei L, Slonim DK, Howes SH;
XX
XX WPI; 2005-075568/08.
XX
XX Pharmaceutical composition comprising an agent capable of modulating an
XX expression level or protein activity of a gene, e.g. ABC4, or a T cell
XX activated by the polypeptide or antibody, and a carrier, useful for
XX treating cancer.
XX
XX Claim 3; SEQ ID NO 8052; 113pp; English.
XX
XX The present invention relates to a novel pharmaceutical composition
XX comprising: (a) an agent capable of modulating an expression level or
XX protein activity of a cancer-related transmembrane protein (CRTP) or gene
XX ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and
XX (b) a carrier. The pharmaceutical composition may also comprise a
XX polynucleotide capable of inhibiting or decreasing the expression of the
XX CRTP by RNA interference or an antisense mechanism. The CRTPs of the
XX invention are selected from ABC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
CC FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
CC pharmaceutical composition is useful for treating cancer, e.g. colon
CC cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney

CC cancer, stomach cancer, and esophageal cancer. The present sequence is a
CC CRP short interfering RNA (siRNA) oligonucleotide. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 21 BP; 3 A; 4 C; 4 G; 0 T; 10 U; 0 Other;

Query Match 6.5%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 18;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 163 AACAGAGACCTGTTAAG 181
Db 20 AACGGAACACCTGTTAAG 2

RESULT 16
ACLA6620/C
ID ACLA6620 standard; RNA; 21 BP.

XX ACLA6620;
XX
XX 24-MAR-2005 (first entry)

DE ENPP3 siRNA antisense sequence, SEQ ID 7692.

KM Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss;
KM short interfering RNA; gene silencing.

XX Synthetic.

OS
XX WO2005001092-A2.

PN 06-JAN-2005.

XX 19-MAY-2004; 2004WO-US015645.

XX 20-MAY-2003; 2003US-0471729P.

XX (AMHP) WYETH.

PI Be X, Wei L, Slonim DK, Howes SH;

XX WPI; 2005-075568/08.

PT Pharmaceutical composition comprising an agent capable of modulating an
PT expression level or protein activity of a gene, e.g. ABC4, or a T cell
PT activated by the polypeptide or antibody, and a carrier, useful for
PT treating cancer.

XX Claim 3; SEQ ID NO 7692; 113pp; English.

XX The present invention relates to a novel pharmaceutical composition
XX comprising: (a) an agent capable of modulating an expression level or
XX protein activity of a cancer-related transmembrane protein (CRTP) or gene
XX; an antibody specific for a CRTP, or a T cell activated by a CRTP; and
XX (b) a carrier. The pharmaceutical composition may also comprise a
XX polynucleotide capable of inhibiting or decreasing the expression of the
XX CRTP by RNA interference or an antisense mechanism. The CRTPs of the
XX invention are selected from ABC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
XX FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
XX pharmaceutical composition is useful for treating cancer, e.g. colon
XX cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
XX cancer, stomach cancer, and esophageal cancer. The present sequence is a
XX CRP short interfering RNA (siRNA) oligonucleotide. Note: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

XX Sequence 21 BP; 3 A; 4 C; 4 G; 0 T; 10 U; 0 Other;

Query Match 6.5%; Score 15.8; DB 1; Length 21;

Best Local Similarity 89.5%; Pred. No. 18;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 163 AACAGAGACCTGTTAAG 181
Db 21 AACGGAACACCTGTTAAG 3

RESULT 17
ACLA6978
ID ACLA6978 standard; DNA; 21 BP.

XX ACLA6978;
XX
XX 24-MAR-2005 (first entry)

DE ENPP3 target oligonucleotide, SEQ ID 8050.

KM Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss.

XX Homo sapiens.

XX WO2005001092-A2.

XX 06-JAN-2005.

XX 19-MAY-2004; 2004WO-US015645.

XX 20-MAY-2003; 2003US-0471729P.

XX (AMHP) WYETH.

PI Be X, Wei L, Slonim DK, Howes SH;

XX WPI; 2005-075568/08.

PT Pharmaceutical composition comprising an agent capable of modulating an
PT expression level or protein activity of a gene, e.g. ABC4, or a T cell
PT activated by the polypeptide or antibody, and a carrier, useful for
PT treating cancer.

XX Claim 3; SEQ ID NO 8050; 113pp; English.

XX The present invention relates to a novel pharmaceutical composition
XX comprising: (a) an agent capable of modulating an expression level or
XX protein activity of a cancer-related transmembrane protein (CRTP) or gene
XX; an antibody specific for a CRTP, or a T cell activated by a CRTP; and
XX (b) a carrier. The pharmaceutical composition may also comprise a
XX polynucleotide capable of inhibiting or decreasing the expression of the
XX CRTP by RNA interference or an antisense mechanism. The CRTPs of the
XX invention are selected from ABC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
XX FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
XX pharmaceutical composition is useful for treating cancer, e.g. colon
XX cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
XX cancer, stomach cancer, and esophageal cancer. The present sequence is a
XX target oligonucleotide from one such CRTP for which short interfering
XX RNA (siRNA) were produced. Note: The sequence data for this patent did
XX not form part of the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

XX Sequence 21 BP; 9 A; 5 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 6.5%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 18;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 163 AACAGAGACCTGTTAAG 181
Db 2 AACGGAACACCTGTTAAG 20

RESULT 18

```

AAD45780
ID   AAD45780 standard; DNA; 22 BP.
XX
AC   AAD45780;
XX
DT   27-DEC-2002 (first entry)
XX
DE   Human promoter -147 CYP4503A5 specific probe #1.
XX
KM   Human; cytochrome P450; CYP3A4; CYP3A5; glutathione S-transferase;
KM   polymorphism; GSTM1; breast cancer; therapy; chemotherapeutic agent;
KM   drug-drug interaction; drug adverse effect; anti-cancer agent; enzyme;
KM   probe; promoter; ss.
XX
OS   Homo sapiens.
XX
PN   WO200268448-A1.
XX
PD   06-SEP-2002.
XX
PF   26-FEB-2002; 2002WO-US006135.
XX
PR   26-FEB-2001; 2001US-0271630P.
XX
PA   (DNAS-) DNA SCI INC.
XX
PA   (UYDU-) UNIV DUKE.
XX
PI   Guida M, Hall J, Petros WP, Vredenburg JJ, Colvin OM, Marks JR;
XX
DR   WPI; 2002-691652/74.
XX
PT   New nucleic acid molecule useful for identifying polymorphisms associated
PT   with CYP3A4, CYP3A5 or GSTM1 substrates which influence breast cancer
PT   treatments, comprises at least one base variation from human CYP3A4 or
PT   CYP3A5 sequence.
XX
PS   Example 3; Page 27; 41pp; English.
XX
CC   The invention relates to a nucleic acid molecule comprising at least one
CC   base variation from human cytochrome P450 (CYP) 3A4 or CYP3A5 sequence.
CC   Nucleic acid molecules of the invention are useful for identifying
CC   polymorphisms associated with CYP3A4, CYP3A5 or glutathione S-transferase
CC   (GST) M1 substrates which influence breast cancer treatments. They are
CC   also useful in diagnostic purposes to identify individuals having a
CC   polymorphic genotype which influence the outcome of breast cancer
CC   treatments and the selection of chemotherapeutic agents used to treat
CC   breast cancer. The polymorphisms detected are used to screen altered
CC   metabolism of CYP3A4, CYP3A5 or GSTM1 substrates, potential drug-drug
CC   interactions, drug adverse effects, likelihood of successful clinical
CC   outcome following treatment with anti-cancer agents such as cisplatin,
CC   cyclophosphamide and/or BCNU. The present sequence is human promoter -147
CC   CYP4503A5 specific probe
XX
SQ   Sequence 22 BP; 2 A; 13 C; 2 G; 5 T; 0 U; 0 Other;
XX
Query Match          6.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY      56 CTGCTGCTCACTGCTTTTCC 77
      ||||| ||||| ||||| |||||
DB      1 CTGCAGCCCACTCTCTCTCC 22

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XX
KM   anti-HIV; cytostatic; vaccine; expression; cell culture;
KM   acquired immune deficiency syndrome; immune disorder; cancer; neoplasm;
KM   protein production; antibody production; PCR; primer; ss.
XX
OS   Unidentified.
XX
PN   WO2005054467-A1.
XX
PD   16-JUN-2005.
XX
PF   03-DEC-2004; 2004WO-JP018006.
XX
PR   03-DEC-2003; 2003JP-00405269.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
PI   Teunoda H, Habu K;
XX
DR   WPI; 2005-425413/43.
XX
PT   Novel DNA construct comprising mammalian beta actin promoter being
PT   functionally coupled to enhancer, useful for producing protein e.g.
PT   antibody or treating AIDS or cancer.
XX
PS   Example 1; SEQ ID NO 33; 48pp; Japanese.
XX
CC   The invention describes a DNA construct (I) comprising a mammalian beta
CC   actin promoter being functionally coupled to the enhancer. Also described
CC   are: a vector (II) comprising (I); a cell (III) comprising (II); a
CC   transgenic non-human animal comprising (II); a totipotent cell comprising
CC   (II); and increasing (M1) an expression of a DNA, comprising integrating
CC   beta actin promoter to the upstream of the DNA, where the promoter is
CC   obtained from a host cell, in which the DNA exist. (II) is useful for
CC   expressing a DNA in a host cell such as mammalian cell e.g. rodent cell.
CC   (III) is useful for producing protein which involves culturing (II) in a
CC   culture medium and recovering protein from the culture and medium. (I) or
CC   (II) is useful for producing protein e.g. antibody or treating AIDS or
CC   cancer. (I) enables to produce large quantities of protein e.g. antibody.
CC   This sequence represents a DNA construct associated primer.
XX
SQ   Sequence 22 BP; 4 A; 10 C; 5 G; 3 T; 0 U; 0 Other;
XX
Query Match          6.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY      110 GTGCCACTAGCGCTCTGTTTC 131
      ||||| ||||| ||||| |||||
DB      1 GTGCACACGACGCGACGTTGCC 22

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RESULT 19
AEA33500
ID   AEA33500 standard; DNA; 22 BP.
XX
AC   AEA33500;
XX
DT   25-AUG-2005 (first entry)
XX
DE   Expression system associated primer SEQ ID NO 33.
XX

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RESULT 20
AAF26513
ID   AAF26513 standard; DNA; 18 BP.
XX
AC   AAF26513;
XX
DT   27-MAR-2001 (first entry)
XX
DE   Human SRC-3 antisense oligonucleotide #17.
XX
KM   Steroid receptor coactivator-3; SRC-3; antisense; infection;
KM   inflammation; tumour; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   US6156571-A.
XX
PD   05-DEC-2000.
XX
PF   15-NOV-1999; 99US-00440612.
XX

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PR 15-NOV-1999; 99US-00440612.
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Coweart LM;
XX
DR WPI; 2001-079549/09.
XX
PT Novel antisense compound useful to prevent or delay infection,
PT inflammation or tumor formation, specifically hybridizes with, and
PT inhibits the expression of human steroid receptor coactivator-3.
XX
PS Claim 1; Col 40; 36pp; English.
XX
CC The present invention relates to an antisense oligonucleotide, targeted
CC to a nucleic acid molecule encoding human steroid receptor coactivator-3
CC (SRC-3). The invention is useful for inhibiting the expression of SRC-3
CC in human cells or tissues in vitro. It is useful for diagnostics,
CC therapeutics, prophylaxis and as research reagents and kits. It is useful
CC prophylactically, to prevent or delay infection, inflammation or tumor
CC formation
XX
SQ Sequence 18 BP; 3 A; 4 C; 5 G; 6 T; 0 U; 0 Other;

Query Match          6.4%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      14 CACTGATTTTGGTCAC 30
        |||||
Db      1 CACTGATTTTGGTCGC 17

RESULT 21
AA91393
ID AAX91393 standard; DNA; 20 BP.
XX
AC AAX91393;
XX
DT 24-SEP-1999 (first entry)
XX
XX Primer for RT-PCR analysis of T. gondii immunogenic protein DNA.
XX
XX Immunogenic protein; Toxoplasma gondii protein; oocyst shedding; cat;
XX T. gondii infection; enteric apicomplexa oocyst; Cryptosporidium oocyst;
XX Toxoplasma oocyst; RT-PCR primer; ss.
XX
OS Synthetic.
OS Toxoplasma gondii.
XX
XX W09932633-A1.
XX
PD 01-JUL-1999.
XX
PF 18-DEC-1998; 98WO-US027137.
XX
PR 19-DEC-1997; 97US-00994825.
XX
PA (HESK-) HESKA CORP.
XX
PI Milhausen MJ, Lutz SB, Ng RK;
XX
DR WPI; 1999-418930/35.
XX
XX New isolated Toxoplasma gondii nucleic acids used, e.g. to treat
PT infection caused by this microorganism.
XX
PS Example 2; Page 69; 381pp; English.
XX
CC The invention provides isolated Toxoplasma gondii nucleic acids that
CC encode immunogenic polypeptides. The T. gondii nucleic acid molecules,
CC immunogenic proteins and antibodies to the proteins can be used to
CC inhibit T. gondii oocyst shedding in a cat due to infection with T.

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CC gondii. They can be used for preventing T. gondii infection and for
CC preventing the spread of T. gondii infection. They can also be used for
CC detecting T. gondii infection. The detection method can be used to detect
CC parasite cysts or oocysts in feces, e.g. from enteric apicomplexa oocysts
CC such as Cryptosporidium oocysts and Toxoplasma oocysts. Sequences
CC AAX91276-395 primers used in RT-PCR analysis of nucleic acid sequences
CC encoding immunogenic T. gondii proteins
XX
SQ Sequence 20 BP; 0 A; 2 C; 9 G; 9 T; 0 U; 0 Other;

Query Match          6.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 23;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      189 TGTCTAGGCTGTCTAG 208
        |||||
Db      1 TGGCTGTTGGTGTCTCG 20

RESULT 22
AAS42716
ID AAS42716 standard; DNA; 20 BP.
XX
AC AAS42716;
XX
DT 17-DEC-2001 (first entry)
XX
XX T. gondii immunogenic protein PCR primer nTG78 #2.
XX
XX Immunogenic protein; oocyst; faeces; ss; enteric apicomplexa oocyst;
XX Cryptosporidium oocyst; Toxoplasma oocyst; Giardia cyst; vaccine;
XX oocyst shedding; PCR primer.
XX
OS Toxoplasma gondii.
OS
XX
XX US2001014447-A1.
XX
PD 16-AUG-2001.
XX
PF 18-DEC-1998; 98US-00216393.
XX
PR 19-DEC-1997; 97US-00994825.
XX
PA (MILH/) MILHAUSEN M J.
XX
PI Milhausen MJ;
XX
DR WPI; 2001-529100/58.
XX
XX
XX Detecting parasite oocysts or cysts in feces, comprises eluting DNA from
PT sample into aqueous solution by heating, amplifying DNA with primers
PT specific for oocysts or cysts being detected, and detecting amplification
PT product.
XX
PS Example 2; Page 25; 188pp; English.
XX
XX The invention relates to detection of parasite oocysts or cysts in a
XX faeces sample comprising contacting the sample with a solid support,
XX drying and then washing the sample with an aqueous wash solution, adding
XX an aqueous elution solution and eluting DNA from the sample by heating
XX and amplifying by PCR oocyst/cyst-specific DNA and detecting the
XX amplification products. The method is useful for detecting parasite
XX oocysts e.g., enteric apicomplexa oocysts such as Cryptosporidium oocysts
XX or Toxoplasma oocysts, or for detecting parasite cysts e.g. Giardia
XX cysts. The method is also useful for developing vaccines to prevent
XX oocyte shedding in cats. The present sequence is a PCR primer used to
XX isolate DNAs encoding immunogenic proteins from Toxoplasma gondii
XX
SQ Sequence 20 BP; 0 A; 2 C; 9 G; 9 T; 0 U; 0 Other;

Query Match          6.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 23;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

OY 189 TGTCTGTAGGTTGTCTAG 208
 XX |||||
 DB 1 TGGCTGTTGGGTTGCTCG 20

RESULT 23

ID ADG17312 standard; DNA; 20 BP.

XX ADG17312;

XX 26-FEB-2004 (first entry)

XX T. gondii sequencing primer #118.

XX Toxoplasma gondii; oocyst shedding; genetic vaccine; vaccine; ss; primer.

XX Toxoplasma gondii.

XX US2003194393-A1.

XX 16-OCT-2003.

XX 17-DEC-2002; 2002US-00321856.

XX 19-DEC-1997; 97US-00994825.

XX 18-DEC-1998; 98US-00216393.

XX (MILH/) MILHAUSEN M J.

XX Milhausen MJ;

XX WPI; 2003-899768/82.

XX Novel immunogenic Toxoplasma gondii proteins useful for inhibiting oocyst shedding by cats infected with Toxoplasma gondii.

XX Example 2; SEQ ID NO 262; 198pp; English.

XX The invention relates to an isolated Toxoplasma gondii protein. The CC protein is useful for inhibit oocyst shedding by cats infected with CC Toxoplasma gondii. The protein is useful for preventing or ameliorating CC diseases caused by infection with T. gondii. The nucleic acid can be used CC as genetic vaccine which encodes the protein. The protein and the nucleic CC acid are used as diagnostic reagents for detection of T. gondii CC infection. The present sequence is used in the exemplification of the CC invention.

XX Sequence 20 BP; 0 A; 2 C; 9 G; 9 T; 0 U; 0 Other;

XX Query Match 6.3%; Score 15.2; DB 1; Length 20;

XX Best Local Similarity 85.0%; Pred. No. 23;

XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 189 TGTCTGTAGGTTGTCTAG 208
 |||||
 DB 1 TGGCTGTTGGGTTGCTCG 20

RESULT 24
 ID ADP78412 standard; DNA; 20 BP.

XX ADP78412;

XX 12-AUG-2004 (first entry)

XX Chimeric phosphorothioate oligonucleotide #2211.

XX GFAT; Antidiabetic; Cardiant;

XX Glutamine-fructose-6-phosphate amidotransferase; diabetes; ischemia;
 KW reperfusion; ss.

XX Synthetic.

XX Key Location/Qualifiers
 XX modified_base 1..4
 FT /*tag= a

FT /mod_base= other

FT /note= "2-methoxyethyl wing"

FT modified_base 17..20

FT /*tag= b

FT /mod_base= other

FT /note= "2-methoxyethyl wing"

XX WO2004035763-A2.

XX 29-APR-2004.

XX 02-OCT-2003; 2003WO-US033332.

XX 17-OCT-2002; 2002US-0419268P.

XX (PHAA) PHARMACIA CORP.

XX Broscat KO, Crosby SD;

XX WPI; 2004-348453/32.

XX Claim 4; SEQ ID NO 2211; 175pp; English.

XX The present invention relates to a compound which specifically hybridizes CC with a nucleic acid molecule encoding GFAT, and inhibits the expression CC of GFAT. Specifically claimed are antisense oligonucleotides capable of CC modulating the expression of GFAT, and which comprise any of the 1063 CC sequences of 20 base pairs, given in the specification. The compound, CC composition and methods are useful for treating a disease or condition CC associated with GFAT, such as a disease or condition, e.g. diabetes, a CC cardiovascular or neurological disorder, ischemia/reperfusion injury. CC They are also useful in research and diagnostics for modulating the CC expression of GFAT. The present sequence represents a chimeric CC phosphorothioate oligonucleotide with 2'-MOE wings and a deoxy gap, these CC oligonucleotides inhibit human GFAT expression.

XX Sequence 20 BP; 3 A; 6 C; 3 G; 8 T; 0 U; 0 Other;

XX Query Match 6.3%; Score 15.2; DB 1; Length 20;

XX Best Local Similarity 85.0%; Pred. No. 23;

XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 54 AGCTGCTGCTCAGCTGCTT 73
 |||||
 DB 1 ATCTGCTGCTCAGCTGATT 20

RESULT 25
 AAC69341
 ID AAC69341 standard; DNA; 21 BP.

XX AAC69341;

XX 29-JAN-2001 (first entry)

XX Human ABC1 gene intron 14 polymorphic site, SEQ ID NO:240.

XX Human ABC1 cholesterol transporter; chromosome 9q31;

XX ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
 KW Tangier disease; TD; familial HDL deficiency; FHD; polymorphism;

KW cardiovascular disease; coronary artery disease; coronary restenosis;
 KW cerebrovascular disease; peripheral vascular disease;

KW Alzheimer's disease; Niemann-Pick disease; Huntington's disease;
KW X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
KW prognosis; prophylaxis; drug screening; transgenic animal; ds.
XX Homo sapiens.
XX MO20005318-A2.
XX
XX 21-SEP-2000.
XX
XX 15-MAR-2000; 2000WO-IB000532.
XX
XX 15-MAR-1999; 99US-0124702P.
XX 08-JUN-1999; 99US-0138048P.
XX 17-JUN-1999; 99US-0139600P.
XX 01-SEP-1999; 99US-0151977P.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX (XENO-) XENON BIORESEARCH INC.
XX
XX Hayden MR, Wilson AR, Pimstone SN;
XX WPI; 2000-587528/55.
XX
XX New ABC1 polypeptide is useful for treating diseases associated with ABC1
XX biological activity, e.g. Alzheimer's disease, Huntington's disease and
XX cancer.
XX
XX Example; Fig 11; 229pp; English.
XX
XX The invention relates to the human ABC1 cholesterol transporter protein
XX (B38082) and to nucleic acid sequences (C69120) which encode it. ABC1 is
XX a member of the ATP-binding cassette (ABC transporter) superfamily of
XX proteins, and plays a crucial role in cholesterol transport, particularly
XX intracellular cholesterol trafficking in monocytes and fibroblasts, being
XX involved in cholesterol efflux from the cell. The gene encoding ABC1 is
XX located on chromosome 9q31, and mutations in this gene are associated
XX with two genetic HDL (high density lipoprotein) deficiency disorders,
XX Tangier disease (TD) and familial HDL deficiency (FHA). These diseases
XX are distinguishable in that TD is an autosomal recessive disorder, while
XX FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good
XX cholesterol") in the blood correlate with a high risk of cardiovascular
XX disease, particularly coronary artery disease, but also cerebrovascular
XX disease, coronary restenosis, and peripheral vascular disease.
XX Conversely, a high level of HDL has protective effects against
XX cardiovascular disease. The invention provides genetic constructs and
XX transgenic cells and non-human animals comprising human ABC1 nucleic
XX acids, and methods of gene therapy for the treatment or prevention of
XX cardiovascular disease comprising the administration of an expression
XX vector encoding ABC1 or an active fragment thereof. The invention also
XX encompasses compounds which mimic ABC1 activity, compounds which
XX stimulate ABC1 expression and methods of screening for such compounds. It
XX further relates to methods for determining whether a patient has an
XX increased risk for cardiovascular disease due to polymorphisms in the
XX ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat or
XX prevent cardiovascular disease, especially coronary artery disease,
XX cerebrovascular disease, coronary restenosis or peripheral vascular
XX disease. They may also be used in the treatment of diseases associated
XX with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick
XX disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.
XX The invention specifically excludes proteins with the exact amino acid
XX sequences of Genbank Accession No: CAA10005.1 and X75926, and the nucleic
XX acid with the exact sequence as Genbank Accession No: AU012376.1. The
XX present sequence represents a polymorphic site of the human ABC1 gene
XX
XX Sequence 21 BP; 2 A; 12 C; 3 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 6.3%; Score 15.2; DB 1; Length 21;
XX Best Local Similarity 85.0%; Pred. No. 22;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 58 GGTGCTCAGCTGCTTTCC 77
XX
XX ||||||||| ||| |||

DB 1 GCAGCTCAGCCGCTTTCC 20
XX
XX RESULT 26
XX AAH62254/C
XX ID AAH62254 standard; DNA; 21 BP.
XX
XX AC AAH62254;
XX
XX DT 09-SEP-2004 (revised)
XX DT 12-SEP-2001 (first entry)
XX
XX DE NF-kappa-B inhibitor polymorphism containing DNA fragment #155.
XX
XX KW Single nucleotide polymorphism; SNP; human; cancer; inflammation;
XX KW heart disease; paternity testing; forensic science; ds.
XX
XX OS Homo sapiens.
XX OS Unidentified.
XX
XX FH Key Location/Qualifiers
XX FT 11
XX FT variation /*tag=a
XX FT /standard_name="single nucleotide polymorphism"
XX
XX PM WO200138576-A2.
XX
XX PD 31-MAY-2001.
XX
XX PF 17-NOV-2000; 2000WO-US031639.
XX
XX PR 24-NOV-1999; 99US-0167334P.
XX
XX PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
XX
XX PI Cargill M, Ireland JS, Lander ES;
XX WPI; 2001-367705/38.
XX
XX DR New nucleic acid segments of the human genome, particularly from genes
XX including polymorphic sites, for phenotype correlation, forensics,
XX paternity testing, medicine and genetic analysis.
XX
XX PS Claim 1; Page 42; 80pp; English.
XX
XX XX DNA sequences AAH62100 - AAH62688 represent segments of human genes which
XX contain single nucleotide polymorphisms (SNPs). A method is included in
XX the invention for analysing a nucleic acid sample, which consists of
XX determining the base occupying any one of the polymorphic sites given in
XX the SNP containing sequences. The nucleotide sequences can be used in the
XX diagnosis or monitoring of diseases, such as cancer, inflammation, heart
XX diseases, diseases of the cardiovascular system, and infection by
XX microorganisms. The oligonucleotides are also useful in the manufacture
XX of a medicament for the treatment or prophylaxis of the diseases, and as
XX a pharmaceutical. SNP containing oligonucleotides are useful in
XX applications such as phenotype correlation, forensics, paternity testing,
XX medicine and genetic analysis
XX
XX Revised record issued on 09-SEP-2004 : Correction to Feature Table Key
XX
XX Sequence 21 BP; 2 A; 6 C; 10 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 6.3%; Score 15.2; DB 1; Length 21;
XX Best Local Similarity 85.0%; Pred. No. 22;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 37 GCGAGCTCCAGCTCCGAGC 56
XX
XX DB 21 GAGAGCTCCAGCTCCGAGC 2
XX
XX RESULT 27
XX ADU66202

ID		ADU66202 standard; RNA; 21 BP.
XX		
AC		ADU66202;
XX		
DT		27-JAN-2005 (first entry)
XX		
DE		Human MAP kinase 8/JNK1 modified siRNA #27.
XX		
KW	RNA interference; mitogen activated protein kinase inhibitor; inflammation; immunosuppressive; immune disorder; autoimmune disease; allergy; anti-allergic; cytostatic; neoplasm; cancer; ss; siRNA; gene silencing; small interfering RNA; MAP kinase inhibitor.	
XX		
OS	Homo sapiens.	
PV	MO2004097020-A2.	
XX		
PD	11-NOV-2004.	
XX		
PF	23-APR-2004; 2004WO-USO12517.	
XX		
PR	25-APR-2003; 2003US-00424339. 30-APR-2003; 2003US-00427160. 23-MAY-2003; 2003US-00444853. 23-OCT-2003; 2003US-00693059. 24-NOV-2003; 2003US-00720448. 14-JAN-2004; 2004US-00757803.	
XX		
PA	(SIRN-) SIRNA THERAPEUTICS INC.	
XX	Meswigen J, Beigelman L, Ueman N, Haeblerl P, Chowrira B; Polsky B; WPI, 2005-012649/01.	
PT	Novel short interfering nucleic acid molecule useful for inhibiting mitogen activated protein kinase gene expression e.g., c-jun associated with diseases e.g., inflammatory disease or autoimmune disease.	
XX		
PS	Disclosure; SEQ ID NO 1705; 322pp; English.	
CC	The invention relates to a chemically synthesized double stranded short interfering nucleic acid (siRNA) molecule (I) that directs cleavage of a c -JUN RNA through RNA interference (RNAi), where one strand of the siRNA molecule comprises nucleotide sequence having sufficient complementarity to the c-jun RNA for the siRNA molecule to direct cleavage of the c-jun RNA through RNA interference. (II) is useful for inhibiting mitogen activated protein kinase gene (e.g., c-jun, jnk1, junK, p38, ERK1 or ERK2) expression associated with diseases e.g., inflammatory disease, autoimmune disease, allergy, cancer. (I) exhibits improved RNA interference activity and nuclease resistance. The present sequence represents a human MAP kinase 8/JNK1 modified siRNA.	
CO	Sequence 21 BP, 5 A, 3 C, 5 G, 2 T, 6 U, 0 Other;	
OY	Query Match 6.3%; Score 15.2; DB 1; Length 21; Best Local Similarity 55.0%; Pred. No. 22; Matches 11; Conservative 6; Mismatches 3; Indels 0; Gaps 0;	
DB	196 TAGGTTGTCTAGCGTAT 215 : :: :: : 1 YACAGUGUCUAGCUGAAT 20	
RESULT 28		
ID	ADM72412/C	
XX	ADM72412 standard; DNA; 21 BP.	
AC	ADM72412;	
XX		
DT	24-MAR-2005 (first entry)	
XX		
DE	Mitochondrial polymerase Polg target DNA #59.	

XX Cell transduction; organelle; chloroplast; mitochondria; Alpers Disease;
KW carnitine deficiency; pyruvate carboxylase deficiency;
KW mitochondrial cytopathy; mitochondrial DNA depletion;
KW mitochondrial encephalopathy; mitochondrial myopathy; neuropathy; ataxia;
KW retinitis pigmentosa; pyruvate dehydrogenase deficiency;
KW Alzheimer's disease; Parkinson's disease; diabetes; aging; heart disease;
KW mitochondrial polymerase; Polg; muscular-gen.; ophthalmological;
KW cerebroprotective; anticonvulsant; antiparkinsonian; nootropic;
KW neuroprotective; cardiovascular-gen.; anti-diabetic; ds.
XX
OS Synthetic.
XX
XX WO200501062-A2.
XX
XX
PD 06-JAN-2005.
XX
XX 25-JUN-2004; 2004MO-US020454.
PP 25-JUN-2003; 2003US-0482603P.
PR (GENC-) GENCIA CORP.
PA
XX Khan S;
PI
XX MPI; 2005-075550/08.
DR
XX
PT New polynucleotide encoding a polypeptide having an organelle or
PT chloroplast localization signal, and a protein transduction domain,
PT useful for treating diseases with defective mitochondrial function.

Claim 96; SEQ ID NO 370; 98pp; English.

The invention relates to a polynucleotide encoding a recombinant polypeptide comprising an organelle and/or chloroplast localization signal and a protein transduction domain. The invention also relates to a recombinant viral vector comprising the polynucleotide, a cell comprising a modified organelle comprising a bacteriophage, a method of transfecting a cell comprising contacting the cell with a vector operably linked to a polypeptide having a protein transduction domain and an organelle targeting signal, a method of modifying an organelle comprising transfecting the cell with a recombinant lambda phage, the recombinant lambda phage comprising a polynucleotide encoding an organelle localization signal operably linked to a bacteriophage lambda surface protein, where the organelle localization signal is displayed on a surface of the recombinant lambda phage and directs the recombinant lambda phage to the organelle, and where the recombinant lambda phage introduces a polynucleotide into the organelle, a composition comprising a recombinant polypeptide comprising an organelle localization signal operably linked to a protein transduction domain, where the recombinant polypeptide is operably linked to a polynucleotide, a method for modifying the metabolism of a cell comprising contacting the cell with a recombinant vector displaying a recombinant polypeptide comprising a mitochondrial localization signal operably linked to a protein transduction domain, the recombinant vector comprising a polynucleotide encoding a functional respiratory chain component, where the functional respiratory chain component compensates for the at least one defective respiratory chain component when expressed by the cell, a method for modifying cytochrome oxidase activity in a cell, and a method of treating a mitochondrial disease in a host, comprising contacting a host's cell with a recombinant vector displaying a recombinant polypeptide comprising a mitochondrial localization signal operably linked to a protein transduction domain, the recombinant vector encoding a functional mitochondrial polypeptide, where the recombinant vector transfects at least one of the host's mitochondria enabling the host's cell to express the functional mitochondrial polypeptide in the at least one transfected mitochondrion. The methods and compositions are useful for transfecting cells and organelle DNA in living cells directly, in particular for transfecting mitochondria and chloroplasts, and for treating diseases related to organelle dysfunction, such as Alpers Disease, carnitine deficiency, pyruvate carboxylase deficiency, mitochondrial cytopathy, mitochondrial DNA depletion, mitochondrial encephalopathy, mitochondrial myopathy, neuropathy, ataxia, retinitis pigmentosa, pyruvate

CC dehydrogenase deficiency, Alzheimers disease, Parkinsons disease,
CC diabetes, aging and heart disease. This sequence represents mitochondrial
CC polymerase PolG target DNA used in the scope of the invention.
XX
SQ Sequence 21 BP; 8 A; 4 C; 8 G; 1 T; 0 U; 0 Other;
Query Match 6.3%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 22;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 53 CAGCTGCTGCTCCTCCTGCT 72
Db 20 CAGCTGCTGCTCCTCCTGCT 1
RESULT 29
ID ADW72414 standard; RNA; 21 BP.
XX
AC ADW72414;
XX
DT 24-MAR-2005 (first entry)
XX
DE Mitochondrial polymerase PolG siRNA strand #118.
XX
KM Cell transduction; organelle; chloroplast; mitochondria; Alpers Disease;
KM carnitine deficiency; pyruvate carboxylase deficiency;
KM mitochondrial cytopathy; mitochondrial DNA depletion;
KM mitochondrial encephalopathy; mitochondrial myopathy; neuropathy; ataxia;
KM retinitis pigmentosa; pyruvate dehydrogenase deficiency;
KM Alzheimers disease; Parkinsons disease; diabetes; aging; heart disease;
KM mitochondrial polymerase; PolG; muscular-gen.; ophthalmological;
KM cerebroprotective; anticonvulsant; antiparkinsonian; nootropic;
KM neuroprotective; cardiovascular-gen.; antidiabetic; ss;
KM short interfering RNA; siRNA; RNA interference; gene silencing.
XX
OS Synthetic.
XX
PN WO200501062-A2.
XX
PD 06-JAN-2005.
XX
PF 25-JUN-2004; 2004WO-US020454.
XX
PR 25-JUN-2003; 2003US-0482603P.
XX
PA (GENC-) GENCIA CORP.
XX
PI Khan S;
XX
PS WPI; 2005-075550/08.
XX
PT New polynucleotide encoding a polypeptide having an organelle or
PT chloroplast localization signal, and a protein transduction domain,
PT useful for treating diseases with defective mitochondrial function.
XX
XX Claim 96; SEQ ID NO 372; 98bp; English.
XX
XX The invention relates to a polynucleotide encoding a recombinant
XX polypeptide comprising an organelle and/or chloroplast localization
XX signal and a protein transduction domain. The invention also relates to a
XX recombinant viral vector comprising the polynucleotide, a cell comprising
XX a modified organelle comprising a bacteriophage, a method of transfecting
XX a cell comprising contacting the cell with a vector operably linked to a
XX polypeptide having a protein transduction domain and an organelle
XX targeting signal, a method of modifying an organelle comprising
XX transfecting the cell with a recombinant lambda phage, the recombinant
XX lambda phage comprising a polynucleotide encoding an organelle
XX localization signal operably linked to a bacteriophage lambda surface
XX protein, where the organelle localization signal is displayed on a
XX surface of the recombinant lambda phage and directs the recombinant
XX lambda phage to the organelle, and where the recombinant lambda phage
XX introduces a polynucleotide into the organelle, a composition comprising

CC a recombinant polypeptide comprising an organelle localization signal
CC operably linked to a protein transduction domain, where the recombinant
CC polypeptide is operably linked to a polynucleotide, a method for
CC modifying the metabolism of a cell comprising contacting the cell with a
CC recombinant vector displaying a recombinant polypeptide comprising a
CC mitochondrial localization signal operably linked to a protein
CC transduction domain, the recombinant vector comprising a polynucleotide
CC encoding a functional respiratory chain component, where the functional
CC respiratory chain component compensates for the at least one defective
CC respiratory chain component when expressed by the cell, a method for
CC modifying cytochrome oxidase activity in a cell, and a method of treating
CC a mitochondrial disease in a host, comprising contacting a host's cell
CC with a recombinant vector displaying a recombinant polypeptide comprising
CC a mitochondrial localization signal operably linked to a protein
CC transduction domain, the recombinant vector encoding a functional
CC mitochondrial polypeptide, where the recombinant vector transfects at
CC least one of the host's mitochondria enabling the host's cell to express
CC the functional mitochondrial polypeptide in the at least one transfected
CC mitochondrion. The methods and compositions are useful for transfecting
CC cells and organelle DNA in living cells directly, in particular for
CC transfecting mitochondria and chloroplasts, and for treating diseases
CC related to organelle dysfunction, such as Alpers Disease, carnitine
CC deficiency, pyruvate carboxylase deficiency, mitochondrial cytopathy,
CC mitochondrial DNA depletion, mitochondrial encephalopathy, mitochondrial
CC myopathy, neuropathy, ataxia, retinitis pigmentosa, pyruvate
CC dehydrogenase deficiency, Alzheimers disease, Parkinsons disease,
CC diabetes, aging and heart disease. This sequence represents mitochondrial
CC polymerase PolG siRNA used in the scope of the invention.
XX
SQ Sequence 21 BP; 1 A; 8 C; 4 G; 2 T; 6 U; 0 Other;
Query Match 6.3%; Score 15.2; DB 1; Length 21;
Best Local Similarity 65.0%; Pred. No. 22;
Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Oy 53 CAGCTGCTGCTCCTCCTGCT 72
Db 2 CAGCTGCTGCTCCTCCTGCT 21
RESULT 30
AEC03076/c
ID AEC03076 standard; DNA; 21 BP.
XX
AC AEC03076;
XX
DT 03-NOV-2005 (first entry)
XX
DE Human IGE short interfering nucleic acid SEQ ID NO 679.
XX
XX antiallergic; antiinflammatory; antiasthmatic; dermatological;
XX immunosuppressive; expression; RNA interference; allergy;
XX atopic dermatitis; urticaria; dermatological; dermatological disease;
XX immediate type hypersensitivity; immunosuppressive; asthma;
XX antiasthmatic; allergic rhinitis; antiallergic; antiinflammatory;
XX ear, nose, throat disease; inflammation; respiratory diseases;
XX immune disorder; IGE; short interfering nucleic acid; siRNA;
XX gene silencing; ss.
XX
XX Homo sapiens.
XX
OS
XX
PN WO2005080410-A1.
XX
PD 01-SEP-2005.
XX
PF 21-FEB-2005; 2005WO-NZ000021.
XX
PR 20-FEB-2004; 2004US-0546434P.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI Watson JD, Murison GJ, Grigor MR, Havukkala JU, Munro G,
PI Abernethy N, Webster G;

```
XX WPI, 2005-591970/60.
DR
XX
PT New composition comprises small interfering nucleic acid molecule (siNA)
PT capable of reducing expression of a target gene that is active in a IGE-
PT mediated disorder, useful for treating, e.g. allergic rhinitis or atopic
PT dermatitis.
XX
XX Example 2, SEQ ID NO 679; 178bp; English.
PS
XX The invention describes a composition comprising a small interfering
CC nucleic acid molecule (siNA) capable of reducing expression of a target
CC gene that is active in a IGE-mediated disorder, a genetic construct that
CC expresses the siNA, and a binding agent that specifically binds to a
CC target antigen expressed on the surface of the cell. Also described are:
CC a method for the treatment of an IGE-mediated disorder in a patient;
CC prevention of IGE-mediated disorder in a patient; reduction of
CC eosinophilia in a patient; modulating an IGE-mediated immune response to
CC of an immune response to a specific antigen in a patient. The composition
CC is useful in the preparation of a medicament useful for the treatment of
CC an IGE-mediated disorder, e.g. allergic rhinitis, asthma, anaphylaxis,
CC urticaria, atopic dermatitis, food allergies, diseases that benefit from
CC the reduction of eosinophilia in the tissues of the respiratory system,
CC or disorders having hypersensitivity immune reaction. This sequence
CC represents a siNA for suppression of human IGE expression.
XX
SQ Sequence 21 BP; 6 A; 5 C; 6 G; 4 T; 0 U; 0 Other;
Query Match 6.3%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 22;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 142 AGCAGCTCTCAGCTGAGCT 161
Db 21 AGTACTTCTCAGCGAGCT 2
RESULT 31
AAV13327
ID AAV13327 standard; DNA; 18 BP.
XX
AC AAV13327;
XX
XX 14-MAY-1998 (first entry)
DE Sense primer Exon 9 for human 5-lipoxygenase gene.
XX
XX Inflammatory disease; polymorphism; 5-lipoxygenase; asthma;
KM ulcerative colitis; bronchitis; sinusitis; psoriasis; rhinitis;
KM arthritis; diagnosis; treatment; PCR primer; ss.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO9742347-A2.
XX
XX 13-NOV-1997.
XX
XX 29-APR-1997; 97WO-US007137.
XX
XX 06-MAY-1996; 96US-0016890P.
XX
XX 25-APR-1997; 97US-00846020.
XX
XX (BGM ) BRIGHAM & WOMENS HOSPITAL.
XX
XX Drazen JM, In K, Asano K, Belier D, Grobholz J;
DR WPI, 1997-558997/51.
XX
PT Classifying patients with inflammatory disease, specifically asthma -
PT according to polymorphisms in 5-lipoxygenase gene regulatory region, e.g.
PT to identify candidates for lipoxygenase inhibitor treatment.
```

```
XX Example 1, Page 19; 56pp; English.
XX
XX The present sequence was used in the development of a novel method for
CC classifying patients suffering from an inflammatory disease. The method
CC comprises identifying in DNA from at least 1 patient a sequence
CC polymorphism, as compared with the normal 5-lipoxygenase (5-LOX) gene
CC (AA88431), in a 5-LOX regulatory gene sequence. The method can be
CC applied to subjects with asthma, ulcerative colitis, bronchitis,
CC sinusitis, psoriasis, allergic and non-allergic rhinitis, lupus or
CC rheumatoid arthritis. Specifically it can be used to diagnose asthma or
CC susceptibility to disease, identify treatments suitable for individual
CC patients or assess the likely success of treatment
XX
SQ Sequence 18 BP; 1 A; 9 C; 4 G; 4 T; 0 U; 0 Other;
Query Match 6.2%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 47 CCGCCCGAGCTGCTG 61
Db 2 CCGCCCGAGCTGCTG 16
RESULT 32
ADJ95475
ID ADJ95475 standard; DNA; 18 BP.
XX
AC ADJ95475;
XX
XX 06-MAY-2004 (first entry)
DE Equine herpesvirus type 1-related PCR primer #2.
XX
XX virulence; herpesvirus; Equine herpesvirus type 1; EHV-1; EHV-4;
KM Equine herpesvirus type 4; genetic marker; ORF30-ml region marker;
KM virucide; vaccine; EHV-1 strain V592 polymerase ORF30-ml region;
KM neurovirulence; herpesvirus disease; PCR; primer; ss.
XX
XX Equine herpesvirus 1.
OS
XX WO2004011677-A2.
XX
XX 05-FEB-2004.
XX
XX 23-JUL-2003; 2003WO-GB003279.
XX
XX 26-JUL-2002; 2002US-0398576P.
XX
XX (ANIM-) ANIMAL HEALTH TRUST.
XX
XX Davis Poynter N, Nugent J, Birch-Machin I, Allen G;
PI WPI, 2004-143877/14.
DR
XX
XX Assessing the virulence of a herpesvirus isolate, useful in preventing or
PT treating herpesvirus infection, by using virulence marker corresponding
PT to an ORF30-ml region.
XX
XX Claim 24; Page 60; 63pp; English.
XX
XX This invention relates to a novel method of assessing the virulence of a
CC herpesvirus isolate, for example Equine herpesvirus type 1 (EHV-1) or
CC type 4 (EHV-4), which comprises using a genetic marker, especially an
CC ORF30-ml region marker. The invention may be useful for the production of
CC compounds with a virucide activity or for the development of a vaccine.
CC The method, kit and sequence of the EHV-1 strain V592 polymerase ORF30-ml
CC region are useful for assessing the virulence of a herpesvirus or
CC neurovirulence. The vaccine is useful for immunising a host against a
CC herpesvirus disease and for treating disease. The present sequence is
CC that of a PCR primer which was used in the exemplification of the
CC invention.
```

XX SQ Sequence 18 BP; 5 A; 7 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 6.1%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTCTCAGCAGCA 15
1 |||||
1 TTCTCAGCAGCA 15
DB 1 TTCTCAGCAGCA 15

RESULT 33
AEE10387/C
ID AEE10387 standard; DNA; 18 BP.
XX AC AEE10387;
XX DT 26-JAN-2006 (first entry)
XX DE Maize gamma-zein PCR primer SEQ ID NO:2.
XX DE Maize gamma-zein PCR primer SEQ ID NO:2.
XX KW ss; PCR; primer; gamma-zein; transgenic plant; mucopolysaccharidosis;
XX KW metabolic; metabolic disorder.
XX OS Zea mays.
XX FN WO2005113775-A1.
XX PD 01-DEC-2005.
XX PF 19-MAY-2005; 2005WO-CA000762.
XX PR 21-MAY-2004; 2004US-0573777P.
XX PR 04-AUG-2004; 2004US-0598428P.
XX PA (UFR-) UNIV FRASER SIMON.
XX PI Kermode AR, He X, Clarke L;
XX DR WPI; 2005-812257/82.
XX PT New nucleotide sequence comprising a first nucleic acid sequence encoding
PT a gamma-zein signal peptide; a second nucleic acid sequence encoding the
PT protein of interest; and a regulatory element, useful for producing
PT transgenic plants.
XX PS Example 2; SEQ ID NO 2; 53pp; English.
XX CC The invention relates to a new nucleotide sequence which comprises: a
CC first nucleic acid sequence encoding a signal peptide that localizes a
CC protein of interest fused to the signal peptide to an endoplasmic
CC reticulum-derived protein body within a cell; a second nucleic acid
CC sequence encoding the protein of interest; and a regulatory element
CC operatively linked with the first nucleotide sequence, where one or more
CC than one of the first nucleic acid, the second nucleic acid and the
CC regulatory element, is heterologous with respect to one or more than one
CC of first nucleic acid, the second nucleic acid and the regulatory
CC element. Also described are: a nucleotide sequence comprising, a gamma-
CC zein regulatory element operatively linked with a nucleic acid sequence
CC encoding a gamma-zein signal peptide fused to a heterologous protein of
CC interest, and a gamma-zein 3' UTR operatively linked to the nucleic acid
CC sequence; a vector comprising the nucleotide sequence; a plant comprising
CC the nucleotide sequence; a plant cell comprising the nucleotide sequence;
CC a seed comprising the nucleotide sequence; a method of producing a
CC protein of interest comprising providing a plant comprising the
CC nucleotide sequence; and expressing the protein of interest; and an
CC expression construct comprising the following operatively linked elements
CC P-35'-UTR-GSP-X-3'-UTR. The nucleotide sequence is useful for producing
CC transgenic plants and seeds having heterologous protein, such as gamma-
CC zein peptide, localized to the endoplasmic reticulum protein bodies in
CC the transgenic plant. The produced proteins are useful in treatment of,
CC e.g., lysosomal diseases such as mucopolysaccharidosis. The present

CC CC Sequence represents a PCR primer used with primer ABE10386 to amplify and
CC clone the 5'UTR and signal peptide-encoding sequences of gamma-zein.
XX SQ Sequence 18 BP; 2 A; 5 C; 9 G; 2 T; 0 U; 0 Other;
Query Match 6.1%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 28;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 34 GCTGGAGCTTCACCTCC 51
|||
18 GCTGGAGCTTCACCTCC 1
DB 18 GCTGGAGCTTCACCTCC 1

RESULT 34
ADG31596/C
ID ADG31596 standard; DNA; 20 BP.
XX AC ADG31596;
XX DT 26-FEB-2004 (first entry)
XX DE PCR primer used to amplify human PKHD1 exon 57 for mutation analysis.
XX DE PCR; ss; polycystic kidney and hepatic disease 1; PKHD1;
XX KW autosomal recessive polycystic kidney disease; ARPKD;
XX KW congenital hepatic fibrosis; human; nephrotropic; cell proliferation;
XX KW cellular adhesion; repulsion; primer.
XX OS Homo sapiens.
XX FN WO2003085088-A2.
XX PN 16-OCT-2003.
XX PD 03-FEB-2003; 2003WO-US003410.
XX PF 01-FEB-2002; 2002US-0353472P.
XX PR (UABR-) UAB RES FOUND.
XX PA Germine GG, Onuchic LF, Nagasawa Y, Guay-Woodford LM, Somolo S;
XX PI Furu VM;
XX DR WPI; 2003-877030/81.
XX PT New polycystic kidney and hepatic disease 1 polynucleotides and
PT polypeptides, useful in diagnostic testing and for developing targeted
PT therapeutic interventions for patients with autosomal recessive
PT polycystic kidney disease.
XX PS Disclosure; Page 40; 41pp; English.
XX CC This invention relates to a novel nucleic acid that encodes the
CC polycystic kidney and hepatic disease 1 (PKHD1) polypeptide. It has been
CC identified that a mutation in the PKHD1 gene is associated with autosomal
CC recessive polycystic kidney disease (ARPKD), which is characterised by
CC enlarged kidneys and congenital hepatic fibrosis, and is most commonly
CC observed in children and infants. The present invention describes the
CC identification of the PKHD1 gene, mapped to human chromosome 6p21.1-p12,
CC and splice variants thereof. The PKHD1 polynucleotides and polypeptides
CC are useful in diagnostic testing and for developing targeted therapeutic
CC interventions for patients with ARPKD. Furthermore, they exhibit
CC nephrotropic activity and are involved in the regulation of cell
CC proliferation, cellular adhesion and repulsion. This oligonucleotide
CC sequence is a PCR primer used to amplify human PKHD1 exons for mutation
CC analysis, in an exemplification of the invention.
XX SQ Sequence 20 BP; 6 A; 7 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 6.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 25;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

OY      22  TTGTGTCACCTGCTGGG 39
Db      20  TTGTGTAACCTAGCTGGG 3

RESULT 35
ID      ADP78946 standard; DNA; 20 BP.
XX
AC      ADP78946;
XX
DT      12-AUG-2004 (first entry)
XX
DE      Chimeric phosphorothioate oligonucleotide #2745.
XX
KW      GFAT; Antidiabetic; Cardiant;
KW      Glutamine-fructose-6-phosphate amidotransferase; diabetes; ischemia;
KW      reperfusion; ss.
XX
OS      Synthetic.
XX
FH      Key      Location/Qualifiers
FT      modified_base 1..4
FT      /*tag= a
FT      /mod_base= other
FT      /note= "2-methoxyethyl wing"
FT      modified_base 17..20
FT      /*tag= b
FT      /mod_base= other
FT      /note= "2-methoxyethyl wing"

WO2004035763-A2.
XX
PD      29-APR-2004.
XX
PF      02-OCT-2003; 2003WO-US033332.
XX
PR      17-OCT-2002; 2002US-0419268P.
XX
PA      (PHAA ) PHARMACIA CORP.
XX
PI      Broschat KO, Crosby SD;
XX
DR      WPI; 2004-348453/32.
XX
PT      New compounds, particularly antisense oligonucleotides targeted to a
PT      nucleic acid encoding glutamine-fructose-6-phosphate amidotransferase
PT      (GFAT), for treating diabetes, a cardiovascular or neurologic disorder,
PT      ischemia/reperfusion injury.
XX
PS      Claim 4; SEQ ID NO 2745; 175pp; English.
XX
CC      The present invention relates to a compound which specifically hybridizes
CC      with a nucleic acid molecule encoding GFAT, and inhibits the expression
CC      of GFAT. Specifically claimed are antisense oligonucleotides capable of
CC      modulating the expression of GFAT, and which comprise any of the 3063
CC      sequences of 20 base pairs, given in the specification. The compound,
CC      composition and methods are useful for treating a disease or condition
CC      associated with GFAT, such as a disease or condition, e.g. diabetes, a
CC      cardiovascular or neurological disorder, ischemia/reperfusion injury.
CC      They are also useful in research and diagnostics for modulating the
CC      expression of GFAT. The present sequence represents a chimeric
CC      phosphorothioate oligonucleotide with 2'-MOE wings and a deoxy gap, these
CC      oligonucleotides inhibit human GFAT expression.
XX
SQ      Sequence 20 BP; 3 A; 6 C; 4 G; 7 T; 0 U; 0 Other;
Query Match      6.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 25;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY      56  CTGCTGCTCACCCTGCTT 73

```

```

Db      1  CTGCTGCTCACCCTGATT 18

RESULT 36
ID      ADP78939 standard; DNA; 20 BP.
XX
AC      ADP78939;
XX
DT      12-AUG-2004 (first entry)
XX
DE      Chimeric phosphorothioate oligonucleotide #2738.
XX
KW      GFAT; Antidiabetic; Cardiant;
KW      Glutamine-fructose-6-phosphate amidotransferase; diabetes; ischemia;
KW      reperfusion; ss.
XX
OS      Synthetic.
XX
FH      Key      Location/Qualifiers
FT      modified_base 1..4
FT      /*tag= a
FT      /mod_base= other
FT      /note= "2-methoxyethyl wing"
FT      modified_base 17..20
FT      /*tag= b
FT      /mod_base= other
FT      /note= "2-methoxyethyl wing"

WO2004035763-A2.
XX
PD      29-APR-2004.
XX
PF      02-OCT-2003; 2003WO-US033332.
XX
PR      17-OCT-2002; 2002US-0419268P.
XX
PA      (PHAA ) PHARMACIA CORP.
XX
PI      Broschat KO, Crosby SD;
XX
DR      WPI; 2004-348453/32.
XX
PT      New compounds, particularly antisense oligonucleotides targeted to a
PT      nucleic acid encoding glutamine-fructose-6-phosphate amidotransferase
PT      (GFAT), for treating diabetes, a cardiovascular or neurologic disorder,
PT      ischemia/reperfusion injury.
XX
PS      Claim 4; SEQ ID NO 2738; 175pp; English.
XX
CC      The present invention relates to a compound which specifically hybridizes
CC      with a nucleic acid molecule encoding GFAT, and inhibits the expression
CC      of GFAT. Specifically claimed are antisense oligonucleotides capable of
CC      modulating the expression of GFAT, and which comprise any of the 3063
CC      sequences of 20 base pairs, given in the specification. The compound,
CC      composition and methods are useful for treating a disease or condition
CC      associated with GFAT, such as a disease or condition, e.g. diabetes, a
CC      cardiovascular or neurological disorder, ischemia/reperfusion injury.
CC      They are also useful in research and diagnostics for modulating the
CC      expression of GFAT. The present sequence represents a chimeric
CC      phosphorothioate oligonucleotide with 2'-MOE wings and a deoxy gap, these
CC      oligonucleotides inhibit human GFAT expression.
XX
SQ      Sequence 20 BP; 2 A; 6 C; 4 G; 8 T; 0 U; 0 Other;
Query Match      6.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 25;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY      56  CTGCTGCTCACCCTGCTT 73
Db      2  CTGCTGCTCACCCTGATT 19

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```
RESULT 37
ADP81801/C
ID ADP81801 standard; DNA; 20 BP.
XX
XX AC ADP81801;
XX
XX DT 26-AUG-2004 (first entry)
XX
DE Human MD-1 RP105-associated antisense oligo, ISIS 260183.
XX
XX MD-1 RP105-associated; MD-1; MD1; autoimmune disorder; gene therapy;
XX human; antisense; phosphorochioate backbone; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX Key modified_base Location/Qualifiers
XX FT 1..20
XX FT /*tag= b
XX FT /mod_base= OTHER
XX FT /note= "Phosphorochioate backbone in which all cytidine
XX modified_base residues are 5-methylcytidines"
XX FT 1..5
XX FT /*tag= a
XX FT /mod_base= OTHER
XX FT /note= "2'-methoxyethyl (2'-MOE) bases"
XX FT 16..20
XX FT /*tag= c
XX FT /mod_base= OTHER
XX FT /note= "2'-methoxyethyl (2'-MOE) bases"
XX
XX US2004110146-A1.
XX
XX 10-JUN-2004.
XX
XX 09-DEC-2002; 2002US-00316242.
XX
XX 09-DEC-2002; 2002US-00316242.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX PA
XX
XX PI Dobie KM;
XX
XX WPI; 2004-440335/41.
XX
XX New oligonucleotide compound that inhibits expression of MD-1 RP105-
XX associated, useful for preparing a composition for treating autoimmune
XX disorder.
XX
XX Example 15; SEQ ID NO 40; 63pp; English.
XX
XX The invention relates to compounds, compositions and methods for
XX modulating the expression of MD-1 RP105-associated (also called as MD-1
XX and MD1) DNA. The composition comprise antisense oligonucleotides
XX targeted to MD-1 RP105-associated DNA. The compound is useful for
XX preparing a composition for treating autoimmune disorder. It is also
XX useful in gene therapy. The present sequence is an antisense
XX oligonucleotide targeted to human MD-1 RP105-associated DNA. This
XX sequence is used to illustrate the method of the invention.
XX
XX Sequence 20 BP; 6 A; 2 C; 8 G; 4 T; 0 U; 0 Other;
XX
Query Match 6.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred.No. 25;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 59 CTGCTCTACCTGCTTTTC 76
DB 18 CAGACTCAGCTGCTTTTC 1
```

```
RESULT 38
ADP81821
ID ADP81821 standard; DNA; 20 BP.
XX
XX AC ADP81821;
XX
XX DT 26-AUG-2004 (first entry)
XX
DE Human MD-1 RP105-associated DNA target region #11.
XX
XX MD-1 RP105-associated; MD-1; MD1; autoimmune disorder; gene therapy;
XX human; ds.
XX
OS Homo sapiens.
XX
XX US2004110146-A1.
XX
XX 10-JUN-2004.
XX
XX 09-DEC-2002; 2002US-00316242.
XX
XX 09-DEC-2002; 2002US-00316242.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX PA
XX
XX PI Dobie KM;
XX
XX WPI; 2004-440335/41.
XX
XX New oligonucleotide compound that inhibits expression of MD-1 RP105-
XX associated, useful for preparing a composition for treating autoimmune
XX disorder.
XX
XX Example 15; SEQ ID NO 60; 63pp; English.
XX
XX The invention relates to compounds, compositions and methods for
XX modulating the expression of MD-1 RP105-associated (also called as MD-1
XX and MD1) DNA. The composition comprise antisense oligonucleotides
XX targeted to MD-1 RP105-associated DNA. The compound is useful for
XX preparing a composition for treating autoimmune disorder. It is also
XX useful in gene therapy. The present sequence is human MD-1 RP105-
XX associated DNA target region. This sequence is used to illustrate the
XX method of the invention.
XX
XX Sequence 20 BP; 4 A; 8 C; 2 G; 6 T; 0 U; 0 Other;
XX
Query Match 6.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred.No. 25;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 59 CTGCTCTACCTGCTTTTC 76
DB 3 CAGACTCAGCTGCTTTTC 20
XX
RESULT 39
ADR70686/C
ID ADR70686 standard; DNA; 20 BP.
XX
XX ADR70686;
XX
XX DT 02-DEC-2004 (first entry)
XX
XX Solanum glycosylase related PCR primer SEQ ID NO:23.
XX
XX glycosylase; enzyme; saccharide; pharmaceutical; food additive;
XX industrial raw material; PCR; primer; ss; plant.
XX
XX Solanum.
XX
XX Synthetic.
XX
XX WO2004078979-A1.
XX
```

```

PD 16-SEP-2004.
XX
PF 03-MAR-2004; 2004WO-JP002675.
XX
PR 03-MAR-2003; 2003JP-00055468.
XX
PR 31-MAR-2003; 2003JP-00093642.
XX
PA (RIKE ) RIKEN KK.
XX
PI Muranaka T, Kohara A;
XX
DR WPI; 2004-662429/64.
XX
PT New glycosylase protein derived from Solanaceae plant, useful for
XX manufacturing pharmaceuticals and food additive.
XX
PS Example 5; SEQ ID NO 23; 61pp; Japanese.
XX
CC The present invention describes a glycosylase protein (I) having a
CC sequence of SEQ ID NO:1, 3, 7, 9 or 11 (S1) (ADR70664, ADR70666,
CC ADR70670, ADR70672 or ADR70674), a sequence comprising (S1) in which one
CC or more amino acids are deleted, substituted and/or added, or a sequence
CC exhibiting 70% or more homology with (S1), where the amino acid sequence
CC exhibits glycosylase activity. Also described: (1) a gene (II) encoding
CC host (1); (2) a recombinant vector (III) containing: (1) a gene (II) encoding
CC host (IV) comprising (II) or (III); and (4) producing (I), using (IV).
CC (I) is useful for combining a saccharide with a substrate, which involves
CC reacting saccharide and a substrate in the presence of (I). (I) can be
CC used in manufacturing pharmaceuticals, food additive or as industrial raw
CC material. (I) has high substrate specificity. The present sequence
CC represents a PCR primer for a Solanum glycosylase protein, which is used
CC in the exemplification of the present invention.
XX
SQ Sequence 20 BP; 3 A; 5 C; 7 G; 5 T; 0 U; 0 Other;
XX
Query Match 6.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 25;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 38 GGAGCTCACCTCCCGAG 55
DB 19 GGAGCTCAACATCCCGAG 2
XX
RESULT 40
ADZ47085
ID ADZ47085 standard; DNA; 20 BP.
XX
AC ADZ47085;
XX
DT 14-JUL-2005 (first entry)
XX
DE Human phosphodiesterase 4B antisense oligo target site SEQ ID NO:113.
XX
KW ss; antisense; phosphodiesterase 4b; PDE 4b; immunosuppressive;
XX expression; autoimmune disease; immune disorder.
XX
OS Homo sapiens.
XX
US2005101000-A1.
XX
PD 12-MAY-2005.
XX
PF 11-DEC-2002; 2002US-00317869.
XX
PR 11-DEC-2002; 2002US-00317869.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Dobie KW;
XX
DR WPI; 2005-345404/35.
XX

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PT New compound 8-80 nucleobases in length targeted to a nucleic acid
PT molecule encoding phosphodiesterase 4B, useful for diagnosing or treating
PT diseases associated with expression of phosphodiesterase 4B, e.g.
PT autoimmune disease.
XX
PS Example 15; SEQ ID NO 113; 25pp; English.
XX
CC The invention relates to a novel compound 8-80 nucleotides in length
CC targeted to a nucleic acid molecule encoding phosphodiesterase 4B, where
CC the compound specifically hybridizes with the nucleic acid molecule
CC encoding phosphodiesterase 4B (ADZ46976) and inhibits the expression of
CC phosphodiesterase 4B. A compound of the invention has immunosuppressive
CC activity. The compound is useful for modulating the expression of
CC phosphodiesterase 4B. It is useful for diagnosing or treating diseases
CC associated with expression of phosphodiesterase 4B, including autoimmune
CC disease. The present sequence is used in the exemplification of the
CC invention.
XX
SQ Sequence 20 BP; 3 A; 6 C; 2 G; 9 T; 0 U; 0 Other;
XX
Query Match 6.1%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 25;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 61 GCCTCACCTGCTTTTCCA 78
DB 1 GCCTCACATGCTTTTCTTA 18
XX
RESULT 41
ADZ47045/c
ID ADZ47045 standard; DNA; 20 BP.
XX
AC ADZ47045;
XX
DT 14-JUL-2005 (first entry)
XX
DE Human phosphodiesterase 4B antisense oligonucleotide SEQ ID NO:73.
XX
KW ss; antisense; phosphodiesterase 4b; PDE 4b; immunosuppressive;
XX expression; autoimmune disease; immune disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note="OTHER=phosphorothioate backbone. All cytidines
FT are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note="2-methoxyethyl nucleotides"
FT modified_base 15..20
FT /*tag= c
FT /mod_base= OTHER
FT /note="2-methoxyethyl nucleotides"
XX
US2005101000-A1.
XX
PD 12-MAY-2005.
XX
PF 11-DEC-2002; 2002US-00317869.
XX
PR 11-DEC-2002; 2002US-00317869.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Dobie KW;
XX
DR WPI; 2005-345404/35.
XX

```

PT New compound 8-80 nucleobases in length targeted to a nucleic acid
PT molecule encoding phosphodiesterase 4B, useful for diagnosing or treating
PT diseases associated with expression of phosphodiesterase 4B, e.g.
PT autoimmune disease.
XX
XX Example 15; SEQ ID NO 73; 25pp; English.
XX
XX The invention relates to a novel compound 8-80 nucleotides in length
XX targeted to a nucleic acid molecule encoding phosphodiesterase 4B, where
XX the compound specifically hybridizes with the nucleic acid molecule
XX encoding phosphodiesterase 4B (ADZ46976) and inhibits the expression of
XX phosphodiesterase 4B. A compound of the invention has immunosuppressive
XX activity. The compound is useful for modulating the expression of
XX phosphodiesterase 4B. It is useful for diagnosing or treating diseases
XX associated with expression of phosphodiesterase 4B, including autoimmune
XX disease. The present sequence is used in the exemplification of the
XX invention.
SQ Sequence 20 BP; 9 A; 2 C; 6 G; 3 T; 0 U; 0 Other;
XX
XX
XX Query Match 6.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 25;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 61 GCCTCAGCTGCTTTCCA 78
Db 20 GCCTCAGCTGCTTTCTTA 3
XX
XX
XX RESULT 42
XX AEC80212/c
XX ID AEC80212 standard; DNA; 20 BP.
XX AC AEC80212;
XX DT 01-DEC-2005 (first entry)
XX DE Skin permeabilization associated mouse gene RT-PCR primer SEQ ID NO 63.
XX KW drug delivery; permeabilization; reverse transcriptase PCR; RT-PCR; PCR;
XX KM primer; ss.
XX OS Mus sp.
XX PN WO200508299-A1.
XX PD 22-SEP-2005.
XX PF 10-SEP-2004; 2004WO-JP013219.
XX PR 10-MAR-2004; 2004JP-00068249.
XX PA (HISA-) HISAMITSU MEDICAL CO LTD.
XX PA (UYKA-) UNIV KANAZAWA TECHNOLOGY LICENSING ORG.
XX PI Tsuji A, Kato M, Sai Y, Li Q;
XX DR WPI; 2005-676484/69.
XX PT Estimation of percutaneous drug permeability, involves pouring drug
XX solution into chamber having subcutaneous tissue side and epidermal side,
XX PT injecting specific solution, and measuring permeability mediated by
XX transporter.
XX Example 1; SEQ ID NO 63; 37pp; Japanese.
XX
XX The invention describes permeability of a percutaneous drug is assayed by
XX pouring a solution containing percutaneous drug into a chamber having
XX subcutaneous tissue side and epidermal side, injecting polyhydric alcohol
XX -containing solution into the epidermal side, and measuring the degree of
XX permeability mediated by a dermal transporter. Also described is a
XX method of secreting for an inhibitory substance, which involves
XX performing comparative evaluation showing the extent of skin

CC permeability. The method is useful for assaying permeability of
CC percutaneous drugs e.g. indomethacin. The skin permeability of a
CC percutaneous drug can be assayed more efficiently. This sequence
CC represents a mouse gene specific primer associated with skin permeability
CC to a percutaneous drug. Note: This sequence is also available in
CC electronic format directly from wipo at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX SQ Sequence 20 BP; 3 A; 4 C; 7 G; 6 T; 0 U; 0 Other;
XX
XX
XX Query Match 6.1%; Score 14.8; DB 1; Length 20;
XX Best Local Similarity 88.9%; Pred. No. 25;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 212 GTATCAGTATCCCACTA 229
Db 19 GTATCAGTATCCCACTA 2
XX
XX
XX RESULT 43
XX AAV25273/c
XX ID AAV25273 standard; DNA; 21 BP.
XX AC AAV25273;
XX DT 11-JUN-1998 (first entry)
XX DE Primer F2 for H.pylori gly gene.
XX KW Cytoplasmic; vaccine; prevention; treatment; infection; envelope;
XX identification; binding compound; bacteria; life cycle; activator;
XX inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis;
XX KM PCR primer; ss.
XX OS Synthetic.
XX OS Helicobacter pylori.
XX PN WO9737044-A1.
XX PD 09-OCT-1997.
XX PF 27-MAR-1997; 97WO-US005223.
XX PR 29-MAR-1996; 96US-00625811.
XX PR 02-APR-1996; 96US-00758731.
XX PR 25-OCT-1996; 96US-00736905.
XX PR 28-OCT-1996; 96US-00738859.
XX PR 06-DEC-1996; 96US-00761318.
XX PA (ASTR) ASTRA AB.
XX PI Smith D, Alm RA;
XX DR WPI; 1997-503122/46.
XX PT Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) -
XX PT useful in vaccines to treat or prevent H. pylori infection and for
XX PT diagnosis of H. pylori infection.
XX Example; Page 108; 1145pp; English.
XX
XX This sequence represents a primer for the H.pylori gly gene. The
XX amplified sequence was used to compare homology of the coding sequences
XX of the invention with other known proteins. The protein encoded by the
XX DNA of the invention may be used in a vaccine to prevent or treat
XX H. pylori infection or to identify H.pylori polypeptide binding compounds,
XX useful as potential H.pylori life cycle activators or inhibitors. The DNA
XX and probes derived from it may be used for the identification of H.pylori
XX in a sample and the diagnosis of H.pylori infection. Nucleic acid
XX sequences complementary to the DNA act as antisense sequences and can be
XX used to prevent the translation of H.pylori mRNA. Antibodies against the
XX protein can be used in immunoassays to evaluate the abundance and
XX distribution of H.pylori-specific antigens. The genomic sequence of


```
CC H.pylori (ATCC 55679) was determined from overlapping contigs generated
CC by mechanically shearing the bacterial DNA. The sequences were analysed
CC for ORF of at least 180 nucleotides, and the predicted coding regions
CC defined by computer evaluation. To identify likely H.pylori antigens for
CC vaccine development, the amino acid sequences predicted from various ORF
CC were analysed for significant homology to other known or exported
CC membrane proteins. Having identified and determined the sequences of
CC interest, particular regions can be isolated from H.pylori by PCR
CC amplification for recombinant polypeptide production, e.g. in E. coli
CC hosts
XX
SQ Sequence 21 BP; 4 A; 2 C; 7 G; 8 T; 0 U; 0 Other;
Query Match 6.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 64 TCACCTGCTTTCCCAAC 81
DB 19 TCACCAAGATTTCACAC 2
```

```
RESULT 44
ADH77769/C
XX ADH77769 standard; DNA; 21 BP.
XX
XX ADH77769;
XX
XX 22-APR-2004 (first entry)
XX
XX Human Alstrom's syndrome-related gene (ALMS1) PCR primer #10.
XX
XX human; ALMS1; Alstrom's syndrome; PCR; ss; primer.
XX
XX Homo sapiens.
XX
XX FR2832420-A1.
XX
XX 23-MAY-2003.
XX
XX 12-NOV-2002; 2002FR-00014097.
XX
XX 09-NOV-2001; 2001US-0345883P.
XX
XX (HOPE) HOFEMANN LA ROCHE & CO AG F.
XX (JACK-) JACKSON LAB.
XX
XX Collin GB, Marshall J, Martin ML, Naggett JK, Nishina MP, Sow V;
XX WPI; 2003-610292/58.
XX
XX New DNA associated with Alstrom syndrome, useful for diagnosis and
XX identification of carriers, also related polypeptides, antibodies and
XX transgenic animals.
XX
XX Example; SEQ ID NO 12; 71bp; French.
XX
XX The invention comprises the amino acid and coding sequence of the human
XX protein ALMS1 which is associated with Alstrom's syndrome. The DNA and
XX protein sequences of the invention are useful in the diagnosis of
XX Alstrom's syndrome. The present DNA sequence represents a PCR primer for
XX the human ALMS1 gene.
XX
SQ Sequence 21 BP; 7 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
```

```
Query Match 6.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 13 GCACCTGAGTTTGGTCAC 30
DB 21 GCACCTGAGCTTTGTGCAC 4
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```
RESULT 45
ACL48195
XX ACL48195 standard; RNA; 21 BP.
XX
XX ACL48195;
XX
XX 24-MAR-2005 (first entry)
XX
XX FOLH1 siRNA antisense sequence, SEQ ID 9267.
XX
XX Cytostatic; Gene therapy; Vaccine; RNA interference; cancer; ss;
XX short interfering RNA; gene silencing.
XX
XX Synthetic.
XX
XX WO2005001092-A2.
XX
XX 06-JAN-2005.
XX
XX 19-MAY-2004; 2004WO-US015645.
XX
XX 20-MAY-2003; 2003US-0471729P.
XX
XX (AMHP) WYETH.
XX
XX Be X, Wei L, Slonim DK, Howes SH;
XX
XX WPI; 2005-075568/08.
XX
XX Pharmaceutical composition comprising an agent capable of modulating an
XX expression level or protein activity of a gene, e.g. ABC4, or a T cell
XX activated by the polypeptide or antibody, and a carrier, useful for
XX treating cancer.
XX
XX Claim 3; SEQ ID NO 9267; 113bp; English.
XX
XX The present invention relates to a novel pharmaceutical composition
XX comprising: (a) an agent capable of modulating an expression level or
XX protein activity of a cancer-related transmembrane protein (CRTP) or gene
XX; an antibody specific for a CRTP, or a T cell activated by a CRTP; and
XX (b) a carrier. The pharmaceutical composition may also comprise a
XX polynucleotide capable of inhibiting or decreasing the expression of the
XX CRTP by RNA interference or an antisense mechanism. The CRTPs of the
XX invention are selected from ABC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
XX FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
XX pharmaceutical composition is useful for treating cancer, e.g. colon
XX cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
XX cancer, stomach cancer, and esophageal cancer. The present sequence is a
XX CRTP short interfering RNAs (siRNA) oligonucleotide. Note: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 21 BP; 4 A; 7 C; 3 G; 0 T; 7 U; 0 Other;
```

```
Query Match 6.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
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```
QY 1 TTCTCCAGCAGACACATG 18
DB 1 TTCTCCAGCAGACAGATG 18
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RESULT 46
ACL48194/C
XX ACL48194 standard; RNA; 21 BP.
XX
XX ACL48194;
XX
XX 24-MAR-2005 (first entry)
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XX
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DE FOLH1 siRNA sense sequence, SEQ ID 9266.
XX
XX Cycostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss;
KW short interfering RNA; gene silencing.
XX
XX Synthetic.
XX
XX WO2005001092-A2.
XX
XX 06-JAN-2005.
XX
XX 19-MAY-2004; 2004WO-US015645.
XX
XX 20-MAY-2003; 2003US-0471729P.
XX
XX (AMHP) WYETH.
XX
XX Be X, Wei L, Slonim DK, Howes SH;
XX
XX WPI, 2005-075568/08.
XX
XX
XX Pharmaceutical composition comprising an agent capable of modulating an
PT expression level or protein activity of a gene, e.g. ABC4, or a T cell
PT activated by the polypeptide or antibody, and a carrier, useful for
PT treating cancer.
XX
XX
XX Claim 3; SEQ ID NO 9266; 113pp; English.
XX
XX The present invention relates to a novel pharmaceutical composition
CC comprising: (a) an agent capable of modulating an expression level or
CC protein activity of a cancer-related transmembrane protein (CRP) or gene
CC ; an antibody specific for a CRP, or a T cell activated by a CRP; and
CC (b) a carrier. The pharmaceutical composition may also comprise a
CC polynucleotide capable of inhibiting or decreasing the expression of the
CC CRP by RNA interference or an antisense mechanism. The CRPs of the
CC invention are selected from ABC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
CC FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
CC pharmaceutical composition is useful for treating cancer, e.g. colon
CC cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
CC cancer, stomach cancer, and esophageal cancer. The present sequence is a
CC CRP short interfering RNA (siRNA) oligonucleotide. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX
SQ Sequence 21 BP; 5 A; 3 C; 7 G; 0 T; 6 U; 0 Other;
Query Match 6.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 TTCTCCAGCAGCAGCTG 18
DB 19 TTCTCCAGCAGCAGCTG 2

RESULT 47
ACL48196/c
ID ACL48196 standard; DNA; 21 BP.
XX
XX ACL48196;
XX
XX 24-MAR-2005 (first entry)
XX
XX FOLH1 target oligonucleotide, SEQ ID 9268.
XX
XX Cycostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss.
XX
XX Homo sapiens.
XX
XX WO2005001092-A2.
XX
XX 06-JAN-2005.

XX
XX 19-MAY-2004; 2004WO-US015645.
XX
XX Cycostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss;
KW short interfering RNA; gene silencing.
XX
XX Synthetic.
XX
XX WO2005001092-A2.
XX
XX 06-JAN-2005.
XX
XX 19-MAY-2004; 2004WO-US015645.
XX
XX 20-MAY-2003; 2003US-0471729P.
XX
XX (AMHP) WYETH.
XX
XX Be X, Wei L, Slonim DK, Howes SH;
XX
XX WPI, 2005-075568/08.
XX
XX
XX Pharmaceutical composition comprising an agent capable of modulating an
PT expression level or protein activity of a gene, e.g. ABC4, or a T cell
PT activated by the polypeptide or antibody, and a carrier, useful for
PT treating cancer.
XX
XX
XX Claim 3; SEQ ID NO 9268; 113pp; English.
XX
XX The present invention relates to a novel pharmaceutical composition
CC comprising: (a) an agent capable of modulating an expression level or
CC protein activity of a cancer-related transmembrane protein (CRP) or gene
CC ; an antibody specific for a CRP, or a T cell activated by a CRP; and
CC (b) a carrier. The pharmaceutical composition may also comprise a
CC polynucleotide capable of inhibiting or decreasing the expression of the
CC CRP by RNA interference or an antisense mechanism. The CRPs of the
CC invention are selected from ABC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
CC FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
CC pharmaceutical composition is useful for treating cancer, e.g. colon
CC cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
CC cancer, stomach cancer, and esophageal cancer. The present sequence is a
CC target oligonucleotide from one such CRP for which short interfering
CC RNA (siRNA) were produced. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX
SQ Sequence 21 BP; 7 A; 3 C; 7 G; 4 T; 0 U; 0 Other;
Query Match 6.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 TTCTCCAGCAGCAGCTG 18
DB 20 TTCTCCAGCAGCAGCTG 3

RESULT 48
ACL48430/c
ID ACL48430 standard; DNA; 21 BP.
XX
XX ACL48430;
XX
XX 24-MAR-2005 (first entry)
XX
XX FOLH1 target oligonucleotide, SEQ ID 9502.
XX
XX Cycostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss.
XX
XX Homo sapiens.
XX
XX WO2005001092-A2.
XX
XX 06-JAN-2005.
XX
XX 19-MAY-2004; 2004WO-US015645.
XX
XX 20-MAY-2003; 2003US-0471729P.
XX
XX (AMHP) WYETH.
XX
XX Be X, Wei L, Slonim DK, Howes SH;
XX

DR WPI; 2005-075568/08.

XX Pharmaceutical composition comprising an agent capable of modulating an

PT expression level or protein activity of a gene, e.g. ABCC4, or a T cell

PT activated by the polypeptide or antibody, and a carrier, useful for

PT treating cancer.

XX

PS Claim 3; SEQ ID NO 9502; 113pp; English.

XX

CC The present invention relates to a novel pharmaceutical composition

CC comprising: (a) an agent capable of modulating an expression level or

CC protein activity of a cancer-related transmembrane protein (CRTP) or gene

CC ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and

CC (b) a carrier. The pharmaceutical composition may also comprise a

CC polynucleotide capable of inhibiting or decreasing the expression of the

CC CRTP by RNA interference or an antisense mechanism. The CRTPs of the

CC invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPE3,

CC FLJ11866, GPR34, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The

CC pharmaceutical composition is useful for treating cancer, e.g. colon

CC cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney

CC cancer, stomach cancer, and esophageal cancer. The present sequence is a

CC target oligonucleotide from one such CRTP for which short interfering

CC RNA (siRNA) were produced. Note: The sequence data for this patent did

CC not form part of the printed specification, but was obtained in

CC electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

CC

SQ Sequence 21 BP; 5 A; 4 C; 7 G; 5 T; 0 U; 0 Other;

OY Query March 6.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 TTCTCAGCACAGCACTG 18
18 TTCTCACCACAGCACTG 1

RESULT 49
ACL48198
ID ACL48198 standard; RNA; 21 BP.
XX
XX ACT48198;
DT 24-MAR-2005 (first entry)
XX
DE FOLH1 siRNA antisense sequence. SEQ ID 9270.
XX
XX Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss;
KW short interfering RNA; gene silencing.
XX
OS Synthetic.
XX
PN WO2005001092-A2.
PD 06-JAN-2005.
PF 19-MAY-2004; 2004MO-US015645.
XX
XX 20-MAY-2003; 2003US-0471723P.
PR
XX (AMHP) WYETH.
PA
PI Be X, Wei L, Slonim DK, Howes SH;
XX WPI; 2005-075568/08.
XX
PT Pharmaceutical composition comprising an agent capable of modulating an
PT expression level or protein activity of a gene, e.g. ABCC4, or a T cell
PT activated by the polypeptide or antibody, and a carrier, useful for
PT treating cancer.
PS Claim 3; SEQ ID NO 9270; 113pp; English.

XX The present invention relates to a novel pharmaceutical composition
CC comprising: (a) an agent capable of modulating an expression level or
CC protein activity of a cancer-related transmembrane protein (CRTP) or gene
CC ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and
CC (b) a carrier. The pharmaceutical composition may also comprise a
CC polynucleotide capable of inhibiting or decreasing the expression of the
CC CRTP by RNA interference or an antisense mechanism. The CRTPs of the
CC invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
CC FHL18b6, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
CC pharmaceutical composition is useful for treating cancer, e.g. colon
CC cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
CC cancer, stomach cancer, and esophageal cancer. The present sequence is a
CC CRTP short interfering RNAs (siRNA) oligonucleotide. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 21 BP; 4 A; 7 C; 3 G; 0 T; 7 U; 0 Other;

Query Match 6.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 12; Conservative 4; Mismatches 2; Indels 0; Gaps 0.

Oy 1 TTCTCCAGCACAGCACTG 18
Db :::||| ||||| :::
2 UUCUCCACACAGCAGUG 19

RESULT 50
ACTL48197/c
ID ACTL48197 standard; RNA; 21 BP.
XX AC ACTL48197;
XX DT 24-MAR-2005 (first entry)
DE FOLH1 siRNA sense sequence, SEQ ID 9269.
XX KW Cytostatic; Gene therapy; Vaccine; RNA interference; cancer; ss;
XX KM short interfering RNA; gene silencing.
XX OS Synthetic.
XX PN WO2005001092-A2.
PD 06-JAN-2005.
PF 19-MAY-2004; 2004WO-US015645.
PX 20-MAY-2003; 2003US-0471729P.
PR (AMHP) WYETH.
PA Be X, Wei L, Slonim DK, Howes SH;
PI WPI; 2005-075568/08.
DR
XX
PT Pharmaceutical composition comprising an agent capable of modulating an
PT expression level or protein activity of a gene, e.g. ABCC4, or a T cell
PT activated by the polypeptide or antibody, and a carrier, useful for
PT treating cancer.
PS Claim 3; SEQ ID NO 9269; 113pp; English.
XX
CC The present invention relates to a novel pharmaceutical composition
CC comprising: (a) an agent capable of modulating an expression level or
CC protein activity of a cancer-related transmembrane protein (CRTP) or gene
CC ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and
CC (b) a carrier. The pharmaceutical composition may also comprise a
CC polynucleotide capable of inhibiting or decreasing the expression of the
CC CRTP by RNA interference or an antisense mechanism. The CRTPs of the
CC invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,

RESULT 53
ID ADW72413/c standard; RNA; 21 BP.
XX
AC ADW72413;
XX
DT 24-MAR-2005 (first entry)
XX
DE Mitochondrial polymerase Polg siRNA strand #117.
XX
XX Cell transduction; organelle; chloroplast; mitochondria; Alpers Disease;
KM carnitine deficiency; pyruvate carboxylase deficiency;
KM mitochondrial cytopathy; mitochondrial DNA depletion;
KM mitochondrial encephalopathy; mitochondrial myopathy; neuropathy; ataxia;
KM retinitis pigmentosa; pyruvate dehydrogenase deficiency;
KM Alzheimers disease; Parkinsons disease; diabetes; aging; heart disease;
KM mitochondrial polymerase; Polg; muscular-gen.; ophthalmological;
KM cerebroprotective; anticonvulsant; antiparkinsonian; nootropic;
KM neuroprotective; cardiovascular-gen.; antidiabetic; ss;
KM short interfering RNA; siRNA; RNA interference; gene silencing.
XX
OS Synthetic.
XX
PN WO200501062-A2.
XX
PD 06-JAN-2005.
XX
PF 25-JUN-2004; 2004WO-US020454.
XX
PR 25-JUN-2003; 2003US-0482603P.
XX
PA (GENC-) GENCIA CORP.
XX
PI Khan S;
XX
PI WPI; 2005-075550/08.
XX
PT New polynucleotide encoding a polypeptide having an organelle or
PT chloroplast localization signal, and a protein transduction domain,
PT useful for treating diseases with defective mitochondrial function.
XX
PS Claim 96; SEQ ID NO 371; 98bp; English.
XX
XX The invention relates to a polynucleotide encoding a recombinant
XX polypeptide comprising an organelle and/or chloroplast localization
XX signal and a protein transduction domain. The invention also relates to a
XX recombinant viral vector comprising the polynucleotide, a cell comprising
XX a modified organelle comprising a bacteriophage, a method of transfecting
XX a cell comprising contacting the cell with a vector operably linked to a
XX polypeptide having a protein transduction domain and an organelle
XX targeting signal, a method of modifying an organelle comprising
XX transfecting the cell with a recombinant lambda phage, the recombinant
XX lambda phage comprising a polynucleotide encoding an organelle
XX localization signal operably linked to a bacteriophage lambda surface
XX protein, where the organelle localization signal is displayed on a
XX surface of the recombinant lambda phage and directs the recombinant
XX lambda phage to the organelle, and where the recombinant lambda phage
XX introduces a polynucleotide into the organelle, a composition comprising
XX a recombinant polypeptide comprising an organelle localization signal
XX operably linked to a protein transduction domain, where the recombinant
XX polypeptide is operably linked to a polynucleotide, a method for
XX modifying the metabolism of a cell comprising contacting the cell with a
XX recombinant vector displaying a recombinant polypeptide comprising a
XX mitochondrial localization signal operably linked to a protein
XX transduction domain, the recombinant vector comprising a polynucleotide
XX encoding a functional respiratory chain component, where the functional
XX respiratory chain component compensates for the at least one defective
XX respiratory chain component when expressed by the cell, a method for
XX modifying cytochrome oxidase activity in a cell, and a method of treating
XX a mitochondrial disease in a host, comprising contacting a host's cell
XX with a recombinant vector displaying a recombinant polypeptide comprising

CC a mitochondrial localization signal operably linked to a protein
CC transduction domain, the recombinant vector encoding a functional
CC mitochondrial polypeptide, where the recombinant vector transfects at
CC least one of the host's mitochondria enabling the host's cell to express
CC the functional mitochondrial polypeptide in the at least one transfected
CC mitochondrion. The methods and compositions are useful for transfecting
CC cells and organelle DNA in living cells directly, in particular for
CC transfecting mitochondria and chloroplasts, and for treating diseases
CC related to organelle dysfunction, such as Alpers Disease, carnitine
CC deficiency, pyruvate carboxylase deficiency, mitochondrial cytopathy,
CC mitochondrial DNA depletion, mitochondrial encephalopathy, mitochondrial
CC myopathy, neuropathy, ataxia, retinitis pigmentosa, pyruvate
CC dehydrogenase deficiency, Alzheimers disease, Parkinsons disease,
CC diabetes, aging and heart disease. This sequence represents mitochondrial
CC polymerase Polg siRNA used in the scope of the invention.
XX
SQ Sequence 21 BP; 6 A; 4 C; 8 G; 2 T; 1 U; 0 Other;
XX
Query Match 6.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 53 CAGCTGCTGCTCAGCTG 70
Db 18 CAGCTGCTGCTCCTCG 1
XX
RESULT 54
ID ADY33887/c standard; DNA; 21 BP.
XX
AC ADY33887;
XX
DT 19-MAY-2005 (first entry)
XX
DE Up-regulated renal cell carcinoma gene, RT-PCR primer SEQ ID No:54.
XX
XX diagnosis; renal cell carcinoma; gene expression; gene silencing;
KM RNA interference; vaccine; cytostatic; reverse transcriptase-PCR; RT-PCR;
KM primer; ss.
XX
OS Homo sapiens.
XX
PN WO2005019475-A2.
XX
PD 03-MAR-2005.
XX
PF 20-AUG-2004; 2004WO-JP012411.
XX
PR 20-AUG-2003; 2003US-0496552P.
PR 27-FEB-2004; 2004US-0548201P.
XX
PA (ONCO-) ONCOTHERAPY SCI INC.
PA (UITY) UNIV TOKYO.
XX
PI Nakamura Y, Katagiri T;
XX
PI WPI; 2005-202667/21.
XX
PT Diagnosing renal cell carcinoma (RCC), comprises determining an increased
PT expression level of an RCC-associated gene, in a biological sample
PT derived from a subject, compared to a normal control level of the gene.
XX
PS Example 1; SEQ ID NO 54; 122bp; English.
XX
XX The invention relates to a method (M1) of diagnosing renal cell carcinoma
XX (RCC) or a predisposition for developing RCC in a subject. The method
XX comprises determining in a biological sample derived from a subject, an
XX expression level of an RCC-associated gene chosen from genes of RCCX 1-
XX 32, where an increase in the level as compared to a normal control level
XX of the gene indicates that the subject suffers from or is at risk of
XX developing RCC. Also described are (1) an RCC reference expression
XX profile, comprising a pattern of gene expression of two or more genes

chosen from the genes of RCCX 1-32, (iii) a method (M2) screening for a compound for treating or preventing RCC, comprising contacting a test compound with a polypeptide encoded by a nucleic acid chosen from genes of RCCX 1-32, detecting the binding activity between the polypeptide and the test compound, and selecting the test compound that binds to the polypeptide, contacting a candidate compound with a cell expressing one or more marker genes, where the one or more marker genes is chosen from the genes of RCCX 1-32, and selecting the candidate compound that reduces the expression level of one or more marker genes chosen from the genes of RCCX 1-32, contacting a test compound with a polypeptide encoded by a nucleic acid chosen from genes of RCCX 1-32, detecting the biological activity of the polypeptide of the contacting step, and selecting the test compound that suppresses the biological activity of the polypeptide encoded by a nucleic acid chosen from genes of RCCX 1-32 in comparison with the biological activity detected in the absence of the test compound, or contacting a candidate compound with a cell into which a vector comprising the transcriptional regulatory region of one or more marker genes and a reporter gene that is expressed under the control of the transcriptional regulatory region has been introduced, where one or more marker genes are chosen from genes of RCCX 1-32, measuring the activity or expression level of the reporter gene, and selecting the candidate compound that reduces activity or expression level of the reporter gene, when the marker gene is an up-regulated marker gene chosen from genes of RCCX 1-32 as compared to a control, (iii) a kit for the diagnosis of RCC, comprising a detection reagent which binds to two or more genes chosen from genes of RCCX 1-32, or a detection reagent which binds to at least one protein encoded by any one of genes chosen from genes of RCCX 1-32, (iv) an array comprising a nucleic acid which binds to two or more nucleic acid sequences chosen from genes of RCCX 1-32, (v) a method (M3) of treating or preventing RCC in a subject comprising administering to the subject, a compound that decreases the expression or activity of a polypeptide encoded by a gene chosen from genes of RCCX 1-32, administering to the subject, an antisense polynucleotide or its derivative having a nucleotide sequence complementary to a coding sequence chosen from the genes of RCCX 1-32, administering to the subject, a small interfering RNA (siRNA), which reduces the expression of a nucleic acid sequence chosen from the genes of RCCX 1-32, administering to the subject, a vaccine comprising a polypeptide encoded by a nucleic acid chosen from the genes of RCCX 1-32 or an immunologically active fragment of the polypeptide, or a polynucleotide encoding the polypeptide, or administering a compound that is obtained by method (M2), (vi) a method (M4) of inducing anti-tumor immunity against RCC comprising contacting an antigen presenting cell with a polypeptide encoded by a nucleic acid chosen from the genes of RCCX 1-32 or an immunologically active fragment of the polypeptide, or a polynucleotide encoding the polypeptide or a vector comprising the polynucleotide, (vii) a composition for treating or preventing RCC, comprising an antisense polynucleotide or siRNA against a polynucleotide chosen from the genes of RCCX 1-32, an antibody or its fragment that binds to a protein encoded by any one gene chosen from the genes of RCCX 1-32, or a compound selected by method (M2), as an active ingredient and a carrier, and (viii) an antibody binding to a protein encoded by the hypoxia-inducible protein 2 (HIF2) gene, where the antibody recognizes an epitope consisting of a specific amino acid sequence. Method (M1) is useful for diagnosing RCC or a predisposition for developing RCC in a subject. The composition or method (M3) is useful for treating or preventing RCC in a subject. The antibody is useful for treating or preventing RCC in a subject, which involves administering to the subject, the antibody or its fragment that binds to a protein encoded by any one gene chosen from the genes of RCCX 1-32, preferably to a protein encoded by the HIF2 gene. The antibody or its fragments bind to a protein comprising at least the C-terminal region of a protein encoded by HIF2 gene. Method (M4) is useful for inducing anti-tumor immunity against RCC. This sequence represents a reverse transcriptase (RT)-PCR primer used in a semi-quantitative RT-PCR experiment.

Sequence 21 BP; 6 A; 2 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 6.1%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

59 CTGCTCAGCTGCTTTTC 76

Db 19 CAGACTCACCTGCTTTTC 2

RESULT 55
AAA66613
ID AAA66613 standard; DNA; 20 BP.

AAA66613;

09-OCT-2000 (first entry)

Dog genomic marker oligonucleotide sequence SEQ ID NO:475.

Dog; genome; genomic marker; radiation hybrid map; identification;
KM chromosome location; gene marker; polymorphic microsatellite marker;
KW phenotype; behaviour; pedigree; ss.

Canis familiaris.

WO200029615-A2.

25-MAY-2000.

15-NOV-1999; 99WO-IB001907.

13-NOV-1998; 98US-0108193P.

(CNRS) CNRS CENT NAT RECH SCI.

Gallbert F, Andre C;

WPI: 2000-387821/33.

New radiation hybrid map of the dog, Canine familiaris, genome, useful for e.g. identifying genes implicated in phenotypic and behavioral traits or in genetic diseases and for studying dog pedigrees.

Claim 1; Page 73; 87pp; English.

The present invention describes a radiation hybrid map of the dog (Canine familiaris) genome comprising the genome location of a marker selected from AAA66139 to AAA66942. The radiation hybrid map is useful for identifying and localizing dog genes, since it covers approximately 80 % of the dog genome and provides a dense map integrating different types (i.e. Type I and Type II) of markers. The map and the dog genome markers (or complementary sequences) are especially useful to identify genes responsible for phenotypic and behavioural traits in dogs, to identify morbid genes, to analyse diseases and identify implicated genes in such diseases and their alleles, and to study dog pedigrees. They may also be useful for isolating corresponding human gene sequences e.g. genes involved in genetic diseases

Sequence 20 BP; 5 A; 7 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 6.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 28;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

149 CTGACGTGAGCTGAA 164
1 CTGACGTGAGCTGAA 16

RESULT 56

AAA66531
ID AAA66531 standard; DNA; 20 BP.

AAA66531;

09-OCT-2000 (first entry)

Dog genomic marker oligonucleotide sequence SEQ ID NO:393.

```

XX Dog; genome; genomic marker; radiation hybrid map; identification;
KM chromosome location; gene marker; polymorphic microsatellite marker;
KM phenotype; behaviour; pedigree; ss.
XX Canis familiaris.
XX WO200029615-A2.
XX
XX 25-MAY-2000.
XX
XX 15-NOV-1999; 99WO-IB001907.
XX
XX 13-NOV-1998; 98US-0108193P.
XX
XX (CNRS ) CNRS CENT NAT RECH SCI.
XX
XX Galibert F, Andre C;
XX
XX WPI; 2000-387821/33.
XX
XX New radiation hybrid map of the dog, Canine familiaris, genome, useful
PT for e.g. identifying genes implicated in phenotypic and behavioral traits
PT or in genetic diseases and for studying dog pedigrees.
XX
XX Claim 1; Page 70; 87pp; English.
XX
XX The present invention describes a radiation hybrid map of the dog (Canine
CC familiaris) genome comprising the genome location of a marker selected
CC from AA66139 to AA66942. The radiation hybrid map is useful for
CC identifying and localising dog genes, since it covers approximately 80 %
CC of the dog genome and provides a dense map integrating different types
CC (i.e. Type I and Type II) of markers. The map and the dog genome markers
CC (or complementary sequences) are especially useful to identify genes
CC responsible for phenotypic and behavioural traits in dogs, to identify
CC morbid genes, to analyse diseases and identify implicated genes in such
CC diseases and their alleles, and to study dog pedigrees. They may also be
CC useful for isolating corresponding human gene sequences e.g. genes
CC involved in genetic diseases
XX
XX Sequence 20 BP; 5 A; 7 C; 4 G; 4 T; 0 U; 0 Other;
SQ
Query Match 6.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 28;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 149 CTCACGTCGAGCTGAA 164
DB 1 CTCACGTCGAGCTGAA 16

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RESULT 57
ADP10727/C
ID ADP10727 standard; DNA; 20 BP.
XX
XX ADP10727;
XX
XX 12-AUG-2004 (first entry)
XX
XX Set 1 left PCR primer for marker probe #72.
XX
XX transplant rejection; immune system; rheumatoid arthritis; lupus;
KM inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss; primer.
XX
XX Homo sapiens.
XX
XX WO2004042346-A2.
XX
XX 21-MAY-2004.
XX
XX 24-APR-2003; 2003WO-US012946.
XX
XX 24-APR-2002; 2002US-00131831.
PR

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PR 20-DEC-2002; 2002US-00325899.
XX
XX (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
XX Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
XX Rosenberg S;
XX
XX WPI; 2004-400724/37.
XX
XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT rejection, in an individual, comprises detecting the expression level of
PT the genes.
XX
XX Claim 58; SEQ ID NO 736; 1762pp; English.
XX
XX The present invention relates to diagnosing or monitoring transplant
CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
CC comprises detecting the expression level of one or more genes. The
CC methods, system and kits are useful in diagnosing or monitoring
CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
CC islet, lung, bone marrow or stem cell transplant rejection, in an
CC xenotransplant rejection or mechanical organ replacement rejection, in an
CC individual. The method is also useful in assessing the immune status of
CC an individual. The methods are also useful in diagnosing and monitoring
CC diseases that involve the immune system, e.g. rheumatoid arthritis,
CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
CC viral, bacterial or fungal infection. The present sequence represents a
CC primer, for a 50 mer oligonucleotide marker for diagnosis and monitoring
CC of allograft rejection and other disorders.
XX
XX Sequence 20 BP; 5 A; 3 C; 8 G; 4 T; 0 U; 0 Other;
SQ
Query Match 6.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 28;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 76 CCAAACCCCACTCTGT 91
DB 20 CCAAACCCCACTCTGT 5

```

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RESULT 58
ADX81409/C
ID ADX81409 standard; DNA; 20 BP.
XX
XX ADX81409;
XX
XX 05-MAY-2005 (first entry)
XX
XX Melanoma associated SNP allelotyping primer, #636.
XX
XX melanoma; DNA polymorphism; SNP detection; cytostatic; gene therapy; PCR;
KM primer; ss.
XX
XX Homo sapiens.
XX
XX WO2005017176-A2.
XX
XX 24-FEB-2005.
XX
XX 05-MAY-2004; 2004WO-US014238.
XX
XX 23-JUL-2003; 2003US-0489703P.
XX
XX 06-NOV-2003; 2003US-00703789.
XX
XX 06-NOV-2003; 2003US-00703817.
XX
XX 06-NOV-2003; 2003US-00704513.
XX
XX (SEQU-) SEQUENOM INC.
XX
XX Roth RB, Nelson MR, Kammerer SM, Braun A, Hoyal-Wrightson CR;
XX WPI; 2005-182387/19.
DR

```


XX Identifying a subject at risk of melanoma by detecting presence or
 PT absence of a polymorphic variation associated with melanoma, where the
 PT presence of polymorphic variations is indicative of the subject being at
 PT risk of melanoma.

PS Example 7; Page 119; 418bp; English.

XX The invention relates to a novel method for identifying a subject at risk
 CC of melanoma. The method comprises detecting the presence or absence of a
 CC polymorphic variation associated with melanoma, where the presence of the
 CC one or more polymorphic variations is indicative of the subject being at
 CC risk of melanoma. The invention further comprises: a method for
 CC identifying a polymorphic variation associated with melanoma proximal to
 CC an incident polymorphic variation associated with melanoma; an isolated
 CC nucleic acid which comprises a portion of or all of a nucleotide sequence
 CC comprising fully defined 68400-213300 base pairs sequences (SEQ ID NO. 3,
 CC 4, 5, 6, and/or 7) given in the specification, and comprises one or more
 CC polymorphic variations; an oligonucleotide comprising a nucleotide
 CC sequence complementary to a portion of the nucleotide sequence above,
 CC where the 3' end of the oligonucleotide is adjacent to a polymorphic
 CC variation; a microarray comprising the isolated nucleic acid linked to a
 CC solid support; an isolated polypeptide encoded by the isolated nucleic
 CC acid sequence; genotyping a nucleic acid; a method for identifying a
 CC candidate molecule that modulates cell proliferation; treating melanoma
 CC in a subject; and treating melanoma in a subject or preventing melanoma
 CC in a subject. The methods and sequences have cytostatic activity. The
 CC polynucleotides may be used in gene therapy. The methods are useful for
 CC identifying a subject at risk of melanoma, treating melanoma in a
 CC subject, or preventing melanoma in a subject. This polynucleotide
 CC sequence represents a primer used in the exemplification of the
 CC invention.

XX SQ Sequence 20 BP; 4 A; 4 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 6.0%; Score 14.4; DB 1; Length 20;

Best Local Similarity 93.8%; Pred. No. 28;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 147 CTCTACGCTGAGCTG 162

Db 16 CTCTACGCTGAGCTG 1

Searched completed: October 2, 2006, 15:44:33
 Job time : 0.001 secs

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OM nucleic - nucleic search, using sw model

Run on: October 2, 2006, 15:41:58 : Search time 0.001 Seconds
(without alignments)
1309.220 Million cell updates/sec

Title: US-10-642-946-6_1967-2208

Perfect score: 242
Sequence: 1 ttccacgacacacacacacgca.....ccaactaactgattcac 242

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 0.5

Searched: 124 seqs, 2705 residues

Total number of hits satisfying chosen parameters: 248

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 124 summaries

Database : pubmaindb1:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19.8	8.2	25	1 US-11-036-317-967319	Sequence 987319, A
2	18.2	7.5	25	1 US-10-310-914A-116991	Sequence 116991, A
3	18.2	7.5	25	1 US-10-809-189-18892	Sequence 18892, A
4	18.2	7.5	25	1 US-11-036-317-87349	Sequence 87349, A
5	18.2	7.5	25	1 US-11-036-317-392205	Sequence 392205, A
6	18.2	7.5	25	1 US-11-036-317-957321	Sequence 957321, A
7	17.8	7.4	25	1 US-10-310-914A-120416	Sequence 120416, A
8	17.8	7.4	25	1 US-11-036-317-915497	Sequence 915497, A
9	17.8	7.4	25	1 US-11-060-756-16184	Sequence 16184, A
10	17.8	7.4	25	1 US-11-060-756-162607	Sequence 162607, A
11	17.8	7.4	25	1 US-11-060-756-165160	Sequence 165160, A
12	17.8	7.4	25	1 US-11-060-756-272361	Sequence 272361, A
13	17.8	7.4	25	1 US-11-121-849-3059	Sequence 3059, A
14	17.6	7.3	25	1 US-10-719-900-615502	Sequence 615502, A
15	17.6	7.3	25	1 US-10-719-900-729485	Sequence 729485, A
16	17.6	7.3	25	1 US-10-932-182A-9117	Sequence 9117, A
17	17.6	7.3	25	1 US-10-932-182A-9117	Sequence 9117, A
18	17.6	7.3	25	1 US-10-933-982-210405	Sequence 210405, A
19	17.6	7.3	25	1 US-11-036-317-651088	Sequence 651088, A
20	17.6	7.3	25	1 US-11-036-317-678385	Sequence 678385, A
21	17.4	7.2	23	1 US-10-310-914A-938303	Sequence 938303, A
22	17.4	7.2	23	1 US-10-310-914A-529952	Sequence 529952, A
23	17.4	7.2	23	1 US-10-310-914A-938303	Sequence 938303, A
24	17.4	7.2	23	1 US-10-310-914A-59879	Sequence 59879, A
25	17.2	7.1	22	1 US-10-310-914A-565232	Sequence 565232, A
26	17.2	7.1	22	1 US-10-084-839-3863	Sequence 3863, A
27	17.2	7.1	24	1 US-09-962-290-9	Sequence 9, App1
28	17.2	7.1	24	1 US-10-310-914A-392849	Sequence 392849, A
29	17.2	7.1	24	1 US-10-310-914A-471177	Sequence 471177, A
30	17	7.0	19	1 US-10-310-914A-382552	Sequence 382552, A
31	17	7.0	19	1 US-10-310-914A-1324851	Sequence 1324851, A
32	16.8	6.9	20	1 US-10-310-914A-1180613	Sequence 1180613, A
33	16.8	6.9	21	1 US-10-310-914A-178653	Sequence 178653, A

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c 107 15.8 6.5 21 1 US-10-831-997-768 Sequence 768, App
108 15.8 6.5 21 1 US-10-310-914A-117008 Sequence 117008,
109 15.8 6.5 21 1 US-10-310-914A-227677 Sequence 227677,
c 110 15.8 6.5 21 1 US-10-310-914A-593921 Sequence 593921,
c 111 15.8 6.5 21 1 US-10-310-914A-800173 Sequence 800173,
c 112 15.8 6.5 22 1 US-10-708-204-288 Sequence 288, App
c 113 15.8 6.5 22 1 US-10-708-204-2661 Sequence 2661, App
114 15.8 6.5 22 1 US-10-310-914A-160067 Sequence 160067,
115 15.8 6.5 22 1 US-10-310-914A-802509 Sequence 802509,
c 116 15.8 6.5 22 1 US-10-310-914A-978748 Sequence 978748,
c 117 15.8 6.5 22 1 US-10-310-914A-1115299 Sequence 1115299,
118 15.6 6.4 22 1 US-10-310-914A-45234 Sequence 45234, A
c 119 15.6 6.4 22 1 US-10-310-914A-419337 Sequence 419337,
c 120 15.6 6.4 22 1 US-10-310-914A-877383 Sequence 877383,
121 15.6 6.4 22 1 US-10-310-914A-955140 Sequence 955140,
c 122 15.6 6.4 22 1 US-10-310-914A-993524 Sequence 993524,
c 123 15.6 6.4 22 1 US-10-310-914A-1134411 Sequence 1134411,
c 124 15.6 6.4 22 1 US-10-310-914A-1326011 Sequence 1326011,

```

ALIGNMENTS

RESULT 1

```

US-11-036-317-987319
; Sequence 987319, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; PRIOR FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 987319
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-987319

```

```

Query Match 8.2%; Score 19.8; DB 1; Length 25;
Best Local Similarity 91.3%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

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Qy 1 TTCTCCAGCAGCAGCTGATTT 23
Db 1 TTCTCCAGCAGCAGCTGATTT 23

```

RESULT 2

```

US-10-310-914A-116991
; Sequence 116991, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kiyazai
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 116991
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-116991

```

```

Query Match 7.5%; Score 18.2; DB 1; Length 24;
Best Local Similarity 73.9%; Pred. No. 21;
Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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```

Qy 45 CACCTCCAGCTGCTGCTTAC 67
Db 1 CCCCCTCCAGCAGCTGCTTAC 23

```

RESULT 3

```

US-10-809-189-18892
; Sequence 18892, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18892
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-809-189-18892

```

```

Query Match 7.5%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy 1 TTCTCCAGCAGCAGCTGATTT 23
Db 3 TTCTCCAGCAGCAGCTGATTT 25

```

RESULT 4

```

US-11-036-317-87349/C
; Sequence 87349, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 87349
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-87349

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```

Query Match 7.5%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy 124 TCGTTTCATCTCTTTGAGAC 146
Db 25 TCTGTCATCTCTTTGAGAC 3

```

```
RESULT 5
US-11-036-317-392205
; Sequence 392205, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 392205
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-392205

Query Match      7.5%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      1 TTCTCCAGACAGCAGCTGATTT 23
Db      1 TTCTCCAGACAGCAGCTGATTT 23

RESULT 6
US-11-036-317-987321
; Sequence 987321, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 987321
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-987321

Query Match      7.5%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      1 TTCTCCAGACAGCAGCTGATTT 23
Db      1 TTCTCCAGACAGCAGCTGATTT 23

RESULT 7
US-10-310-914A-1204416
; Sequence 1204416, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kiyazac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402

; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1204416
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1204416

Query Match      7.4%; Score 17.8; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 27;
Matches 17; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy      33 GGCTGGAGCTCCACCTCCCC 53
Db      1 GGCGGAGGCTCCACCTCC 21

RESULT 8
US-11-036-317-915497
; Sequence 915497, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 915497
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-915497

Query Match      7.4%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      3 CTCCAGACAGCAGCTGATTT 23
Db      1 CTCCAGACAGCAGCTGATTT 21

RESULT 9
US-11-060-756-146184
; Sequence 146184, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 146184
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-146184

Query Match      7.4%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      144 CACCTTCACGTGAGCTGAA 164
Db      2 CACCTTCACGTGAGCTCAA 22
```

```
RESULT 10
US-11-060-756-162607
; Sequence 162607, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 162607
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-162607

Query Match
Best Local Similarity 7.4%; Score 17.8; DB 1; Length 25;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 144 CACCTTCACGTGAGCTGAA 164
Db 3 CACCTATCAGCTGAGCTCAA 23

RESULT 11
US-11-060-756-165160
; Sequence 165160, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 165160
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-165160

Query Match
Best Local Similarity 7.4%; Score 17.8; DB 1; Length 25;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 144 CACCTTCACGTGAGCTGAA 164
Db 1 CACCTATCAGCTGAGCTCAA 21

RESULT 12
US-11-060-756-272361
; Sequence 272361, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
```

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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 272361
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-272361

Query Match
Best Local Similarity 7.4%; Score 17.8; DB 1; Length 25;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 144 CACCTTCACGTGAGCTGAA 164
Db 5 CACCTATCAGCTGAGCTCAA 25

RESULT 13
US-11-121-849-3059
; Sequence 3059, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 3059
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-3059

Query Match
Best Local Similarity 7.4%; Score 17.8; DB 1; Length 25;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 57 TGCTGCTTCACCTGCTTTTCC 77
Db 4 TGCTGCTTCACCTGCTTTTGC 24

RESULT 14
US-10-719-900-615502/c
; Sequence 615502, Application US/10719900
; Publication No. US2005026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 615502
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-615502

Query Match
Best Local Similarity 7.3%; Score 17.6; DB 1; Length 25;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 5 CCAGCACAGCAGCTGATTTTGTC 28
Db 25 CCAGCACATCAGCTGATGATGGC 2
```

```
RESULT 15
US-10-719-900-729485
; Sequence 729485, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 729485
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-729485

Query Match          7.3%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

128 TTCCATCTCTTGGACGACCTCTC 151
Db 2 TTCTAGGCTTTGGACGACCTCTC 25

RESULT 16
US-10-719-900-767611
; Sequence 767611, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 767611
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-767611

Query Match          7.3%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

57 TCGTGGCTCAGCTGCTTTCCAA 80
Db 1 TACTGACGAGCTGCTTTCCAA 24

RESULT 17
US-10-932-182A-49117
; Sequence 49117, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIRO
; APPLICANT: KODAMA, YUKIYO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIRO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
```

```
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 49117
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-49117

Query Match          7.3%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

97 GTAAGTACATTTGGCCCACTAC 120
Db 1 GAAGTACATTTGGCCCACTAC 24

RESULT 18
US-10-933-982-210405
; Sequence 210405, Application US/10933982
; Publication No. US20060051769A1
; GENERAL INFORMATION:
; APPLICANT: Barts, Jennifer
; TITLE OF INVENTION: Methods of Genetic Analysis of E. coli
; FILE REFERENCE: 3700
; CURRENT APPLICATION NUMBER: US/10/933,982
; CURRENT FILING DATE: 2004-09-03
; NUMBER OF SEQ ID NOS: 224976
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 210405
; LENGTH: 25
; TYPE: DNA
; ORGANISM: E. coli
US-10-933-982-210405

Query Match          7.3%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 TTCTCCAGCAGCAGCTGATTTT 24
Db 2 TTCTCCGCGCAGCAGCTGATATT 25

RESULT 19
US-11-036-317-651088/c
; Sequence 651088, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 651088
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-651088

Query Match          7.3%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

37 GGGAGCTCAGCTCCCGAGCTGCT 60
Db 25 GGGAGCTACAGCTCAGAGCTTCT 2
```



```
RESULT 20
US-11-036-317-678385
; Sequence 678385, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 678385
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-678385
```

```
Query Match 7.3%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY 121 GCCGCTTCCATCTCTTGAGC 144
Db 1 GCATCGTTCCATCTGTTTGAGC 24
```

```
RESULT 21
US-10-310-914A-938357
; Sequence 938357, Application US/10310914A
; Publication No. US2006003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 938357
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-938357
```

```
Query Match 7.2%; Score 17.4; DB 1; Length 22;
Best Local Similarity 78.9%; Pred. No. 28;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 74 TTCGAACCCACCCCTGTA 92
Db 2 UCCCAACCCACCCCTGTA 20
```

```
RESULT 22
US-10-310-914A-529952/c
; Sequence 529952, Application US/10310914A
; Publication No. US2006003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
```

```
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 529952
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-529952
```

```
Query Match 7.2%; Score 17.4; DB 1; Length 23;
Best Local Similarity 94.7%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 45 CACCTCCCAAGCTGCTGCC 63
Db 23 CACTCCTCAGCTGCTGCC 5
```

```
RESULT 23
US-10-310-914A-938303
; Sequence 938303, Application US/10310914A
; Publication No. US2006003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 938303
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-938303
```

```
Query Match 7.2%; Score 17.4; DB 1; Length 23;
Best Local Similarity 78.9%; Pred. No. 27;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 74 TTCGAACCCACCCCTGTA 92
Db 5 UCCCAACCCACCCCTGTA 23
```

```
RESULT 24
US-10-310-914A-59879
; Sequence 59879, Application US/10310914A
; Publication No. US2006003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 59879
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-59879
```

```
Query Match 7.1%; Score 17.2; DB 1; Length 22;
Best Local Similarity 72.7%; Pred. No. 30;
Matches 16; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
```

```
OY 47 CCTCCCAAGCTGCTGCTCACC 68
Db 1 CCCCAAGCTGCTGCTCACC 22
```

```
RESULT 25
US-10-310-914A-565232
; Sequence 565232, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Bentwich, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 565232
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-565232

Query Match          7.1%; Score 17.2; DB 1; Length 22;
Best Local Similarity 54.5%; Pred. No. 30;
Matches 12; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy      56  CGGCTGCTCAGCTGCTTTTC 77
Db      1  CUGGCGCCUGCGUGCGUGUCC 22

RESULT 26
US-10-084-839-3863/C
; Sequence 3863, Application US/10084839
; Publication No. US20030186238A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Allawi, Hatim
; APPLICANT: Argue, Brad T.
; APPLICANT: Bartholomay, Christian T.
; APPLICANT: Barthelemy, Luanne
; APPLICANT: Chenak, Luanne
; APPLICANT: Curtis, Michelle L.
; APPLICANT: Els, Peggy S.
; APPLICANT: Hall, Jeff G.
; APPLICANT: IP, Hon S.
; APPLICANT: Ji, Lin
; APPLICANT: Kaiser, Michael
; APPLICANT: Kislackowski, Jr., Robert W.
; APPLICANT: Lukowiak, Andrew A.
; APPLICANT: Lyamichev, Victor
; APPLICANT: Lyamicheva, Natalie E.
; APPLICANT: Ma, Wupo
; APPLICANT: Neri, Bruce P.
; APPLICANT: Olson, Sarah M.
; APPLICANT: Olson-Munoz, Marilyn C.
; APPLICANT: Schaefer, James J.
; APPLICANT: Skrzypczynski, Zbigniew
; APPLICANT: Takova, Teetska Y.
; APPLICANT: Thompson, Lisa C.
; APPLICANT: Vedvik, Kevin L.
; TITLE OF INVENTION: RNA Detection Assays
; FILE REFERENCE: FORS-06666
; CURRENT APPLICATION NUMBER: US/10/084,839
; CURRENT FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 4004
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3863
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-084-839-3863
```

```
Query Match          7.1%; Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 29;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      120  CGCCTCGTTTCCATCTCTTGG 141
Db      23  CGCCTCGTTTCTATCTCTTGG 2

RESULT 27
US-09-962-290-9/C
; Sequence 9, Application US/09962290
; Patent No. US20020092034A1
; GENERAL INFORMATION:
; APPLICANT: Paterson, David
; APPLICANT: Brennan, Miles
; APPLICANT: Hochgeschwender, Ute
; APPLICANT: Flintoff, Wayne
; APPLICANT: Sadlish, Heather
; APPLICANT: Underhill, T. Michael
; APPLICANT: Williams, Frederick
; TITLE OF INVENTION: No. US20020092034A1-Human Model of Gestational and Adult Folate D
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 3718-8
; CURRENT APPLICATION NUMBER: US/09/962,290
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/234,853
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(24)
; OTHER INFORMATION: primer
US-09-962-290-9

Query Match          7.1%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 27;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      14  CACTGATTTGTGTCACCTGGC 35
Db      23  CAATGATGTGTGTCACCTGGC 2

RESULT 28
US-10-310-914A-392849
; Sequence 392849, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 392849
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-392849

Query Match          7.1%; Score 17.2; DB 1; Length 24;
Best Local Similarity 68.2%; Pred. No. 27;
Matches 15; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
```

OY 66 ACCTGCTTTCCAAACCCACC 87
 Db 1 AACUCUCUCCAAACACACC 22

RESULT 29
 US-10-310-914A-471177
 ; Sequence 471177, Application US/10310914A
 ; Publication No. US20060003322A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bentwich, Isaac
 ; APPLICANT: Shlier, Kuzat
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 ; FILE REFERENCE: 06087.0200.CPUS01
 ; CURRENT APPLICATION NUMBER: US/10/310,914A
 ; CURRENT FILING DATE: 2002-12-06
 ; NUMBER OF SEQ ID NOS: 1388402
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 471177
 ; LENGTH: 24
 ; TYPE: RNA
 ; ORGANISM: Human
 US-10-310-914A-471177

Query Match 7.1%; Score 17.2; DB 1; Length 24;
 Best Local Similarity 68.2%; Pred. No. 27;
 Matches 15; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 31 CTGCGCTGGAGCTCCACTCCC 52
 Db 1 CUCACUGGAGCUCACCUCC 22

RESULT 30
 US-10-310-914A-382552
 ; Sequence 382552, Application US/10310914A
 ; Publication No. US20060003322A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bentwich, Isaac
 ; APPLICANT: Shlier, Kuzat
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 ; FILE REFERENCE: 06087.0200.CPUS01
 ; CURRENT APPLICATION NUMBER: US/10/310,914A
 ; CURRENT FILING DATE: 2002-12-06
 ; NUMBER OF SEQ ID NOS: 1388402
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 382552
 ; LENGTH: 19
 ; TYPE: RNA
 ; ORGANISM: Human
 US-10-310-914A-382552

Query Match 7.0%; Score 17; DB 1; Length 19;
 Best Local Similarity 64.7%; Pred. No. 37;
 Matches 11; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

OY 62 CCTCACCCTGCTTTTCCA 78
 Db 1 CCUCACCCUGCUUCCCA 17

RESULT 31
 US-10-310-914A-1324851/C
 ; Sequence 1324851, Application US/10310914A
 ; Publication No. US20060003322A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bentwich, Isaac
 ; APPLICANT: Shlier, Kuzat
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 ; FILE REFERENCE: 06087.0200.CPUS01
 ; CURRENT APPLICATION NUMBER: US/10/310,914A
 ; CURRENT FILING DATE: 2002-12-06
 ; NUMBER OF SEQ ID NOS: 1388402
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 1324851
 ; LENGTH: 21
 ; TYPE: RNA
 ; ORGANISM: Human
 US-10-310-914A-1324851

FILE REFERENCE: 06087.0200.CPUS01
 ; CURRENT APPLICATION NUMBER: US/10/310,914A
 ; CURRENT FILING DATE: 2002-12-06
 ; NUMBER OF SEQ ID NOS: 1388402
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 1324851
 ; LENGTH: 20
 ; TYPE: RNA
 ; ORGANISM: Human
 US-10-310-914A-1324851

Query Match 7.0%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 62 CCTCACCCTGCTTTTCCA 78
 Db 20 CCTCACCCTGCTTTTCCA 4

RESULT 32
 US-10-310-914A-1180613
 ; Sequence 1180613, Application US/10310914A
 ; Publication No. US20060003322A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bentwich, Isaac
 ; APPLICANT: Shlier, Kuzat
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 ; FILE REFERENCE: 06087.0200.CPUS01
 ; CURRENT APPLICATION NUMBER: US/10/310,914A
 ; CURRENT FILING DATE: 2002-12-06
 ; NUMBER OF SEQ ID NOS: 1388402
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 1180613
 ; LENGTH: 20
 ; TYPE: RNA
 ; ORGANISM: Human
 US-10-310-914A-1180613

Query Match 6.9%; Score 16.8; DB 1; Length 20;
 Best Local Similarity 70.0%; Pred. No. 37;
 Matches 14; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 TTCTCCAGCAGCAGCTGG 20
 Db 1 UUCUCCAGCAAGCACUGCA 20

RESULT 33
 US-10-310-914A-178653/C
 ; Sequence 178653, Application US/10310914A
 ; Publication No. US20060003322A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bentwich, Isaac
 ; APPLICANT: Shlier, Kuzat
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 ; FILE REFERENCE: 06087.0200.CPUS01
 ; CURRENT APPLICATION NUMBER: US/10/310,914A
 ; CURRENT FILING DATE: 2002-12-06
 ; NUMBER OF SEQ ID NOS: 1388402
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 178653
 ; LENGTH: 21
 ; TYPE: RNA
 ; ORGANISM: Human
 US-10-310-914A-178653

Query Match 6.9%; Score 16.8; DB 1; Length 21;
 Best Local Similarity 90.0%; Pred. No. 35;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 44 CCACCTCCAGCTGCTGCC 63
|||
DB 20 CCACCACTCCAGCTGCTGCC 1

RESULT 34
US-10-310-914A-185040/c
; Sequence 185040, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 185040
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-185040

Query Match 6.9%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 35;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 CAGCAGCAGCTGATTTTG 25
|||
DB 20 CAGCAGCAGCTGATTTTG 1

RESULT 35
US-10-310-914A-1124039/c
; Sequence 1124039, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1124039
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1124039

Query Match 6.9%; Score 16.8; DB 1; Length 23;
Best Local Similarity 90.0%; Pred. No. 32;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 47 CCTCCAGCTGCTGCTCA 66
|||
DB 20 CCACCACTCCAGCTGCTCA 1

RESULT 36
US-10-310-914A-931759
; Sequence 931759, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 931759
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-931759

Query Match 6.9%; Score 16.8; DB 1; Length 24;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 15; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 49 TCCCACTGCTGCTCACC 68
|||
DB 1 UCCCACTGCTGCTCACC 20

RESULT 37
US-10-084-839-3864
; Sequence 3864, Application US/10084839
; Publication No. US20030186238A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Allawi, Hatim
; APPLICANT: Argue, Brad T.
; APPLICANT: Bartholomew, Christian T.
; APPLICANT: Chehak, LuAnne
; APPLICANT: Curtis, Michelle L.
; APPLICANT: Eis, Peggy S.
; APPLICANT: Hall, Jeff G.
; APPLICANT: IP, Hon S.
; APPLICANT: Ji, Lin
; APPLICANT: Kaiser, Michael
; APPLICANT: Kwiatkowski, Jr., Robert W.
; APPLICANT: Lukowiak, Andrew A.
; APPLICANT: Lyamichev, Victor
; APPLICANT: Lyamichev, Natalie E.
; APPLICANT: Ma, Wupo
; APPLICANT: Neri, Bruce P.
; APPLICANT: Olson, Sarah M.
; APPLICANT: Olson-Munoz, Marilyn C.
; APPLICANT: Schaefer, James J.
; APPLICANT: Skrzypczynski, Zdzigniew
; APPLICANT: Takova, Teetaka Y.
; APPLICANT: Thompson, Lisa C.
; APPLICANT: Vedvik, Kevin L.
; TITLE OF INVENTION: RNA Detection Assays
; FILE REFERENCE: FORS-0666
; CURRENT APPLICATION NUMBER: US/10/084,839
; CURRENT FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 4004
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3864
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-084-839-3864

Query Match 6.9%; Score 16.6; DB 1; Length 23;
Best Local Similarity 82.6%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 114 CCACTAGCCTGCTTCATCTC 136
|||
DB 1 CCACTAGCCTGCTTCATCTC 23

RESULT 38
US-10-310-914A-970522

```
; Sequence 970522, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 970522
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-970522
```

```
Query Match 6.8%; Score 16.4; DB 1; Length 19;
Best Local Similarity 77.8%; Pred. No. 43;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 4 TTCACGACGACGACTGAT 21
Db 1 UCCAGCACACUCCUGGAU 18
```

```
RESULT 39
US-11-083-784-1493132/c
; Sequence 1493132, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1493132
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1493132
```

```
Query Match 6.8%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 TTCTCCAGCAGCAGCTG 18
Db 19 TTCTCCAGCAGCAGCTG 2
```

```
RESULT 40
US-11-101-244-1493132/c
; Sequence 1493132, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
```

```
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1493132
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1493132
```

```
Query Match 6.8%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 TTCTCCAGCAGCAGCTG 18
Db 19 TTCTCCAGCAGCAGCTG 2
```

```
RESULT 41
US-10-310-914A-970523
; Sequence 970523, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 970523
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-970523
```

```
Query Match 6.8%; Score 16.4; DB 1; Length 20;
Best Local Similarity 77.8%; Pred. No. 41;
Matches 14; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 4 TTCACGACGACGACTGAT 21
Db 1 UCCAGCACACUCCUGGAU 18
```

```
RESULT 42
US-10-310-914A-853027
; Sequence 853027, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 853027
; LENGTH: 21
```

TYPE: RNA
ORGANISM: Human
US-10-310-914A-853027

Query Match 6.8%; Score 16.4; DB 1; Length 21;
Best Local Similarity 83.3%; Pred. No. 39;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 44 CCACTCCCGAGCTGCT 61
|||:|||||:|
Db 1 CCACCCCGCAGCAGCUG 18

RESULT 43

US-10-310-914A-560231
Sequence 560231, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shlier, Kiyazac
TITLE OF INVENTION: Biointernationally detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310.914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 560231
LENGTH: 22
TYPE: RNA
ORGANISM: Human
US-10-310-914A-560231

Query Match 6.8%; Score 16.4; DB 1; Length 22;
Best Local Similarity 72.2%; Pred. No. 37;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 48 CTCCTGCTGCTGCTGCTC 65
||:|||||:|:|:|
Db 1 CUCCCCAGCUCGCTCUC 18

RESULT 44

US-10-310-914A-998415
Sequence 998415, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shlier, Kiyazac
TITLE OF INVENTION: Biointernationally detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310.914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 998415
LENGTH: 22
TYPE: RNA
ORGANISM: Human
US-10-310-914A-998415

Query Match 6.8%; Score 16.4; DB 1; Length 22;
Best Local Similarity 72.2%; Pred. No. 37;
Matches 13; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 43 TCACCTCCCGAGCTGCT 60
:||||:|||||:|
Db 1 UCCACCTCCCGAGCTGCT 18

RESULT 45
US-10-310-914A-1111010

Sequence 1111010, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shlier, Kiyazac
TITLE OF INVENTION: Biointernationally detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310.914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1111010
LENGTH: 23
TYPE: RNA
ORGANISM: Human
US-10-310-914A-1111010

Query Match 6.8%; Score 16.4; DB 1; Length 23;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 12; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 55 GCTGCTGCTGCTGCTGCT 72
||:|||||:|:|:|
Db 3 GCUCGCTGCTGCTGCTGCT 20

RESULT 46

US-10-310-914A-1111016
Sequence 1111016, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shlier, Kiyazac
TITLE OF INVENTION: Biointernationally detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310.914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1111016
LENGTH: 23
TYPE: RNA
ORGANISM: Human
US-10-310-914A-1111016

Query Match 6.8%; Score 16.4; DB 1; Length 23;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 12; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 55 GCTGCTGCTGCTGCTGCT 72
||:|||||:|:|:|
Db 4 GCUCGCTGCTGCTGCTGCT 21

RESULT 47

US-10-310-914A-1256042/c
Sequence 1256042, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shlier, Kiyazac
TITLE OF INVENTION: Biointernationally detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310.914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1256042
LENGTH: 23
TYPE: RNA

```
; ORGANISM: Human
US-10-310-914A-1256042

Query Match      6.8%; Score 16.4; DB 1; Length 23;
Best Local Similarity 94.4%; Pred. No. 35;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      179 AAGCCACCGTGTCTGTT 196
      |||||
Db      19 AAGCCACCGTGTCTGTT 2

RESULT 48
US-10-310-914A-126098/c
; Sequence 126098, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 126098
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-126098

Query Match      6.7%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      44 CCACCTCCCGAGCTGCTGCT 64
      |||||
Db      21 CCACCTCCCGAAGCTGCTGCT 1

RESULT 49
US-10-310-914A-204775
; Sequence 204775, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 204775
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-204775

Query Match      6.7%; Score 16.2; DB 1; Length 21;
Best Local Similarity 71.4%; Pred. No. 41;
Matches 15; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY      34 GCTGGAGCTCCACCTCCCA 54
      |||||
Db      1 GCTGGAGCTCCACCTCCCA 21

RESULT 50
US-10-310-914A-306631/c
; Sequence 306631, Application US/10310914A

; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 306631
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-306631

Query Match      6.7%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 41;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      70 GCTTTCCGAACCCACCCCTG 90
      |||||
Db      21 GCTTTCCGAGCCCACTCTG 1

RESULT 51
US-10-310-914A-565231
; Sequence 565231, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 565231
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-565231

Query Match      6.7%; Score 16.2; DB 1; Length 21;
Best Local Similarity 52.4%; Pred. No. 41;
Matches 11; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

OY      56 CTGCTGCTCAGCTGCTTTC 76
      |||||
Db      1 CUGGUGCTCUGCTGUGUC 21

RESULT 52
US-10-310-914A-1148315
; Sequence 1148315, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kiyazat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1148315
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
```


US-10-310-914A-1148315

Query Match 6.7%; Score 16.2; DB 1; Length 21;

Best Local Similarity 66.7%; Pred. No. 41;

Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 65 CACGCTTTTCCAAACCCCA 85

DB 1 CACCGCTTTTCCAAACCCCA 21

RESULT 53

US-09-965-422-121

Sequence 121, Application US/09965422

Publication No. US20030216545A1

GENERAL INFORMATION:

APPLICANT: Spytek, Kimberly A

APPLICANT: Casman, Stacie

APPLICANT: Padigaru, Muralidhara

APPLICANT: Dickson, Kevin

APPLICANT: Vernet, Corine

APPLICANT: Spaderma, Steven K

APPLICANT: Shenoy, Suresh G

APPLICANT: Gerlach, Valerie

APPLICANT: Ellerman, Karen

APPLICANT: Edinger, Shlomit

APPLICANT: MacDougall, John R

APPLICANT: Smithson, Glenda

APPLICANT: Li, Li

APPLICANT: Malyanar, Urial M

APPLICANT: Taylor, Sarah

APPLICANT: Gunther, Erik

APPLICANT: Tchernev, Velizar T

TITLE OF INVENTION: No. US20030216545A1

Proteins and Nucleic Acids Encoding Same

FILE REFERENCE: 21401-132

CURRENT FILING DATE: 2001-09-27

PRIOR FILING DATE: 2000-09-28

PRIOR FILING DATE: 2000-09-28

PRIOR FILING DATE: 2000-09-28

PRIOR FILING DATE: 2000-09-28

PRIOR FILING DATE: 2000-09-28

PRIOR FILING DATE: 2000-09-28

PRIOR FILING DATE: 2000-09-28

PRIOR FILING DATE: 2000-09-28

PRIOR FILING DATE: 2000-09-28

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PRIOR FILING DATE: 2000-09-28

PRIOR FILING DATE: 2000-09-28

PRIOR FILING DATE: 2000-09-28

PRIOR FILING DATE: 2000-09-28

PRIOR FILING DATE: 2000-09-28

Query Match 6.7%; Score 16.2; DB 1; Length 22;

Best Local Similarity 85.7%; Pred. No. 39;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 133 TCTCTTGAGACACCTCTAC 153

DB 2 TCTCTTGAGACACCTCTAC 22

RESULT 54

US-10-005-041A-187

Sequence 187, Application US/10005041A

Publication No. US2003023231A1

GENERAL INFORMATION:

APPLICANT: Casman, Stacie J

APPLICANT: Padigaru, Muralidhara

APPLICANT: Burgess, Catherine E

APPLICANT: Shinkens, Richard A

APPLICANT: Spytek, Kimberly A

APPLICANT: Gilbert, Jennifer A

APPLICANT: Mayotte, Jane E

APPLICANT: Baumgartner, Jason C

APPLICANT: Mishra, Vishnu

APPLICANT: Vernet, Corine AM

APPLICANT: Dickinson, Kevin S

APPLICANT: Ballinger, Robert A

APPLICANT: Wolenc, Adam R

APPLICANT: Edinger, Shlomit R

APPLICANT: MacDougall, John R

APPLICANT: Smithson, Glenda

APPLICANT: Ellerman, Karen

APPLICANT: Stone, David J

APPLICANT: Gunther, Erik

APPLICANT: Gerlach, Valerie

TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

FILE REFERENCE: 21402-215

CURRENT FILING DATE: 2001-12-04

PRIOR FILING DATE: 2000-12-05

PRIOR FILING DATE: 2000-12-05

PRIOR FILING DATE: 2000-12-05

PRIOR FILING DATE: 2000-12-05

PRIOR FILING DATE: 2000-12-05

PRIOR FILING DATE: 2000-12-05

PRIOR FILING DATE: 2000-12-05

PRIOR FILING DATE: 2000-12-05

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PRIOR FILING DATE: 2000-12-05

PRIOR FILING DATE: 2000-12-05

PRIOR FILING DATE: 2000-12-05

PRIOR FILING DATE: 2000-12-05

```
; PRIOR APPLICATION NUMBER: 60/271,646
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/276,401
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/311,981
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/312,858
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/271,840
; PRIOR FILING DATE: 2001-02-27,324
; PRIOR APPLICATION NUMBER: 60/277,324
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/286,096
; PRIOR FILING DATE: 2001-04-21
; PRIOR APPLICATION NUMBER: 60/299,695
; PRIOR FILING DATE: 2001-06-20,614
; PRIOR APPLICATION NUMBER: 60/315,614
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/272,405
; PRIOR FILING DATE: 2001-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 653
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 526
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
US-10-085-198-526
```

```
Query Match      6.7%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      133 TCTCTTGAGACCTCTAC 153
Db      2 TCTCTTAGAGCCCTTTCAC 22

RESULT 56
US-10-913-280-144
; Sequence 144, Application US/10913280
; Publication No. US20050089894A1
; GENERAL INFORMATION:
; APPLICANT: Gims, Edward I.
; APPLICANT: Galdizcka, Marzena
; TITLE OF INVENTION: SYSTEMS AND METHODS FOR ANALYZING
; FILE REFERENCE: 07917-238001
; CURRENT APPLICATION NUMBER: US/10/913,280
; CURRENT FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 60/493,238
; PRIOR FILING DATE: 2003-08-06
; PRIOR APPLICATION NUMBER: US 60/568,958
; PRIOR FILING DATE: 2004-05-07
; NUMBER OF SEQ ID NOS: 920
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-913-280-144
```

```
Query Match      6.7%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      126 GTTTCATCTCTTGAGAC 146
        ||||||| ||||| |||
```

```
Db      1 GTTTCATCTATTGTAGAC 21

RESULT 57
US-10-708-204-401/c
; Sequence 401, Application US/10708204
; Publication No. US20050222399A1
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
; FILE REFERENCE: 55033
; CURRENT APPLICATION NUMBER: US/10/708,204
; CURRENT FILING DATE: 2004-02-16
; NUMBER OF SEQ ID NOS: 7351
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 401
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-708-204-401
```

```
Query Match      6.7%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      52 CCAGCTGCTGCTCCACCTGCT 72
Db      22 CCTGCTGCTGCCACCTCTCT 2
```

```
RESULT 58
US-10-708-204-668/c
; Sequence 668, Application US/10708204
; Publication No. US20050222399A1
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
; FILE REFERENCE: 55033
; CURRENT APPLICATION NUMBER: US/10/708,204
; CURRENT FILING DATE: 2004-02-16
; NUMBER OF SEQ ID NOS: 7351
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 668
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-708-204-668
```

```
Query Match      6.7%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      52 CCAGCTGCTGCTCCACCTGCT 72
Db      22 CCTGCTGCTGCCACCTCTCT 2
```

```
RESULT 59
US-10-708-204-1098/c
; Sequence 1098, Application US/10708204
; Publication No. US20050222399A1
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
; FILE REFERENCE: 55033
; CURRENT APPLICATION NUMBER: US/10/708,204
; CURRENT FILING DATE: 2004-02-16
```

NUMBER OF SEQ ID NOS: 7351
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1098
LENGTH: 22
TYPE: RNA
ORGANISM: Homo Sapiens
US-10-708-204-1098

Query Match 6.7%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 52 CCAGCTGCTGCTCACCCTGCT 72
DB 22 CCTGCTGCTGCCCACTCCT 2

RESULT 60
US-10-708-204-1209/c
Sequence 1209, Application US/10708204
Publication No. US2005022399A1
GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
FILE REFERENCE: 55033
CURRENT APPLICATION NUMBER: US/10/708,204
CURRENT FILING DATE: 2004-02-16
NUMBER OF SEQ ID NOS: 7351
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1209
LENGTH: 22
TYPE: RNA
ORGANISM: Homo Sapiens
US-10-708-204-1209

Query Match 6.7%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 52 CCAGCTGCTGCTCACCCTGCT 72
DB 22 CCTGCTGCTGCCCACTCCT 2

RESULT 61
US-10-708-204-1976/c
Sequence 1976, Application US/10708204
Publication No. US2005022399A1
GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
FILE REFERENCE: 55033
CURRENT APPLICATION NUMBER: US/10/708,204
CURRENT FILING DATE: 2004-02-16
NUMBER OF SEQ ID NOS: 7351
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1976
LENGTH: 22
TYPE: RNA
ORGANISM: Homo Sapiens
US-10-708-204-1976

Query Match 6.7%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 52 CCAGCTGCTGCTCACCCTGCT 72
DB 22 CCTGCTGCTGCCCACTCCT 2

RESULT 62
US-10-708-204-1991/c
Sequence 1991, Application US/10708204
Publication No. US2005022399A1
GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
FILE REFERENCE: 55033
CURRENT APPLICATION NUMBER: US/10/708,204
CURRENT FILING DATE: 2004-02-16
NUMBER OF SEQ ID NOS: 7351
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1991
LENGTH: 22
TYPE: RNA
ORGANISM: Homo Sapiens
US-10-708-204-1991

Query Match 6.7%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 52 CCAGCTGCTGCTCACCCTGCT 72
DB 22 CCTGCTGCTGCCCACTCCT 2

RESULT 63
US-10-708-204-2118/c
Sequence 2118, Application US/10708204
Publication No. US2005022399A1
GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
FILE REFERENCE: 55033
CURRENT APPLICATION NUMBER: US/10/708,204
CURRENT FILING DATE: 2004-02-16
NUMBER OF SEQ ID NOS: 7351
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2118
LENGTH: 22
TYPE: RNA
ORGANISM: Homo Sapiens
US-10-708-204-2118

Query Match 6.7%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 52 CCAGCTGCTGCTCACCCTGCT 72
DB 22 CCTGCTGCTGCCCACTCCT 2

RESULT 64
US-10-708-204-2334/c
Sequence 2334, Application US/10708204
Publication No. US2005022399A1
GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
FILE REFERENCE: 55033
CURRENT APPLICATION NUMBER: US/10/708,204
CURRENT FILING DATE: 2004-02-16
NUMBER OF SEQ ID NOS: 7351
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2334
LENGTH: 22
TYPE: RNA
ORGANISM: Homo Sapiens
US-10-708-204-2334

Query Match 6.7%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 52 CCAGCTGCTGCTCACCCTGCT 72
DB 22 CCTGCTGCTGCCCACTCCT 2

RESULT 65
US-10-708-204-2118/c
Sequence 2118, Application US/10708204
Publication No. US2005022399A1
GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
FILE REFERENCE: 55033
CURRENT APPLICATION NUMBER: US/10/708,204
CURRENT FILING DATE: 2004-02-16
NUMBER OF SEQ ID NOS: 7351
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2118
LENGTH: 22
TYPE: RNA
ORGANISM: Homo Sapiens
US-10-708-204-2118

Query Match 6.7%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 52 CCAGCTGCTGCTCACCCTGCT 72
DB 22 CCTGCTGCTGCCCACTCCT 2

RESULT 66
US-10-708-204-2118/c
Sequence 2118, Application US/10708204
Publication No. US2005022399A1
GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
FILE REFERENCE: 55033
CURRENT APPLICATION NUMBER: US/10/708,204
CURRENT FILING DATE: 2004-02-16
NUMBER OF SEQ ID NOS: 7351
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2118
LENGTH: 22
TYPE: RNA
ORGANISM: Homo Sapiens
US-10-708-204-2118

Query Match 6.7%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 52 CCAGCTGCTGCTCACCCTGCT 72
DB 22 CCTGCTGCTGCCCACTCCT 2

RESULT 67
US-10-708-204-2334/c
Sequence 2334, Application US/10708204
Publication No. US2005022399A1
GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
FILE REFERENCE: 55033
CURRENT APPLICATION NUMBER: US/10/708,204
CURRENT FILING DATE: 2004-02-16
NUMBER OF SEQ ID NOS: 7351
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2334
LENGTH: 22
TYPE: RNA
ORGANISM: Homo Sapiens
US-10-708-204-2334

Query Match 6.7%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 52 CCAGCTGCTGCTCACCCTGCT 72
DB 22 CCTGCTGCTGCCCACTCCT 2

```

; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2334
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-708-204-2334

Query Match
Best Local Similarity 6.7%; Score 16.2; DB 1; Length 22;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 52 CCAGCTGCTGCTCCTCCTCT 72
DB 22 CCGCTGCTGCTGCTGCTCCTCT 2

RESULT 65
US-10-708-204-2487/c
; Sequence 2487, Application US/10708204
; Publication No. US2005022399A1
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATICALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
; FILE REFERENCE: 55033
; CURRENT APPLICATION NUMBER: US/10/708,204
; CURRENT FILING DATE: 2004-02-16
; NUMBER OF SEQ ID NOS: 7351
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2487
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-708-204-2487

Query Match
Best Local Similarity 6.7%; Score 16.2; DB 1; Length 22;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 52 CCAGCTGCTGCTCCTCCTCT 72
DB 22 CCGCTGCTGCTGCTGCTCCTCT 2

RESULT 66
US-10-310-914A-222541/c
; Sequence 222541, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 222541
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-222541

Query Match
Best Local Similarity 6.7%; Score 16.2; DB 1; Length 22;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 46 ACCGCCAGCTGCTGCTCA 66
DB 22 ACTTCCCGAGCTTGTGCCCA 2
```

```

RESULT 67
US-10-310-914A-653245/c
; Sequence 653245, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 653245
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-653245

Query Match
Best Local Similarity 6.7%; Score 16.2; DB 1; Length 22;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 33 GGCTGGAGCTCCACCTCCC 53
DB 21 GACTGAGATCCACCTCCC 1

RESULT 68
US-10-310-914A-853475/c
; Sequence 853475, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 853475
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-853475

Query Match
Best Local Similarity 6.7%; Score 16.2; DB 1; Length 22;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 32 TGGCTGGAGCTCCACCTCCC 52
DB 22 TTGCTGGAGCTCCCTGCC 2

RESULT 69
US-10-310-914A-1084017/c
; Sequence 1084017, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patentin version 3.3
```

SEQ ID NO 1084017
LENGTH: 22
TYPE: RNA
ORGANISM: Human
US-10-310-914A-1084017

Query Match 6.7%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 33 GGCTGGAGCTCCACCTCCCC 53
DB 21 GACTGGAGATCCACCTCCCC 1

RESULT 70
US-10-310-914A-1084697/c
Sequence 1084697, Application US/10310914A
Publication No. US2006003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087, 0200, CPUS01
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1084697
LENGTH: 22
TYPE: RNA
ORGANISM: Human
US-10-310-914A-1084697

Query Match 6.7%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 33 GGCTGGAGCTCCACCTCCCC 53
DB 21 GACTGGAGATCCACCTCCCC 1

RESULT 71
US-10-310-914A-1084916/c
Sequence 1084916, Application US/10310914A
Publication No. US2006003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087, 0200, CPUS01
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1084916
LENGTH: 22
TYPE: RNA
ORGANISM: Human
US-10-310-914A-1084916

Query Match 6.7%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 33 GGCTGGAGCTCCACCTCCCC 53
DB 21 GACTGGAGATCCACCTCCCC 1

RESULT 72
US-10-310-914A-1215444/c
Sequence 1215444, Application US/10310914A
Publication No. US2006003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087, 0200, CPUS01
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1215444
LENGTH: 22
TYPE: RNA
ORGANISM: Human
US-10-310-914A-1215444

Query Match 6.7%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 33 GGCTGGAGCTCCACCTCCCC 53
DB 21 GACTGGAGATCCACCTCCCC 1

RESULT 73
US-10-310-914A-1215686/c
Sequence 1215686, Application US/10310914A
Publication No. US2006003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087, 0200, CPUS01
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1215686
LENGTH: 22
TYPE: RNA
ORGANISM: Human
US-10-310-914A-1215686

Query Match 6.7%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 33 GGCTGGAGCTCCACCTCCCC 53
DB 21 GACTGGAGATCCACCTCCCC 1

RESULT 74
US-10-310-914A-1217123/c
Sequence 1217123, Application US/10310914A
Publication No. US2006003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087, 0200, CPUS01
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1217123

Query Match 6.7%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

LENGTH: 22
 TYPE: RNA
 ORGANISM: Human
 US-10-310-914A-1217123

Query Match 6.7%; Score 16.2; DB 1; Length 22;
 Best Local Similarity 85.7%; Pred. No. 39;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 33 GGCTGGAGCTCCACCTCCCC 53
 DB 21 GACTGGAAGATCCACCTCCCC 1

RESULT 75

US-10-310-914A-1263320/c
 ; Sequence 1263320, Application US/10310914A
 ; Publication No. US20060003322A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bentwich, Isaac
 ; APPLICANT: Shlier, Kvuza
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 ; FILE REFERENCE: 06087.0200.CPUS01
 ; CURRENT APPLICATION NUMBER: US/10/310.914A
 ; CURRENT FILING DATE: 2002-12-06
 ; NUMBER OF SEQ ID NOS: 1388402
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 1263320
 ; LENGTH: 22
 ; TYPE: RNA
 ; ORGANISM: Human
 US-10-310-914A-1263320

Query Match 6.7%; Score 16.2; DB 1; Length 22;
 Best Local Similarity 85.7%; Pred. No. 39;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 33 GGCTGGAGCTCCACCTCCCC 53
 DB 21 GACTGGAAGATCCACCTCCCC 1

RESULT 76

US-10-310-914A-1287830/c
 ; Sequence 1287830, Application US/10310914A
 ; Publication No. US20060003322A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bentwich, Isaac
 ; APPLICANT: Shlier, Kvuza
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 ; FILE REFERENCE: 06087.0200.CPUS01
 ; CURRENT APPLICATION NUMBER: US/10/310.914A
 ; CURRENT FILING DATE: 2002-12-06
 ; NUMBER OF SEQ ID NOS: 1388402
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 1287830
 ; LENGTH: 22
 ; TYPE: RNA
 ; ORGANISM: Human
 US-10-310-914A-1287830

Query Match 6.7%; Score 16.2; DB 1; Length 22;
 Best Local Similarity 85.7%; Pred. No. 39;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 33 GGCTGGAGCTCCACCTCCCC 53
 DB 21 GACTGGAAGATCCACCTCCCC 1

RESULT 77

US-10-913-280-562
 ; Sequence 562, Application US/10913280
 ; Publication No. US20050089894A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ginn, Edward I.
 ; APPLICANT: Galdicka, Marzena
 ; TITLE OF INVENTION: SYSTEMS AND METHODS FOR ANALYZING
 ; FILE REFERENCE: 07917-238001
 ; CURRENT APPLICATION NUMBER: US/10/913.280
 ; CURRENT FILING DATE: 2004-08-06
 ; PRIOR APPLICATION NUMBER: US 60/493,238
 ; PRIOR FILING DATE: 2003-08-06
 ; PRIOR APPLICATION NUMBER: US 60/568,958
 ; PRIOR FILING DATE: 2004-05-07
 ; NUMBER OF SEQ ID NOS: 920
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 562
 ; LENGTH: 23
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE: Primer
 US-10-913-280-562

Query Match 6.7%; Score 16.2; DB 1; Length 23;
 Best Local Similarity 85.7%; Pred. No. 37;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 126 GTTCCATCTCTTGGAGCAGC 146
 DB 1 GTTCCATCTATTGGTACAC 21

RESULT 78

US-10-310-914A-126107/c
 ; Sequence 126107, Application US/10310914A
 ; Publication No. US20060003322A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bentwich, Isaac
 ; APPLICANT: Shlier, Kvuza
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 ; FILE REFERENCE: 06087.0200.CPUS01
 ; CURRENT APPLICATION NUMBER: US/10/310.914A
 ; CURRENT FILING DATE: 2002-12-06
 ; NUMBER OF SEQ ID NOS: 1388402
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 126107
 ; LENGTH: 23
 ; TYPE: RNA
 ; ORGANISM: Human
 US-10-310-914A-126107

Query Match 6.7%; Score 16.2; DB 1; Length 23;
 Best Local Similarity 85.7%; Pred. No. 37;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 44 CCACCTCCCAAGCTGCTGCT 64
 DB 22 CCACCTCCCAACTCCTGCT 2

RESULT 79

US-10-310-914A-445725
 ; Sequence 445725, Application US/10310914A
 ; Publication No. US20060003322A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bentwich, Isaac
 ; APPLICANT: Shlier, Kvuza
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 ; FILE REFERENCE: 06087.0200.CPUS01

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; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 445725
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-445725

Query Match
Best Local Similarity 66.7%; Pred. No. 37;
Matches 14; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Cy 6 CAGCACGACACTGATTTTGG 26
Db 1 CAGCACGACACUGGAGUUCUG 21

RESULT 80
US-10-310-914A-1335478
; Sequence 1335478, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kynzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087, 0200, CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1335478
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1335478

Query Match
Best Local Similarity 61.9%; Pred. No. 37;
Matches 13; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Cy 3 CTCGACGACGACGATTTT 23
Db 1 CUCGACGACGACCCUGGAGU 21

RESULT 81
US-11-083-784-1311431/C
; Sequence 1311431, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1311431
; LENGTH: 19
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```

; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1311431

Query Match
Best Local Similarity 100.0%; Pred. No. 47;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 TTCTCCAGCACGAC 16
Db 16 TTCTCCAGCACGAC 1

RESULT 82
US-11-083-784-1488626
; Sequence 1488626, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1488626
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1488626

Query Match
Best Local Similarity 81.2%; Pred. No. 47;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Cy 28 CACCTGGCTGGGAGCT 43
Db 2 CACCTGGCTGGGAGCT 17

RESULT 83
US-11-101-244-1311431/C
; Sequence 1311431, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1311431
```



```

; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1311431
```

```
Query Match
Best Local Similarity 100.0%; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 TTCTCCAGCACGAC 16
Db 16 TTCTCCAGCACGAC 1
```

```
RESULT 84
US-11-101-244-1488626
; Sequence 1488626, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; PRIOR FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1488626
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1488626
```

```
Query Match
Best Local Similarity 81.2%; DB 1; Length 19;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 28 CACCTGGCTGGGAGCT 43
Db 2 CACCTGGCTGGGAGCT 17
```

```
RESULT 85
US-10-310-914A-178568/C
; Sequence 178568, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 178568
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-178568
```

```
Query Match
Best Local Similarity 89.5%; DB 1; Length 19;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 42 CTCACCTCCCGAGCTGCT 60
Db 19 CCCACACCCCGAGCTGCT 1
```

```
RESULT 86
US-10-310-914A-178650/C
; Sequence 178650, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 178650
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-178650
```

```
Query Match
Best Local Similarity 89.5%; DB 1; Length 19;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 44 CCACCTCCCGAGCTGCTGC 62
Db 19 CCACACCCCGAGCTGCTGC 1
```

```
RESULT 87
US-10-310-914A-370776/C
; Sequence 370776, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 370776
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-370776
```

```
Query Match
Best Local Similarity 89.5%; DB 1; Length 19;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 35 CTGGAGCTCCACCTCCCTCC 53
Db 19 CTGGAGCTCCACCTCCCTCC 1
```

```
RESULT 88
US-10-310-914A-851035/C
; Sequence 851035, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
```

```
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310.914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patent version 3.3
SEQ ID NO 851035
LENGTH: 19
TYPE: RNA
ORGANISM: Human
US-10-310-914A-851035

Query Match
Best Local Similarity 6.5%; Score 15.8; DB 1; Length 19;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 75 TCCAAACCCACCTGTAA 93
Db 19 TCCAAACCCACCTGTCAA 1

RESULT 89
US-10-310-914A-115160/c
Sequence 115160, Application US/10310914A
Publication No. US2006000322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiler, Kyzac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310.914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patent version 3.3
SEQ ID NO 115160
LENGTH: 19
TYPE: RNA
ORGANISM: Human
US-10-310-914A-115160

Query Match
Best Local Similarity 6.5%; Score 15.8; DB 1; Length 19;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 50 CCCAGCTGCTGCTCACC 68
Db 19 CCTCAGCTGCTGCTGACC 1

RESULT 90
US-11-083-784-207366
Sequence 207366, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083.784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714.333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502.050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426.137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 207366
```

```
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-207366

Query Match
Best Local Similarity 6.5%; Score 15.8; DB 1; Length 19;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 146 CCTCTCAGCTGAGCTGAA 164
Db 1 CCUACACGUCGAGCUCAA 19

RESULT 91
US-11-083-784-207502
Sequence 207502, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmoon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083.784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714.333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502.050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426.137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 207502
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-207502

Query Match
Best Local Similarity 6.5%; Score 15.8; DB 1; Length 19;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CAGCAGACACTGATTTT 24
Db 1 CAGCAGACCTCUGAGNUCU 19

RESULT 92
US-11-083-784-675126
Sequence 675126, Application US/11083784
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmoon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083.784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714.333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502.050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426.137
PRIOR FILING DATE: 2002-11-14
```

```
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 675126
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-675126
```

```
Query Match          6.5%; Score 15.8; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 50;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      55 GCTGCTGCTTCACCTGCTT 73
      ||:|||||:|||||:
Db      1 GCUCUCUCUCUACUCUCUU 19
```

RESULT 93

```
US-11-083-784-1246640
/ Sequence 1246640, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 134990S
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ PRIOR FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 1246640
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-1246640
```

```
Query Match          6.5%; Score 15.8; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 50;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      6 CAGCAGACACTGGATT 24
      |||:|||||:|||||:
Db      1 CAGCAAGCACUGGAUUU 19
```

RESULT 94

```
US-11-083-784-1358279/c
/ Sequence 1358279, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 134990S
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ PRIOR FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
```

```
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 1358279
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-1358279
```

```
Query Match          6.5%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 50;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      133 TCTCTTGGAGCAGCTCTC 151
      |||:|||||:|||||:
Db      19 TCTCTTGGAGCTTCTCTC 1
```

RESULT 95

```
US-11-101-244-207366
/ Sequence 207366, Application US/1101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 134990S
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ CURRENT FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 207366
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-101-244-207366
```

```
Query Match          6.5%; Score 15.8; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 50;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      146 CCTCTCAGCGAGAGCTGAA 164
      ||:|||||:|||||:
Db      1 CCUADUCAGUGGAGCUCUA 19
```

RESULT 96

```
US-11-101-244-207502
/ Sequence 207502, Application US/1101244
/ Publication No. US20050246794A1
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 134990S
/ CURRENT APPLICATION NUMBER: US/11/101,244
/ CURRENT FILING DATE: 2005-04-07
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
```

```

; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 207502
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-207502
```

```

Query Match      6.5%; Score 15.8; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 50;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      6 CAGCACGACGACTGATTTT 24
Db      1 CAGCACGACGACUCGAGUUCU 19
```

RESULT 97

```

; Sequence 675126, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 675126
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-675126
```

```

Query Match      6.5%; Score 15.8; DB 1; Length 19;
Best Local Similarity 57.9%; Pred. No. 50;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      55 GCTGCTGCTCAGCTGCTT 73
Db      1 GCUCUCGCTCUCGUCUCU 19
```

RESULT 98

```

; Sequence 1246640, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
```

```

; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 1246640
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1246640
```

```

Query Match      6.5%; Score 15.8; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 50;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      6 CAGCACGACGACTGATTTT 24
Db      1 CAGCAAGCAGCUCGAGUUCU 19
```

RESULT 99

```

; Sequence 1358279, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 1358279
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1358279
```

```

Query Match      6.5%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 50;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      133 TCTCTTTGAGACACTCTTC 151
Db      19 TCTCTTTGAGACTCTCTTC 1
```

RESULT 100

```

; Sequence 178569, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 178569
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-178569
```

```
Query Match      6.5%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 47;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      42 CTCGACCTCCCGACTGCT 60
Db      19 CCCGACCAACCCCACTGCT 1

RESULT 101
US-10-310-914A-1139581
; Sequence 1139581, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kyzac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1139581
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1139581

Query Match      6.5%; Score 15.8; DB 1; Length 20;
Best Local Similarity 73.7%; Pred. No. 47;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      35 CTGGAGCTCCACTCCCC 53
Db      2 CUGGAGCUCUCCUCCCC 20

RESULT 102
US-10-310-914A-1204303
; Sequence 1204303, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kyzac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1204303
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1204303

Query Match      6.5%; Score 15.8; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 47;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      33 GCGTGGAGCTCCACTCC 51
Db      2 GCGCGGAGCUCUCCUCC 20

RESULT 103
US-10-847-918-7690
; Sequence 7690, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:

; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Stonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847.918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7690
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-847-918-7690

Query Match      6.5%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 45;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      163 AACGAAACGACTGTTAG 181
Db      1 AACGAAACACCTGTTAG 19

RESULT 104
US-10-847-918-7692/c
; Sequence 7692, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Stonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847.918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7692
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNA1-antisense strand
US-10-847-918-7692

Query Match      6.5%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 45;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      163 AACGAAACGACTGTTAG 181
Db      21 AACGAAACACCTGTTAG 3

RESULT 105
US-10-847-918-8050
; Sequence 8050, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Stonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
```

; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 8050
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-847-918-8050

Query Match 6.5%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 45;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 163 AACGAGCAGCCTGTTAAG 181
DB 2 AACGAGCAGCCTGTTAAG 20

RESULT 106
US-10-847-918-8052/c
; Sequence 8052, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 8052
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNA1-antisense strand
US-10-847-918-8052

Query Match 6.5%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 45;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 163 AACGAGCAGCCTGTTAAG 181
DB 2 AACGAGCAGCCTGTTAAG 20

RESULT 107
US-10-831-997-768/c
; Sequence 768, Application US/10831997
; Publication No. US20050244834A1
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Carelli, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Bolt, Stacey
; APPLICANT: Daley, George O.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
; FILE REFERENCE: 2825.1027-001
; CURRENT APPLICATION NUMBER: US/10/831,997
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: US/09/657,472
; PRIOR FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/153,357
; PRIOR FILING DATE: 1999-09-10

; PRIOR APPLICATION NUMBER: US 60/220,947
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: US 60/225,724
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2551
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 768
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-831-997-768

Query Match 6.5%; Score 15.8; DB 1; Length 21;
Best Local Similarity 81.0%; Pred. No. 45;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 3 CTCGACGACGACCTGATTT 23
DB 21 CTCGACGACGACCTGATTT 1

RESULT 108
US-10-310-914A-117008
; Sequence 117008, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 117008
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-117008

Query Match 6.5%; Score 15.8; DB 1; Length 21;
Best Local Similarity 73.7%; Pred. No. 45;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 49 TCCCGAGCTGCTGCTC 67
DB 1 TCCCGAGCTGCTGCTC 19

RESULT 109
US-10-310-914A-227677
; Sequence 227677, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 227677
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-227677

Query Match 6.5%; Score 15.8; DB 1; Length 21;
Best Local Similarity 57.9%; Pred. No. 45;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 55 GCTGCTGCTCAGCTGCTT 73
||:|:|:|:|:|:|:|:|:|:
Db 1 GCUUCUGGCUUCUCCU 19

RESULT 110
US-10-310-914A-593921/c
; Sequence 593921, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 593921
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-593921

Query Match 6.5%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 45;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 58 GCTGCTGCTCAGCTGCTTTC 76
||:|:|:|:|:|:|:|:|:|:
Db 21 GCTACCTCTCTCTGCTTTTC 3

RESULT 111
US-10-310-914A-800173
; Sequence 800173, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 800173
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-800173

Query Match 6.5%; Score 15.8; DB 1; Length 21;
Best Local Similarity 73.7%; Pred. No. 45;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 35 CTGGAGCTCAGCTCCCC 53
||:|:|:|:|:|:|:|:|:|:
Db 3 CUGGAUCUCCACCCUCC 21

RESULT 112
US-10-708-204-288/c
; Sequence 288, Application US/10708204
; Publication No. US2005022399A1
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 55033
; CURRENT APPLICATION NUMBER: US/10/708,204
; CURRENT FILING DATE: 2004-02-16
; NUMBER OF SEQ ID NOS: 7351
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 288
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-708-204-288

Query Match 6.5%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 47 CCTGCCAGCTGCTGCTC 65
||:|:|:|:|:|:|:|:|:|:
Db 19 CCTCACCAGTGTGCTGCTC 1

RESULT 113
US-10-708-204-2661/c
; Sequence 2661, Application US/10708204
; Publication No. US2005022399A1
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
; FILE REFERENCE: 55033
; CURRENT APPLICATION NUMBER: US/10/708,204
; CURRENT FILING DATE: 2004-02-16
; NUMBER OF SEQ ID NOS: 7351
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2661
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-708-204-2661

Query Match 6.5%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 47 CCTGCCAGCTGCTGCTC 65
||:|:|:|:|:|:|:|:|:|:
Db 19 CCTCACCAGTGTGCTGCTC 1

RESULT 114
US-10-310-914A-160067
; Sequence 160067, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 160067
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-160067

Query Match 6.5%; Score 15.8; DB 1; Length 22;
Best Local Similarity 63.2%; Pred. No. 43;
Matches 12; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 67 CCGCTTTTCCAAACCCCA 85
| : : : : :
Db 1 CAUGUUUUCCAAACCCCA 19

RESULT 115

US-10-310-914A-802509
; Sequence 802509, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 802509
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-802509

Query Match 6.5%; Score 15.8; DB 1; Length 22;
Best Local Similarity 57.9%; Pred. No. 43;
Matches 11; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 59 CTGCTCCTCAGCTGCTTTTCC 77
| : : : : :
Db 2 CUCCCUACACUCCUCCUCC 20

RESULT 116

US-10-310-914A-978748/C
; Sequence 978748, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 978748
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-978748

Query Match 6.5%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 41 GCTCCACTCTCCCAAGCTGC 59
| : : : : :
Db 22 GCTCCACTCTCCCAAGCTGC 4

RESULT 117

US-10-310-914A-1115299/C
; Sequence 1115299, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1115299
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1115299

Query Match

6.5%; Score 15.8; DB 1; Length 22;
Best Local Similarity 89.5%; Pred. No. 43;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 37 GCGACTCCTCCTCCCGC 55
| : : : : :
Db 19 GAGAGCTACACTCCCGC 1

RESULT 118

US-10-310-914A-45234
; Sequence 45234, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 45234
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-45234

Query Match 6.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 72.7%; Pred. No. 45;
Matches 16; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 149 CTCACGTGAGCTGACAGAAC 170
| : : : : :
Db 1 CACACGTGAGCTGACAGAAC 22

RESULT 119

US-10-310-914A-419337/C
; Sequence 419337, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 419337
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-419337

Query Match 6.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No. 45;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 52 CCACTGCTGCTCCTGCTT 73

Db 22 CCAGCTCCAGCTCATTTGCTT 1

RESULT 120

US-10-310-914A-877383/c
 ; Sequence 877383, Application US/10310914A
 ; Publication No. US20060003322A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bentwich, Isaac
 ; APPLICANT: Shiler, Kvuza
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 ; FILE REFERENCE: 06087.0200.CPUS01
 ; CURRENT APPLICATION NUMBER: US/10/310,914A
 ; CURRENT FILING DATE: 2002-12-06
 ; NUMBER OF SEQ ID NOS: 1388402
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 877383
 ; LENGTH: 22
 ; TYPE: RNA
 ; ORGANISM: Human
 US-10-310-914A-877383

Query Match 6.4%; Score 15.6; DB 1; Length 22;
 Best Local Similarity 81.8%; Pred. No. 45;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 131 CATCTCTTTGAGCACTCTCA 152
 Db 22 CATCTCTCTCAGCCCTCTCA 1

RESULT 121

US-10-310-914A-955140
 ; Sequence 955140, Application US/10310914A
 ; Publication No. US20060003322A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bentwich, Isaac
 ; APPLICANT: Shiler, Kvuza
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 ; FILE REFERENCE: 06087.0200.CPUS01
 ; CURRENT APPLICATION NUMBER: US/10/310,914A
 ; CURRENT FILING DATE: 2002-12-06
 ; NUMBER OF SEQ ID NOS: 1388402
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 955140
 ; LENGTH: 22
 ; TYPE: RNA
 ; ORGANISM: Human
 US-10-310-914A-955140

Query Match 6.4%; Score 15.6; DB 1; Length 22;
 Best Local Similarity 63.6%; Pred. No. 45;
 Matches 14; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 47 CTTCCAGCTCGCTCAACC 68
 Db 1 CCGGCCGCGCCGCGCCGCC 22

RESULT 122

US-10-310-914A-993524/c
 ; Sequence 993524, Application US/10310914A
 ; Publication No. US20060003322A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bentwich, Isaac
 ; APPLICANT: Shiler, Kvuza
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 ; FILE REFERENCE: 06087.0200.CPUS01
 ; CURRENT APPLICATION NUMBER: US/10/310,914A

; CURRENT FILING DATE: 2002-12-06
 ; NUMBER OF SEQ ID NOS: 1388402
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 993524
 ; LENGTH: 22
 ; TYPE: RNA
 ; ORGANISM: Human
 US-10-310-914A-993524

Query Match 6.4%; Score 15.6; DB 1; Length 22;
 Best Local Similarity 81.8%; Pred. No. 45;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 188 GTGCTGTTAGGCTGTAGG 209
 Db 22 GTGCTGTTATGCTGATCTATG 1

RESULT 123

US-10-310-914A-1134411/c
 ; Sequence 1134411, Application US/10310914A
 ; Publication No. US20060003322A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bentwich, Isaac
 ; APPLICANT: Shiler, Kvuza
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 ; FILE REFERENCE: 06087.0200.CPUS01
 ; CURRENT APPLICATION NUMBER: US/10/310,914A
 ; CURRENT FILING DATE: 2002-12-06
 ; NUMBER OF SEQ ID NOS: 1388402
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 1134411
 ; LENGTH: 22
 ; TYPE: RNA
 ; ORGANISM: Human
 US-10-310-914A-1134411

Query Match 6.4%; Score 15.6; DB 1; Length 22;
 Best Local Similarity 81.8%; Pred. No. 45;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 186 CCGTGTCTGTAGGTTGTCTA 207
 Db 22 CTTGTTGTGCAAGTTCTCTA 1

RESULT 124

US-10-310-914A-1326011/c
 ; Sequence 1326011, Application US/10310914A
 ; Publication No. US20060003322A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bentwich, Isaac
 ; APPLICANT: Shiler, Kvuza
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 ; FILE REFERENCE: 06087.0200.CPUS01
 ; CURRENT APPLICATION NUMBER: US/10/310,914A
 ; CURRENT FILING DATE: 2002-12-06
 ; NUMBER OF SEQ ID NOS: 1388402
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 1326011
 ; LENGTH: 22
 ; TYPE: RNA
 ; ORGANISM: Human
 US-10-310-914A-1326011

Query Match 6.4%; Score 15.6; DB 1; Length 22;
 Best Local Similarity 81.8%; Pred. No. 45;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 43 TCACCTCCCGAGCTGTGCTT 64
 ||||| ||||| ||||| |||||

Db 22 TCAGCTCCCGACCTTGCT 1

Search completed: October 2, 2006, 15:41:59
Job time : 1 secs

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OM nucleic - nucleic search, using sw model

Run on: October 2, 2006, 15:38:59 ; Search time 0.001 Seconds
(without alignments)
231.836 Million cell updates/sec

Title: US-10-642-946-6_1967-2208

Perfect score: 242

Sequence: 1 ttccacagacacacacacgga.....ccaactaaactgattcac 242

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 0.5

Searched: 26 segs, 479 residues

Total number of hits satisfying chosen parameters: 52

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : pubnewdb1.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17.6	7.3	25	US-11-217-529-49117	Sequence 49117, A
2	15.2	6.3	20	US-11-321-421-262	Sequence 262, App
3	14.4	6.0	20	US-10-511-937-736	Sequence 736, App
4	14.2	5.9	19	US-10-424-339-1303	Sequence 1303, App
5	14.2	5.9	19	US-10-424-339-1303	Sequence 1484, App
6	14.2	5.9	19	US-11-293-697-5004	Sequence 5004, App
7	14.2	5.9	19	US-11-217-936-1113	Sequence 1113, App
8	14.2	5.9	19	US-11-217-936-1113	Sequence 1582, App
9	14.2	5.9	20	US-11-221-332-141	Sequence 141, App
10	13.8	5.7	19	US-11-370-584-6418	Sequence 6418, App
11	13.4	5.5	17	US-11-255-139A-6888	Sequence 6888, App
12	13.4	5.5	17	US-11-255-139A-6889	Sequence 6889, App
13	13.4	5.5	18	US-11-327-689-17	Sequence 17, App1
14	13.4	5.5	19	US-11-217-936-1347	Sequence 1347, App
15	13.4	5.5	19	US-11-217-936-1816	Sequence 1816, App
16	13.2	5.5	18	US-10-517-441-1250	Sequence 1250, App
17	13.2	5.5	18	US-11-184-215-43	Sequence 43, App1
18	12.8	5.3	17	US-11-255-139A-4949	Sequence 4949, App
19	12.8	5.3	18	US-11-293-697-4928	Sequence 4928, App
20	12.4	5.1	17	US-11-327-689-49	Sequence 49, App1
21	12.4	5.1	17	US-11-327-689-50	Sequence 50, App1
22	12.4	5.1	17	US-11-361-627-55	Sequence 55, App1
23	12.4	5.1	17	US-11-255-139A-5820	Sequence 5820, App
24	12.2	5.0	17	US-10-524-432-606	Sequence 606, App
25	12.2	5.0	17	US-11-190-801-1	Sequence 1, App11
26	12.2	5.0	17	US-11-255-139A-4513	Sequence 4513, App

ALIGNMENTS

RESULT 1
US-11-217-529-49117

```

; Sequence 49117, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 49117
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-49117
Query Match 7.3%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.2;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

QY 97 GTACTACATTTTGTGCCACTAC 120
DB 1 GAAGTTACATTTGGTCCACTAC 24

```

RESULT 2
US-11-321-421-262
; Sequence 262, Application US/11321421
; Publication No. US20060115496A1
; GENERAL INFORMATION:
; APPLICANT: Milhausen, Michael James
; TITLE OF INVENTION: TOXOPLASMA GONDI PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: TX-1-C2-1
; CURRENT APPLICATION NUMBER: US/11/321,421
; CURRENT FILING DATE: 2005-12-29
; PRIOR APPLICATION NUMBER: 09/216,393
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/994,825
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 262
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-11-321-421-262
Query Match 6.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 3.9;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

QY 189 TGTCTGTTAGGTTGTCTAG 208
DB 1 TGGCTGTTGGGTTGTCTAG 20

RESULT 3
US-10-511-937-736/C
; Sequence 736, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk

```

; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 736
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-736

Query Match          6.0%; Score 14.4; DB 1; Length 20;
Best Local Similarity 93.8%; Pred. No. 5.2;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      76 CCAAAACCCACCTGT 91
Db      20 CCAAAACCCACCTGT 5

RESULT 4
US-10-424-339-1303
; Sequence 1303, Application US/10424339
; Publication No. US20060127891A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Uzman, Nassim
; APPLICANT: Haeblerli, Peter
; APPLICANT: Chowitra, Bharat
; APPLICANT: Polisky, Barry
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of MAP Kinase Gene
; TITLE OF INVENTION: Expression or Expression of Genes Involved in MAP Kinase Pathway
; FILE REFERENCE: 400/113 (MBH03-388)
; CURRENT APPLICATION NUMBER: US/10/424,339
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: PCT/US 03/02510
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: PCT/US 03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US 03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 1714
; SOFTWARE: PatentIn version 3.2
```

```

; SEQ ID NO 1303
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense re
US-10-424-339-1303

Query Match          5.9%; Score 14.2; DB 1; Length 19;
Best Local Similarity 68.4%; Pred. No. 5.9;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      112 GCCCAGTACGCTCGTTTC 130
Db      1 GCCCTCAGCGCTCGTTC 19

RESULT 5
US-10-424-339-1484/c
; Sequence 1484, Application US/10424339
; Publication No. US20060127891A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Uzman, Nassim
; APPLICANT: Haeblerli, Peter
; APPLICANT: Chowitra, Bharat
; APPLICANT: Polisky, Barry
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of MAP Kinase Gene
; TITLE OF INVENTION: Expression or Expression of Genes Involved in MAP Kinase Pathway
; FILE REFERENCE: 400/113 (MBH03-388)
; CURRENT APPLICATION NUMBER: US/10/424,339
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: PCT/US 03/02510
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: PCT/US 03/05346
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: PCT/US 03/05028
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/386,782
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US 60/440,129
; PRIOR FILING DATE: 2003-01-15
; NUMBER OF SEQ ID NOS: 1714
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1484
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-424-339-1484

Query Match          5.9%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 5.9;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      112 GCCCAGTACGCTCGTTTC 130
Db      19 GCCCTCAGCGCTCGTTC 1
```

```

RESULT 6
US-11-293-697-5004
; Sequence 5004, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5004
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: an artificially synthesized F
US-11-293-697-5004

Query Match          5.9%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 5.9;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      14 CACTGAGATTTCGTACCT 32
Db      1 CACTGAGATTTCGTACCT 19

RESULT 7
US-11-217-936-1113
; Sequence 1113, Application US/11217936
; Publication No. US20060148743A1
; GENERAL INFORMATION:
; APPLICANT: Jadhav, Vasant
; APPLICANT: Carroll, Joseph
; APPLICANT: Sirna Therapeutics, Inc.
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Histone Deacetylase
; TITLE OF INVENTION: (HDAC) Gene Expression Using Short Interfering Nucleic Acid
; FILE REFERENCE: 05-727 (400/271)
; CURRENT APPLICATION NUMBER: US/11/217,936
; CURRENT FILING DATE: 2005-09-01
; NUMBER OF SEQ ID NOS: 5036
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1113
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-217-936-1113

Query Match          5.9%; Score 14.2; DB 1; Length 19;
Best Local Similarity 73.7%; Pred. No. 5.9;
Matches 14; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      141 GAGCAGCTCTCAGCGAG 159
Db      1 GAGCAGCTCTCAGCGAG 19

RESULT 8
US-11-217-936-1582/c
; Sequence 1582, Application US/11217936
; Publication No. US20060148743A1
; GENERAL INFORMATION:
; APPLICANT: Jadhav, Vasant
; APPLICANT: Carroll, Joseph
; APPLICANT: Sirna Therapeutics, Inc.

```

```

; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Histone Deacetylase
; TITLE OF INVENTION: (HDAC) Gene Expression Using Short Interfering Nucleic Acid
; FILE REFERENCE: 05-727 (400/271)
; CURRENT APPLICATION NUMBER: US/11/217,936
; CURRENT FILING DATE: 2005-09-01
; NUMBER OF SEQ ID NOS: 5036
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1582
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-217-936-1582

Query Match          5.9%; Score 14.2; DB 1; Length 19;
Best Local Similarity 84.2%; Pred. No. 5.9;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      141 GAGCAGCTCTCAGCGAG 159
Db      19 GAGCAGCTCTCAGCGAG 1

RESULT 9
US-11-221-332-141/c
; Sequence 141, Application US/11221332
; Publication No. US20060121498A1
; GENERAL INFORMATION:
; APPLICANT: EIRx Therapeutics
; TITLE OF INVENTION: Enzymes involved in apoptosis
; FILE REFERENCE: 8912/2042
; CURRENT APPLICATION NUMBER: US/11/221,332
; CURRENT FILING DATE: 2005-09-07
; PRIOR APPLICATION NUMBER: PCT/GB2004/00957
; PRIOR FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: GB0305267.7
; PRIOR FILING DATE: 2003-05-07
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 141
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: QPCR primer
US-11-221-332-141

Query Match          5.9%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 5.6;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      69 TGCTTTCCAAACCCACC 87
Db      19 TGCTTTCCAAACCCACC 1

RESULT 10
US-11-370-584-6418/c
; Sequence 6418, Application US/11370584
; Publication No. US20060177863A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Ballelic markers for use in constructing a high
; TITLE OF INVENTION: density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/11/370,584
; CURRENT FILING DATE: 2006-03-08
; PRIOR APPLICATION NUMBER: US/10/349,143
; PRIOR FILING DATE: 2003-01-21

```



```
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6418
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer 99-11313 for SEQ 2484,
US-11-370-584-6418
```

```
Query Match          5.7%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 6.9;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY      165 CAGACGACCTGTTAG 181
      |||||
Db       17 CATAACGACCTGATAG 1
```

```
RESULT 11
US-11-255-139A-6888/c
; Sequence 6888, Application US/11255139A
; Publication No. US20060154271A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/11/255,139A
; CURRENT FILING DATE: 2005-10-20
; NUMBER OF SEQ ID NOS: 8014
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6888
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-255-139A-6888
```

```
Query Match          5.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 8.9;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      38 GGAGCTCCACCTCCC 52
      |||||
Db       16 GGTGCTCCACCTCCC 2
```

```
RESULT 12
US-11-255-139A-6889/c
; Sequence 6889, Application US/11255139A
; Publication No. US20060154271A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/11/255,139A
; CURRENT FILING DATE: 2005-10-20
; NUMBER OF SEQ ID NOS: 8014
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6889
; LENGTH: 17
```

```
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-255-139A-6889
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```
Query Match          5.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 8.9;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
OY      38 GGAGCTCCACCTCCC 52
      |||||
Db       15 GGTGCTCCACCTCCC 1
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```
RESULT 13
US-11-327-689-17/c
; Sequence 17, Application US/11327689
; Publication No. US20060177854A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Winston J.
; Drayna, Dennis T.
; Feder, John N.
; Gnirke, Andreas
; Ruddy, David
; Teuchinashi, Zenta
; Wolff, Roger K.
; TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/327,689
; FILING DATE: 05-Jan-2006
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/497,957
; FILING DATE: 04-FEB-2000
; APPLICATION NUMBER: US/08/834,497
; FILING DATE: 04-APR-1997
; APPLICATION NUMBER: US 08/652,265
; FILING DATE: 23-MAY-1996
; APPLICATION NUMBER: US 08/632,673
; FILING DATE: 16-APR-1996
; APPLICATION NUMBER: US 08/630,912
; FILING DATE: 04-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0056-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 1
; OTHER INFORMATION: /mod_base= OTHER
```

```
/note= "N = 5'-phosphorylated cytosine
(P-C)"
FEATURE:
NAME/KEY: modified_base
LOCATION: 18
OTHER INFORMATION: /mod_base= OTHER
/note= "N = 3'-dioxigenin-conjugated
guanine (G-dig)"
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-11-327-689-17

Query Match
Best Local Similarity 5.5%; Score 13.4; DB 1; Length 18;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 35 CTGGAGCTCCACCT 49
Db 17 CTGGGTCTCCACCT 3

RESULT 14
US-11-217-936-1347
; Sequence 1347, Application US/11217936
; Publication No. US20060148743A1
; GENERAL INFORMATION:
; APPLICANT: Jadhav, Vasant
; APPLICANT: Carroll, Joseph
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Histone Deacetylase
; TITLE OF INVENTION: (HDAC) Gene Expression Using Short Interfering Nucleic Acid
; TITLE OF INVENTION: (sIN)
; FILE REFERENCE: 05-727 (400/271)
; CURRENT APPLICATION NUMBER: US/11/217, 936
; CURRENT FILING DATE: 2005-09-01
; NUMBER OF SEQ ID NOS: 5036
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 1347
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-217-936-1347

Query Match
Best Local Similarity 5.5%; Score 13.4; DB 1; Length 19;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 11 CAGCAGTGGATTGG 25
Db 5 CAGCCUGGAUUUG 19

RESULT 15
US-11-217-936-1816/c
; Sequence 1816, Application US/11217936
; Publication No. US20060148743A1
; GENERAL INFORMATION:
; APPLICANT: Jadhav, Vasant
; APPLICANT: Carroll, Joseph
; APPLICANT: Sina Therapeutics, Inc.
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Histone Deacetylase
; TITLE OF INVENTION: (HDAC) Gene Expression Using Short Interfering Nucleic Acid
; TITLE OF INVENTION: (sIN)
; FILE REFERENCE: 05-727 (400/271)
; CURRENT APPLICATION NUMBER: US/11/217, 936
; CURRENT FILING DATE: 2005-09-01
; NUMBER OF SEQ ID NOS: 5036
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 1816
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
```

```
/ FEATURE:
; OTHER INFORMATION: Synthetic
US-11-217-936-1816

Query Match
Best Local Similarity 5.5%; Score 13.4; DB 1; Length 19;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 CAGCAGTGGATTGG 25
Db 15 CAGCCUGGAUUUG 1

RESULT 16
US-10-517-441-1250/c
; Sequence 1250, Application US/10517441
; Publication No. US20060121467A1
; GENERAL INFORMATION:
; APPLICANT: FOEKEN, John
; APPLICANT: HAREBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: MARX, Almuth
; APPLICANT: HOEFLER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
; TITLE OF INVENTION: Proliferative disorders
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517, 441
; CURRENT FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 1250
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Detection oligonucleotide for MGMT
US-10-517-441-1250

Query Match
Best Local Similarity 5.5%; Score 13.2; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 213 TATCAGATACCACTAA 230
Db 18 TACACATACCAATAA 1

RESULT 17
US-11-184-215-43/c
; Sequence 43, Application US/11184215
; Publication No. US20060122790A1
; GENERAL INFORMATION:
; APPLICANT: Fowler, Craig A.
; APPLICANT: Menla, Vinod C.
; APPLICANT: ROSEO, Thomas L.
; TITLE OF INVENTION: OLIGONUCLEOTIDE ORDERING SYSTEM
; FILE REFERENCE: ILLINC.050A
; CURRENT APPLICATION NUMBER: US/11/184, 215
```

CURRENT FILING DATE: 2005-07-15
PRIOR APPLICATION NUMBER: 60/634,154
PRIOR FILING DATE: 2004-12-07
NUMBER OF SEQ ID NOS: 96
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 43
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE: OTHER INFORMATION: Synthetically prepared nucleic acid sequence
US-11-184-215-43

Query Match 5.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 9;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 128 TTCCATCTTTTGAGCA 145
Db 18 TGCCATCTTTTGAGCA 1

RESULT 18
US-11-255-139A-4949
Sequence 4949, Application US/11255139A
Publication No. US20060154271A1
GENERAL INFORMATION:
APPLICANT: Strata Therapeutics, Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
FILE REFERENCE: MBH01-664-A (400/050)
CURRENT FILING DATE: 2005-10-20
NUMBER OF SEQ ID NOS: 8014
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4949
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-11-255-139A-4949

Query Match 5.3%; Score 12.8; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 11;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Oy 64 TCACCTGCTTTCCAA 79
Db 1 UCACCAGCUCUCCAA 16

RESULT 19
US-11-293-697-4928/C
Sequence 4928, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length CDNA
FILE REFERENCE: H1-A0106
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/11/293,697
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4928
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE: OTHER INFORMATION: Description of Artificial Sequence: an artificially synthesized p
US-11-293-697-4928

Query Match 5.3%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 10;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 74 TTCCAAACCCACCCT 89
Db 17 TTCCAAACCCCAACAT 2

RESULT 20
US-11-327-689-49
Sequence 49, Application US/11327689
Publication No. US20060177854A1
GENERAL INFORMATION:
APPLICANT: Thomas, Winston J.
Drayna, Dennis T.
Feder, John N.
Galitke, Andreas
Ruddy, David
Tsuchinashi, Zenta
Wolff, Roger K.

TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE PRODUCTS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2811

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/327,689
FILING DATE: 05-Jan-2006
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/497,957
FILING DATE: 04-FEB-2000
APPLICATION NUMBER: US/08/834,497
FILING DATE: 04-APR-1997
APPLICATION NUMBER: US 08/652,265
FILING DATE: 23-MAY-1996
APPLICATION NUMBER: US 08/632,673
FILING DATE: 16-APR-1996
APPLICATION NUMBER: US 08/630,912
FILING DATE: 04-APR-1996

ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.

REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0056-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-11-327-689-49.

Query Match 5.1%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 13;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 36 TGGAGCTCCACCT 49

Db 1 TGGGTGCTCCACT 14

RESULT 21

US-11-327-689-50
 ; Sequence 50, Application US/11327689
 ; Publication No. US20060177854A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Winston J.
 ; Drayna, Dennis T.
 ; Feder, John N.
 ; Galke, Andreas
 ; Ruddy, David
 ; Tsuchihashi, Zenta
 ; Wolff, Roger K.
 ; TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS GENE, PRODUCTS
 ; NUMBER OF SEQUENCES: 76
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds LLP
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036-2811
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: Windows 95
 ; SOFTWARE: FASTSEQ for Windows Version 2.0b
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/11/327,689
 ; FILING DATE: 05-Jan-2006
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/497,957
 ; FILING DATE: 04-FEB-2000
 ; APPLICATION NUMBER: US/08/834,497
 ; FILING DATE: 04-APR-1997
 ; APPLICATION NUMBER: US 08/652,265
 ; FILING DATE: 23-MAY-1996
 ; APPLICATION NUMBER: US 08/632,673
 ; FILING DATE: 16-APR-1996
 ; APPLICATION NUMBER: US 08/630,912
 ; FILING DATE: 04-APR-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Polissant, Brian M.
 ; REGISTRATION NUMBER: 28,462
 ; REFERENCE/DOCKET NUMBER: 8907-0056-999
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-493-4935
 ; TELEFAX: 650-493-5556
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 50:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 17 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
 US-11-327-689-50

Query Match 5.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 13;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 36 TGGAGCTCCACT 49
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 Db 1 TGGGTGCTCCACT 14

RESULT 22

US-11-361-627-55
 ; Sequence 55, Application US/11361627
 ; Publication No. US20060199208A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Srinivasan, Subha
 ; Bingham, Jonathan
 ; TITLE OF INVENTION: METHODS AND SYSTEMS FOR POLYNUCLEOTIDE DETECTION
 ; FILE REFERENCE: 37087-8002 US 01
 ; CURRENT APPLICATION NUMBER: US/11/361,627
 ; CURRENT FILING DATE: 2006-02-24
 ; PRIOR APPLICATION NUMBER: US/10/272,461
 ; PRIOR FILING DATE: 2002-10-16
 ; PRIOR APPLICATION NUMBER: US 60/343,298
 ; PRIOR FILING DATE: 2001-12-21
 ; NUMBER OF SEQ ID NOS: 104
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 55
 ; LENGTH: 17
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-11-361-627-55

Query Match 5.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 13;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 53 CAGCTGCTGCTCA 66
 |||||
 Db 4 CAGCTGCTGCTCA 17

RESULT 23

US-11-255-139A-5820/C
 ; Sequence 5820, Application US/11255139A
 ; Publication No. US20060154271A1
 ; GENERAL INFORMATION:
 ; APPLICANT: McSwigen, James
 ; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
 ; FILE REFERENCE: MBH01-664-A (400/050)
 ; CURRENT APPLICATION NUMBER: US/11/255,139A
 ; CURRENT FILING DATE: 2005-10-20
 ; NUMBER OF SEQ ID NOS: 8014
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 5820
 ; LENGTH: 17
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 US-11-255-139A-5820

Query Match 5.1%; Score 12.4; DB 1; Length 17;
 Best Local Similarity 92.9%; Pred. No. 13;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 39 GAGCTCCACTCCC 52
 |||||
 Db 17 GTGCTCCACTCCC 4

RESULT 24

US-10-524-432-606
 ; Sequence 606, Application US/10524432
 ; Publication No. US20060127902A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Genzyme Corporation
 ; TITLE OF INVENTION: BRAIN ENDOTHELIAL EXPRESSION PATTERNS
 ; FILE REFERENCE: 003482.00010
 ; CURRENT APPLICATION NUMBER: US/10/524,432
 ; CURRENT FILING DATE: 2005-02-15
 ; PRIOR APPLICATION NUMBER: US 60/403,390
 ; PRIOR FILING DATE: 2002-08-15

PRIOR APPLICATION NUMBER: US 60/458,978
PRIOR FILING DATE: 2003-04-01
NUMBER OF SEQ ID NOS: 869
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 606
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-10-524-432-606

Query Match 5.0%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 14;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 40 AGCTCCAGCTCCCGCAGC 56
|||
Db 1 AGCTCCAGACCCCGCAGC 17

RESULT 25
US-11-190-801-1/C
Sequence 1, Application US/11190801
Publication No. US20060141492A1
GENERAL INFORMATION:
APPLICANT: SOMERS, KEVIN R.
APPLICANT: FAGERVOID, SONJA K.
APPLICANT: MATTS, JOY E. M.
APPLICANT: MAY, HAROLD D.
TITLE OF INVENTION: GENE PROBES FOR THE SELECTIVE DETECTION OF MICROORGANISMS THAT
FILE REFERENCE: 4115-206
CURRENT APPLICATION NUMBER: US/11/190,801
CURRENT FILING DATE: 2005-07-27
PRIOR APPLICATION NUMBER: 60/591,514
PRIOR FILING DATE: 2004-07-27
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1
LENGTH: 17
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Construct
US-11-190-801-1

Query Match 5.0%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 14;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 49 TCCCGAGCTGCTGCCTC 65
|||
Db 17 TTCCTTGCTGCTGCCTC 1

RESULT 26
US-11-255-139A-4513
Sequence 4513, Application US/11255139A
Publication No. US20060154271A1
GENERAL INFORMATION:
APPLICANT: Sigma Therapeutics, Inc.
APPLICANT: McSwiggan, James
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
FILE REFERENCE: MHB01-654-A (400/050)
CURRENT APPLICATION NUMBER: US/11/255,139A
CURRENT FILING DATE: 2005-10-20
NUMBER OF SEQ ID NOS: 8014
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4513
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-11-255-139A-4513

Query Match 5.0%; Score 12.2; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 14;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 36 TGGGAGCTTCACCTCC 52
|||
Db 1 UGGCAGCUCUCUCUCCC 17

Search completed: October 2, 2006, 15:38:59
Job time : 0.001 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2006, 15:34:16 ; Search time 0.001 seconds

(without alignments)
116.160 Million cell updates/sec

Title: US-10-642-946-6_1967-2208
Perfect score: 242
Sequence: 1 tctctccagcacagcactgga.....ccaactaaactgattccac 242

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 11 seqs, 240 residues

Total number of hits satisfying chosen parameters: 22

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 11 summaries

Database : gedbl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Genbank / EMBL

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18.6	7.7	25	1	CS150458
2	16.2	6.7	22	1	AX921533
3	16.2	6.7	22	1	AX528253
4	16.2	6.7	22	1	AX554633
5	16.2	6.7	22	1	AX703110
6	15.8	6.5	21	1	AX529565
7	15.8	6.5	21	1	AX095590
8	15.6	6.4	22	1	DD173031
9	15.6	6.4	22	1	AR704960
10	15.2	6.3	20	1	AR279129
11	15.2	6.3	21	1	AR393701

ALIGNMENTS

RESULT 1
LOCUS CS150458 25 bp DNA linear PAT 07-SEP-2005
DEFINITION Sequence 1578 from Patent WO2005075685.
ACCESSION CS150458
VERSION CS150458.1 GI:74270448
KEYWORDS
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
REFERENCE 1
AUTHORS Middleton, R.P.
JOURNAL Patent: WO 2005075685-A 1578 18-AUG-2005;
NESTEC S.A. (CH)
FEATURES Location/Qualifiers

source

1..25
/organism="Canis familiaris"
/mol_type="unassigned DNA"
/db_xref="taxon:9615"

Query Match 7.7%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 1.3;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 43 TCCACCTCCCACTGCTGCTCAG 67
DB 1 TCTATCTCCCACTGCTGCTCAG 25

RESULT 2
LOCUS AX921533 22 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 526 from Patent WO02068652.
ACCESSION AX921533
VERSION AX921533.1 GI:40215154
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Nov-x proteins and nucleic acids encoding same
TITLE Patent: WO 02068652-A 526 06-SEP-2002;
JOURNAL Location/Qualifiers
FEATURES
source
1..22
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: oligonucleotide primer"

Query Match 6.7%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 3;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 133 TCTCTTGAGCACTCTCAG 153
DB 2 TCTCTTGAGCACTCTCAG 22

RESULT 3
LOCUS AX528253 22 bp DNA linear PAT 21-NOV-2002
DEFINITION Sequence 121 from Patent WO0226985.
ACCESSION AX528253
VERSION AX528253.1 GI:25172560
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.

REFERENCE 1
AUTHORS Spytek, K.A., Caeman, S., Padigaru, M., Dickson, K., Vernet, C.,
Spaderna, S.K., Shenoy, S., Gerlach, V., Ellerman, K., Edinger, S.,
Macdougall, J.R., Smithson, G., Li, L., Malyankar, U.M., Taylor, S.,
Gunter, B. and Tcherenev, V.T.
TITLE G-protein coupled receptors
JOURNAL Patent: WO 0226985-A 121 04-APR-2002;
CURAGEN Corporation (US)
FEATURES Location/Qualifiers
source
1..22
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR Primer Sequence"

Query Match 6.7%; Score 16.2; DB 1; Length 22;
Best Local Similarity 85.7%; Pred. No. 3;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 133 TCTCTTGAGACCTCTCAG 153
 |||||
 Db 2 TCTCTTGAGACCTCTTTCAC 22

RESULT 4
 AX554633
 LOCUS Sequence 187 from Patent WO0246229. 22 bp DNA linear PAT 27-NOV-2002
 DEFINITION AX554633
 ACCESSION AX554633
 VERSION AX554633.1 GI:25898300
 KEYWORDS
 SOURCE
 ORGANISM
 synthetic construct
 other sequences; artificial sequences.

REFERENCE
 AUTHORS 1 Casman,S.J., Padigaru,M., Burgess,C.E., Shinkets,R.A., Spytek,K.A.,
 Gilbert,J.A., Mayoite,J.E., Baumgartner,J.C., Mishra,V.,
 Vernet,C.A., Dickinson,K.S., Ballinger,R.A. and Wolenc,A.R.
 TITLE Novel proteins and nucleic acids encoding same
 JOURNAL Patent: WO 0246229-A 187 13-JUN-2002;
 Curagen Corporation (US)
 FEATURES
 source Location/Qualifiers
 1..22
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="PCR Primer Sequence"

Query Match 6.7%; Score 16.2; DB 1; Length 22;
 Best Local Similarity 85.7%; Pred. No. 3;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 133 TCTCTTGAGACCTCTCAG 153
 |||||
 Db 2 TCTCTTGAGACCTCTTTCAC 22

RESULT 5
 AX703310
 LOCUS Sequence 539 from Patent WO0205913. 22 bp DNA linear PAT 03-APR-2003
 DEFINITION AX703310
 ACCESSION AX703310
 VERSION AX703310.1 GI:29538356
 KEYWORDS
 SOURCE
 ORGANISM
 synthetic construct
 other sequences; artificial sequences.

REFERENCE
 AUTHORS 1 L.L., Ballinger,R.A., Padigaru,M., Kexuda,R., Colman,S.D.,
 Spytek,K.A., Casman,S.J., Vernet,C.A., Shenoy,S.G., Gusev,V.,
 Malyankar,U.M., Edinger,S., Gerlach,V., Smithson,G., Stone,D.J.,
 Setore,P., Macdougall,J.R., Gunther,E., Peyman,J.A., Ellerman,K.,
 Gangoli,E.A. and Millet,I.
 TITLE G-protein coupled receptors and nucleic acids encoding same
 JOURNAL Patent: WO 0205913-A 539 01-AUG-2002;
 Curagen Corporation (US)
 FEATURES
 source Location/Qualifiers
 1..22
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="PCR Primer Sequence"

Query Match 6.7%; Score 16.2; DB 1; Length 22;
 Best Local Similarity 85.7%; Pred. No. 3;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 133 TCTCTTGAGACCTCTCAG 153
 |||||
 Db 2 TCTCTTGAGACCTCTTTCAC 22

RESULT 6
 AR529565/c
 LOCUS AR529565 768 from patent US 6727063. 21 bp DNA linear PAT 08-OCT-2004
 DEFINITION AR529565
 ACCESSION AR529565
 VERSION AR529565.1 GI:53918002
 KEYWORDS
 SOURCE
 ORGANISM
 unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Lander,E.S., Cargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
 McCarthy,J.J.
 TITLE Single nucleotide polymorphisms in genes
 JOURNAL Patent: US 6727063-A 768 27-APR-2004;
 Millennium Pharmaceuticals, Inc. and Whitehead Institute for
 Biomedical Research; Cambridge, MA
 FEATURES
 source Location/Qualifiers
 1..21
 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 6.5%; Score 15.8; DB 1; Length 21;
 Best Local Similarity 81.0%; Pred. No. 3.5;
 Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CTCACAGCAGCACTGATTT 23
 |||||
 Db 21 CTCACAGCAGCACTGCTAT 1

RESULT 7
 AX095590/c
 LOCUS AX095590 768 from Patent WO0118250. 21 bp DNA linear PAT 30-MAR-2001
 DEFINITION AX095590
 ACCESSION AX095590
 VERSION AX095590.1 GI:13511793
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.

REFERENCE
 AUTHORS 1 Lander,E.S., Cargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and
 McCarthy,J.J.
 TITLE Single nucleotide polymorphisms in genes
 JOURNAL Patent: WO 0118250-A 768 15-MAR-2001;
 WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; Millennium
 Pharmaceuticals, Inc. (US)
 FEATURES
 source Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 6.5%; Score 15.8; DB 1; Length 21;
 Best Local Similarity 81.0%; Pred. No. 3.5;
 Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CTCACAGCAGCACTGATTT 23
 |||||
 Db 21 CTCACAGCAGCACTGCTAT 1

RESULT 8
 DD173031
 LOCUS DD173031 22 bp DNA linear PAT 19-DEC-2005
 DEFINITION DD173031
 ACCESSION DD173031
 VERSION DD173031.1 GI:83967286
 KEYWORDS
 WO 2005054467-A/31.

Expression systems using mammalian beta-Actin promoter.


```

SOURCE      unidentified
ORGANISM    unidentified
REFERENCE    1 (bases 1 to 22)
AUTHORS      Tsunoda,H. and Habu,K.
TITLE        Expression systems using mammalian beta-Actin promoter
JOURNAL      Patent: WO 2005054467-A 31 16-JUN-2005;
              CHUGAI PHARMACEUTICAL CO LTD
COMMENT      OS Artificial
              PN WO 2005054467-A/31
              PD 16-JUN-2005
              PF 03-DEC-2004 WO 2004JP018006
              PR 03-DEC-2003 JP 200 3-405269
              PI hiroyuki tsunoda,kiyoshi habu
              CC Description of Artificial Sequence : Artificially Synthesized
              CC Primer
              CC Sequence
FEATURES     Location/Qualifiers
             source          1..22
                           /organism="unidentified"
                           /mol_type="unassigned DNA"
                           /db_xref="taxon:32644"

Query Match      6.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No.3.5;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      110 GTGCCCACTACGCTCTTCC 131
Db      1 GTGCACACACGCGCCGTTGCC 22

RESULT 9
LOCUS      AR704960                22 bp    DNA        linear    PAT 20-SEP-2005
DEFINITION Sequence 23 from patent US 6929912.
ACCESSION  AR704960
VERSION     AR704960.1 GI:75923278
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE    1 (bases 1 to 22)
AUTHORS      Guida,M., Hall,U., Petros,W.P., Vredenburg,J.J., Colvin,O.M. and
              Marks,J.R.
TITLE        Methods for evaluating the ability to metabolize pharmaceuticals
JOURNAL      Patent: US 6929912-A 23 16-AUG-2005;
              Genesee Pharmaceuticals, Inc. and Duke University; New Haven,
              CT
FEATURES     Location/Qualifiers
             source          1..22
                           /organism="unknown"
                           /mol_type="genomic DNA"

Query Match      6.4%; Score 15.6; DB 1; Length 22;
Best Local Similarity 81.8%; Pred. No.3.5;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      56 CTGCTGCTCACCCTCTTCC 77
Db      1 CTGCAGCCCGCCTCTTCTCC 22

RESULT 10
LOCUS      AR279129                20 bp    DNA        linear    PAT 10-APR-2003
DEFINITION Sequence 262 from patent US 6514694.
ACCESSION  AR279129
VERSION     AR279129.1 GI:29713772
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.

```

```

REFERENCE    1 (bases 1 to 20)
AUTHORS      Milhausen,M.J.
TITLE        Methods for the detection of encysted parasites
JOURNAL      Patent: US 6514694-A 262 04-FEB-2003;
              Heeska Corporation; Fort Collins, CO
FEATURES     Location/Qualifiers
             source          1..20
                           /organism="unknown"
                           /mol_type="genomic DNA"

Query Match      6.3%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No.4.4;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      189 TGCTGTAGGTTGCTAG 208
Db      1 TGGCTGTTGGGTTGCTCG 20

RESULT 11
LOCUS      AR393701                21 bp    DNA        linear    PAT 18-DEC-2003
DEFINITION Sequence 240 from patent US 6617122.
ACCESSION  AR393701
VERSION     AR393701.1 GI:40120515
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE    1 (bases 1 to 21)
AUTHORS      Hayden,M.R., Brooke-Wilson,A.R. and Pinstone,S.N.
TITLE        Process for identifying modulators of ABC1 activity
JOURNAL      Patent: US 6617122-A 240 09-SEP-2003;
              Xenon Genetics, Inc.; Burnaby;
              BC, Canada
FEATURES     Location/Qualifiers
             source          1..21
                           /organism="unknown"
                           /mol_type="genomic DNA"

Query Match      6.3%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No.4.1;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      58 GCTGCTCACCCTCTTCC 77
Db      1 GCAGCTCACCCTCTTCC 20

Search completed: October 2, 2006, 15:34:16
Job time : 0.001 secs

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```
US-08-765-340-30
; Sequence 30, Application US/08765340
; Patent No. 6150092
; GENERAL INFORMATION:
; APPLICANT: UCHIDA, K.,
; APPLICANT: UCHIDA, T.,
; APPLICANT: TANAKA, Y.,
; APPLICANT: MATSUDA, Y.,
; APPLICANT: KONDO, S.,
; TITLE OF INVENTION: AN ANTISENSE NUCLEIC ACID
; TITLE OF INVENTION: COMPOUND
; NUMBER OF SEQUENCES: 185
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,340
; FILING DATE: 23-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 145146/94
; FILING DATE: 27-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 311130/94
; FILING DATE: 21-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SERUNIAN, LESLIE
; REGISTRATION NUMBER: 35,353
; REFERENCE/DOCKET NUMBER: 1452-4005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"
US-08-765-340-30

Query Match          6.9%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 10;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      147 CCCTTCCTCTGCGCAT 164
      ||| ||| ||| ||| ||| |||
DB      3 CCCTCTCTCTGCGCAT 20

RESULT 2
US-09-702-251-85
; Sequence 85, Application US/09702251
; Patent No. 6372492
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF TALIN EXPRESSION
; FILE REFERENCE: RTS-0199
; CURRENT APPLICATION NUMBER: US/09/702,251
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 85
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; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-702-251-85

Query Match          6.8%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      105 TCTCATCTCTGCTC 120
      ||| ||| ||| ||| ||| |||
DB      3 TCTCATCTCTGCTC 18

RESULT 3
US-09-574-779B-88/c
; Sequence 88, Application US/09574779B
; Patent No. 6767720
; GENERAL INFORMATION:
; APPLICANT: VILAMS, INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOLOGIE
; TITLE OF INVENTION: No. 6767720el cDNAs encoding catenin-binding proteins with
; FILE REFERENCE: 2676-4415US
; CURRENT APPLICATION NUMBER: US/09/574,779B
; CURRENT FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 99201543.8
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 88
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer FVR1479F
US-09-574-779B-88

Query Match          6.5%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 15;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      182 GACTTCACAGAGCAA 198
      ||| ||| ||| ||| ||| |||
DB      17 GACTTCACAGAGCAA 1

RESULT 4
US-09-593-711A-63
; Sequence 63, Application US/09593711A
; Patent No. 6271030
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF C/EBP BETA EXPRESSION
; FILE REFERENCE: RTS-0118
; CURRENT APPLICATION NUMBER: US/09/593,711A
; CURRENT FILING DATE: 2000-06-14
; NUMBER OF SEQ ID NOS: 244
; SEQ ID NO 63
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-593-711A-63

Query Match          6.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 16;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Oy 133 GAGACACCTGCTCCCTTC 152
 Db 1 GCGACAGCTGCTCCACCTTC 20

RESULT 5

US-09-593-711A-180
 ; Sequence 180, Application US/09593711A
 ; Patent No. 6271030
 ; GENERAL INFORMATION:
 ; APPLICANT: Brett P. Monia
 ; APPLICANT: Madeline M. Butler
 ; APPLICANT: Jacqueline Wyatt
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF C/EBP BETA EXPRESSION
 ; FILE REFERENCE: RTS-0118
 ; CURRENT APPLICATION NUMBER: US/09/593,711A
 ; CURRENT FILING DATE: 2000-06-14
 ; NUMBER OF SEQ ID NOS: 244
 ; SEQ ID NO 180
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Antisense Oligonucleotide
 US-09-593-711A-180

Query Match 6.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 16;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 136 ACACCTGCTCCCTTCCTCC 155
 Db 1 ACAGCTGCTCCACCTTCCTTC 20

RESULT 6

US-09-295-593-9/c
 ; Sequence 9, Application US/09295593
 ; Patent No. 6417169
 ; GENERAL INFORMATION:
 ; APPLICANT: WRIGHT, Jim A.
 ; APPLICANT: YOUNG, Aiping H.
 ; APPLICANT: LEE, Yoon S.
 ; TITLE OF INVENTION: INSULIN-LIKE GROWTH FACTOR II ANTISENSE OLIGONUCLEOTIDE
 ; TITLE OF INVENTION: SEQUENCES AND METHODS OF USING SAME TO MODULATE CELL
 ; FILE REFERENCE: 032396-046
 ; CURRENT APPLICATION NUMBER: US/09/295,593
 ; CURRENT FILING DATE: 1999-04-22
 ; EARLIER APPLICATION NUMBER: US 60/082,791
 ; EARLIER FILING DATE: 1998-04-23
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 9
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Human
 US-09-295-593-9

Query Match 6.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 16;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 98 GGGCCCCCTGCTCTCTCTG 117
 Db 20 GGGCCCCGCTCTCTCTCCG 1

RESULT 7
 US-09-484-629B-28/c
 ; Sequence 28, Application US/09484629B
 ; Patent No. 6998472
 ; GENERAL INFORMATION:

APPLICANT: Medical Research Council
 ; TITLE OF INVENTION: Obesity gene
 ; FILE REFERENCE: 18396/1140
 ; CURRENT APPLICATION NUMBER: US/09/484,629B
 ; CURRENT FILING DATE: 2000-01-18
 ; PRIOR APPLICATION NUMBER: PCT/GB99/02658
 ; PRIOR FILING DATE: 1998-12-08
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 28
 ; LENGTH: 21
 ; TYPE: DNA
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: synthetic primer
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(21)
 ; OTHER INFORMATION: synthetic primer
 US-09-484-629B-28

Query Match 6.4%; Score 15.2; DB 1; Length 21;
 Best Local Similarity 85.0%; Pred. No. 15;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 139 CCGTCTCCCTCTCTCTCTC 158
 Db 20 CCGTCTCCGCTCTCTCTCG 1

RESULT 8

US-08-741-406-10/c
 ; Sequence 10, Application US/08741406
 ; Patent No. 572118
 ; GENERAL INFORMATION:
 ; APPLICANT: Scheffler, Immo E.
 ; TITLE OF INVENTION: Mammalian Artificial Chromosomes and
 ; TITLE OF INVENTION: Methods of Using Same
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell & Flores LLP
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/741,406
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/550,717
 ; FILING DATE: 31-OCT-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A.
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P-UD 2317
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 535-9001
 ; TELEFAX: (619) 535-8949
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 20 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 US-08-741-406-10

Query Match 6.4%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 CAGGAGCTTCACAG 192
Db 16 CAGGAGCTTCACAG 2

RESULT 9

US-09-024-472-10/c
; Sequence 10, Application US/09024472
; Patent No. 6133503
; GENERAL INFORMATION:
; APPLICANT: Schefler, Immo E.
; TITLE OF INVENTION: Mammalian Artificial Chromosomes and
; NUMBER OF INVENTION: Methods of Using Same
; CORRESPONDENCE ADDRESSES: 16
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/024,472
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/741,406
; FILING DATE:
; APPLICATION NUMBER: US 08/550,717
; FILING DATE: 31-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UD 2317
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-09-024-472-10

Query Match 6.4%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 178 CAGGAGCTTCACAG 192
Db 16 CAGGAGCTTCACAG 2

RESULT 10

US-09-517-467B-252
; Sequence 252, Application US/09517467B
; Patent No. 6451602
; GENERAL INFORMATION:
; APPLICANT: Ian Popoff
; APPLICANT: Lex M. Cowbert
; TITLE OF INVENTION: ANTISENSE MODULATION OF PARP EXPRESSION
; FILE REFERENCE: RTS-0150
; CURRENT APPLICATION NUMBER: US/09/517,467B

; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 09/517,467
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 345
; SEQ ID NO 252
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide

US-09-517-467B-252

Query Match 6.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 18;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 41 TGCATCCCTTGAT 58
Db 1 TCCCATCCCTTGAT 18

RESULT 11

US-09-076-259-2/c
; Sequence 2, Application US/09076259
; Patent No. 6548245
; GENERAL INFORMATION:
; APPLICANT: Lilly, Craig M.
; APPLICANT: Luster, Andrew D.
; TITLE OF INVENTION: METHODS FOR DIAGNOSIS, PREDICTION
; TITLE OF INVENTION: AND TREATMENT OF ASTHMA AND OTHER INFLAMMATORY CONDITIONS
; NUMBER OF INVENTION: BASED ON BOTAXIN CODING SEQUENCE POLYMORPHISM
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02210-2211

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/076,259
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/046,720
; FILING DATE: 16-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Plumer, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: B0801/7104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other

US-09-076-259-2

Query Match 6.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 18;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 70 CGTGAGAGCTGTTGTT 87
|||
Db 20 CGTGAGAGCTGTTGTT 3

RESULT 12

US-10-413-255-2/c

Sequence 2, Application US/10413255

Patent No. 6949637

GENERAL INFORMATION:

APPLICANT: Lilly, Craig M.

Luster, Andrew D.

Drazen, Jeffrey M.

TITLE OF INVENTION: METHODS FOR DIAGNOSIS, PREDICTION

AND TREATMENT OF ASTHMA AND OTHER INFLAMMATORY CONDITIONS

BASED ON EOTAXIN CODING SEQUENCE POLYMORPHISM

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Wolf, Greenfield & Sacke, P.C.

STREET: 600 Atlantic Avenue

CITY: Boston

STATE: MA

COUNTRY: U.S.A.

ZIP: 02210-2211

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/413,255

FILING DATE: 14-Apr-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/076,259

FILING DATE: 12-MAY-1998

APPLICATION NUMBER: 60/046,720

FILING DATE: 16-MAY-1997

ATTORNEY/AGENT INFORMATION:

NAME: Trevisan, Maria A.

REGISTRATION NUMBER: 48,207

REFERENCE/DOCKET NUMBER: B00801.70282. US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-720-3500

TELEFAX: 617-720-2441

TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Other

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-413-255-2

Query Match 6.3%; Score 14.8; DB 1; Length 20;

Best Local Similarity 88.9%; Pred. No. 18;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 70 CGTGAGAGCTGTTGTT 87

Db 20 CGTGAGAGCTGTTGTT 3

RESULT 13

US-08-117-952-294/c

Sequence 294, Application US/08117952

Patent No. 3851760

GENERAL INFORMATION:

APPLICANT: Evans, Glen A.

APPLICANT: Smith, Michael W.

TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE

TITLE OF INVENTION: SAMPLED MAPS OF COMPLEX GENOMES
NUMBER OF SEQUENCES: 797
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark

STREET: 444 South Flower Street, Suite 2000

CITY: Los Angeles

STATE: CA

COUNTRY: USA

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/117,952

FILING DATE: 07-SEP-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/078,471

FILING DATE: 15-JUN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Reiter, Stephen E.

REGISTRATION NUMBER: 31,192

REFERENCE/DOCKET NUMBER: P41 9423

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-546-4737

INFORMATION FOR SEQ ID NO: 294:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: Oligonucleotide

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-117-952-294

Query Match 6.3%; Score 14.8; DB 1; Length 21;

Best Local Similarity 88.9%; Pred. No. 17;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 74 AGAGCTGTTGTTGAAA 91

Db 18 AAGCTGTTTGTGAAA 1

RESULT 14

US-09-825-923-6

Sequence 6, Application US/09825923

Patent No. 6696556

GENERAL INFORMATION:

APPLICANT: Snajdr, Amlir

APPLICANT: Heinoonen, Paula

APPLICANT: Alhopuro, Pia

APPLICANT: Karvonen, Matti

APPLICANT: Pesonen, Ullamari

APPLICANT: Scheinin, Mika

APPLICANT: Salonen, Jukka T

APPLICANT: Tuomainen, Tomi-Pekka

APPLICANT: Lakka, Timo A

APPLICANT: Nyysanen, Kristina

APPLICANT: Salonen, Riitta

APPLICANT: Kaunonen, Jussi

APPLICANT: Valkonen, Veli-Pekka

TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor

FILE REFERENCE: Alpha-2B-AR variant

CURRENT APPLICATION NUMBER: US/09/825,923

CURRENT FILING DATE: 2001-04-05

PRIOR APPLICATION NUMBER: 09/422,985


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; PRIOR FILING DATE: 2000-05-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR primer
US-09-825-923-6

Query Match
Best Local Similarity 6.1%; Score 14.4; DB 1; Length 19;
Pred. No. 22;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 143 CTCCTCTCTCTCTC 158
Db 4 CTCCTCTCTCTCTC 19

RESULT 15
US-10-077-870-6
; Sequence 6, Application US/10077870
; Patent No. 7029849
; GENERAL INFORMATION:
; APPLICANT: Salonen, Jukka T
; TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
; FILE REFERENCE: 0933-0183P
; CURRENT APPLICATION NUMBER: US/10/077, 870
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: FI 20010323
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 6
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR primer pair 1, directed
US-10-077-870-6

Query Match
Best Local Similarity 6.1%; Score 14.4; DB 1; Length 19;
Pred. No. 22;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 143 CTCCTCTCTCTCTC 158
Db 4 CTCCTCTCTCTCTC 19

RESULT 16
US-09-056-285A-41
; Sequence 41, Application US/09056285A
; Patent No. 6403307
; GENERAL INFORMATION:
; APPLICANT: Stone, Edwin M.
; Sheffield, Val C.
; Alward, Wallace L.M.
; Fingert, John
; TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESSES: 43
; ADDRESSSEE: FOLEY, HONG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,285A
; FILING DATE: 07-Apr-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: UIA-010.28
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-7000
; TELEFAX: 617-832-1000
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "primer".
; SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-09-056-285A-41

Query Match
Best Local Similarity 6.1%; Score 14.4; DB 1; Length 20;
Pred. No. 21;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 149 CTTCTCTCTCTGCCAT 164
Db 3 CATTCTCTCTGCCAT 18

RESULT 17
US-09-952-464A-41
; Sequence 41, Application US/09952464A
; Patent No. 6956103
; GENERAL INFORMATION:
; APPLICANT: Stone, Edwin M.
; Sheffield, Val C.
; Alward, Wallace L.M.
; Fingert, John
; TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
; FILE REFERENCE: 21087.0017U1
; CURRENT APPLICATION NUMBER: US/09/952,464A
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: 09/473,273
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 09/461,542
; PRIOR FILING DATE: 1999-12-15
; PRIOR APPLICATION NUMBER: 09/366,952
; PRIOR FILING DATE: 1999-08-04
; PRIOR APPLICATION NUMBER: 09/056,285
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: 08/822,999
; PRIOR FILING DATE: 1997-03-21
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6956103e =
US-09-952-464A-41

Query Match
Best Local Similarity 6.1%; Score 14.4; DB 1; Length 20;
Pred. No. 21;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 149 CTTCTCTCTCTGCCAT 164
Db 3 CTTCTCTCTCTGCCAT 164
```

Db 3 CATCTCTTGTGCAT 18

RESULT 18

US-09-422-978-10001/c
; Sequence 10001, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/422,978
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 10001
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: downstream amplification primer 99-8732 for SEQ 2136, in compleme
US-09-422-978-10001

Query Match 6.0%; Score 14.2; DB 1; Length 19;

Best Local Similarity 84.2%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 209 CATGCTCTGTTGTTGCT 227

Db 19 CTACTCTTGTGTGTCT 1

RESULT 19

US-08-850-993-10/c
; Sequence 10, Application US/08850993
; Patent No. 5955277
; GENERAL INFORMATION:
; APPLICANT: Hansen, Torben
; APPLICANT: Andersen, Carsten
; APPLICANT: Pedersen, Oluf B.
; TITLE OF INVENTION: Mutant cDNA Encoding The p53alpha
; TITLE OF INVENTION: Subunit Of Phosphatidylinositol 3-Kinase
; FILE REFERENCE: 4802.200-US
; CURRENT FILING DATE: 1997-05-05
; EARLIER APPLICATION NUMBER: 0539/96
; EARLIER FILING DATE: 1996-05-06
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: human
US-08-850-993-10

Query Match 6.0%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 23;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 77 GCTGTTGTTGAAGAGC 95

Db 20 GCTGAGGTTTGAGAGC 2

RESULT 20

US-09-392-350-35/c
; Sequence 35, Application US/09392350
; Patent No. 6133032
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowert
; TITLE OF INVENTION: ANTISENSE MODULATION OF PI3 KINASE P110 BETA EXPRESSION
; FILE REFERENCE: RTS-0075
; CURRENT APPLICATION NUMBER: US/09/392,350
; CURRENT FILING DATE: 1999-09-08
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-392-350-35

Query Match 6.0%; Score 14.2; DB 1; Length 20;

Best Local Similarity 84.2%; Pred. No. 23;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 64 AGTTCAGTGAGAGCTGCT 82

Db 19 AGTTCATGTCAGGCTGCT 1

RESULT 21

US-09-283-011-35/c
; Sequence 35, Application US/09283011
; Patent No. 6207401
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mosele, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0.
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/283,011
; FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/012,135
FILING DATE: January 22, 1998
APPLICATION NUMBER: 08/755,728
FILING DATE: No. 6207401ember 25, 1996
APPLICATION NUMBER: 60/023,943
FILING DATE: August 14, 1996
APPLICATION NUMBER: 60/008,809
FILING DATE: December 18, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Watburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 231/282
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440

TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-283-011-35

Query Match 6.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 23;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 182 GACTTCACAGAGCAAT 200
Db 20 GTCTTCACAGAGCAAT 2

RESULT 22
US-09-593-711A-62
; Sequence 62, Application US/09593711A
; Patent No. 6271030
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF C/EBP BETA EXPRESSION
; FILE REFERENCE: RFS-0118
; CURRENT APPLICATION NUMBER: US/09/593, 711A
; CURRENT FILING DATE: 2000-06-14
; NUMBER OF SEQ ID NOS: 244
; SEQ ID NO 62
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-09-593-711A-62

Query Match 6.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 23;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 138 ACCTGCTCCCTCTCCT 156
Db 1 AGCTGCTCCACTTCTCT 19

RESULT 23
US-09-422-978-11320
; Sequence 11320, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Balleleic markers for use in constructing a high density...
; FILE REFERENCE: GENSET 020CPI
; CURRENT APPLICATION NUMBER: US/09/422, 978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298, 850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/409, 732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082, 614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 11320
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind

LOCATION: 1..20
; OTHER INFORMATION: downstream amplification primer 99-4207 for SEQ 3455, in complement
US-09-422-978-11320

Query Match 6.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 23;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 104 CTCTCATTCCTGCTCCC 122
Db 2 CTCTCATTCCTGCTCCC 20

RESULT 24
US-09-033-936-35/C
; Sequence 35, Application US/09033936
; Patent No. 6632976
; GENERAL INFORMATION:
; APPLICANT: TOMIZUKA, KAZUMA
; APPLICANT: YOSHIDA, HITOSHI
; APPLICANT: HANAOKA, KAZUNORI
; APPLICANT: OSHIMURA, MITSUO
; APPLICANT: ISHIDA, ISAO
; TITLE OF INVENTION: CHIMERIC ANIMAL AND METHOD FOR PRODUCING THE SAME
; FILE REFERENCE: 081356/0114
; CURRENT APPLICATION NUMBER: US/09/033, 936
; CURRENT FILING DATE: 1998-03-02
; PRIOR APPLICATION NUMBER: PCT/JP96/02427
; PRIOR FILING DATE: 1996-08-29
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-033-936-35

Query Match 6.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 23;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 136 ACACCTGCTCCCTCTCTC 154
Db 20 ACACCTGCTCTCTCTCAC 2

RESULT 25
US-09-012-135A-35/C
; Sequence 35, Application US/09012135A
; Patent No. 6716575
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Mosie, Kevin
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AUR-1
; TITLE OF INVENTION: AND/OR AUR-2 RELATED DISORDERS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/012,135A
FILING DATE: January 22, 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,268
FILING DATE: January 9, 1998
APPLICATION NUMBER: 08/755,728
FILING DATE: No. 6716575ember 25, 1996
APPLICATION NUMBER: 60/023,943
FILING DATE: August 14, 1996
APPLICATION NUMBER: 60/008,809
FILING DATE: December 18, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 231/282
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-012-135A-35

Query Match 6.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 23;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 182 GACTTCACAAGAGCAAT 200
Db 20 GTCTTCACAGAGCAAT 2

RESULT 26
US-09-784-332-35/C
Sequence 35, Application US/09784332
Patent No. 6841579
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF AIR-1
Mossie, Kevin
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/784,332
FILING DATE: 16-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/283,011
FILING DATE: <Unknown>
APPLICATION NUMBER: 09/012,135
FILING DATE: January 22, 1998
APPLICATION NUMBER: 08/755,728
FILING DATE: No. 6841579ember 25, 1996
APPLICATION NUMBER: 60/023,943

FILING DATE: August 14, 1996
APPLICATION NUMBER: 60/008,809
FILING DATE: December 18, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 231/282
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-784-332-35

Query Match 6.0%; Score 14.2; DB 1; Length 20;
Best Local Similarity 84.2%; Pred. No. 23;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 182 GACTTCACAAGAGCAAT 200
Db 20 GTCTTCACAGAGCAAT 2

RESULT 27
US-08-765-340-29
Sequence 29, Application US/08765340
Patent No. 6150092
GENERAL INFORMATION:
APPLICANT: UCHIDA, K.
APPLICANT: UCHIDA, T.
APPLICANT: TANAKA, Y.
APPLICANT: MATSUDA, Y.
APPLICANT: KONDO, S.
TITLE OF INVENTION: AN ANTISENSE NUCLEIC ACID
COMPOUND
NUMBER OF SEQUENCES: 185
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
SOFTWARE: #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,340
FILING DATE: 23-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 145146/94
FILING DATE: 27-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 311130/94
FILING DATE: 21-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: SERUNIAN, LESLIE
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 1452-4005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
US-08-765-340-29

Query Match 5.9%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 152 CTCCTCTGCCATG 165
Db 2 CTCCTCTGCCATG 15

RESULT 28

US-08-373-124A-178
Sequence 178, Application US/08373124A
Patent No. 5646042

GENERAL INFORMATION:

APPLICANT: Stinchcomb, Dan T.

APPLICANT: Draper, Kenneth

APPLICANT: McSwigen, James

APPLICANT: Jarvis, Thale

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR

TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND

NUMBER OF SEQUENCES: 2627

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Suite 4700

STATE: Los Angeles

COUNTRY: California

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/373,124A

FILING DATE: January 13, 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/245,466

FILING DATE: May 18, 1994

APPLICATION NUMBER: 08/192,943

FILING DATE: February 7, 1994

APPLICATION NUMBER: 07/987,132

FILING DATE: December 7, 1992

APPLICATION NUMBER: 07/936,422

FILING DATE: August 26, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 209/035

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 178:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-373-124A-178

Query Match 5.8%; Score 13.8; DB 1; Length 17;

Best Local Similarity 52.9%; Pred. No. 31;
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 140 CTCGCCCCCTTCTCT 156
Db 1 CUCUCUCUCUCUCUCU 17

RESULT 29

US-08-373-124A-180

Sequence 180, Application US/08373124A
Patent No. 5646042

GENERAL INFORMATION:

APPLICANT: Stinchcomb, Dan T.

APPLICANT: Draper, Kenneth

APPLICANT: McSwigen, James

APPLICANT: Jarvis, Thale

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR

TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND

NUMBER OF SEQUENCES: 2627

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Suite 4700

STATE: Los Angeles

COUNTRY: California

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/373,124A

FILING DATE: January 13, 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/245,466

FILING DATE: May 18, 1994

APPLICATION NUMBER: 08/192,943

FILING DATE: February 7, 1994

APPLICATION NUMBER: 07/987,132

FILING DATE: December 7, 1992

APPLICATION NUMBER: 07/936,422

FILING DATE: August 26, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 209/035

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 180:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-373-124A-180

Query Match 5.8%; Score 13.8; DB 1; Length 17;

Best Local Similarity 52.9%; Pred. No. 31;

Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 143 CTCGCCCCCTTCTCT 159
Db 1 CUCUCUCUCUCUCUCU 17

RESULT 30

US-08-435-628-178
; Sequence 178, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth
; APPLICANT: MCSwigen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Filth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,124
; FILING DATE: January 13, 1995
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 178:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-435-628-178
Query Match 5.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 31;
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
CY 140 CTGCTCCCTTCCTTCT 156
DB 1 CUCCUCCUCCUCCUCCU 17
RESULT 31
US-08-435-628-180
; Sequence 180, Application US/08435628
; Patent No. 5817796
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Draper, Kenneth

APPLICANT: MCSwigen, James
; APPLICANT: Jarvis, Thale
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TREATMENT OF RESTENOSIS AND
; TITLE OF INVENTION: CANCER USING RIBOZYMES
; NUMBER OF SEQUENCES: 2627
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Filth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,628
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/373,124
; FILING DATE: January 13, 1995
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 08/192,943
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; APPLICATION NUMBER: 07/936,422
; FILING DATE: August 26, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 180:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-435-628-180
Query Match 5.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 31;
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
CY 143 CTCCTCCCTTCCTTCT 159
DB 1 CUCCUCCUCCUCCUCCU 17
RESULT 32
US-08-311-486C-1151
; Sequence 1151, Application US/08311486C
; Patent No. 5811300
; GENERAL INFORMATION:
; APPLICANT: Sean Sullivan
; APPLICANT: Kenneth Draper
; APPLICANT: Kevin Ksiech
; APPLICANT: Dan T. Stinchcomb
; APPLICANT: James MCSwigen
; TITLE OF INVENTION: RIBOZYME TREATMENT OF
; TITLE OF INVENTION: DISEASES OR CONDITIONS
; TITLE OF INVENTION: RELATED TO LEVELS OF

```

; TITLE OF INVENTION: TNF-
; NUMBER OF SEQUENCES: 1157
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,486C
; FILING DATE: September 23, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/008,895
; FILING DATE: January 19, 1993
; APPLICATION NUMBER: 07/989,849
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 209/166
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1151:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-311-486C-1151

Query Match 5.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 76.5%; Pred. No. 29;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 91 AGAGCTGCGCCCTCT 107
Db 1 AGAGCCAGCCCCCTCT 17

RESULT 33
US-09-422-978-4193/c
; Sequence 4193, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Maria
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020C01
; CURRENT APPLICATION NUMBER: US/09/422,978
; FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4193
; LENGTH: 18
```

```

; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-13878 for SEQ 259,
US-09-422-978-4193

Query Match 5.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 29;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 110 TTCTCGTCCCACTC 126
Db 17 TTCTCGTCCCACTC 1

RESULT 34
PCT-US95-04094-3
; Sequence 3, Application PC/TUS9504094
; GENERAL INFORMATION:
; APPLICANT: ALMS, William
; APPLICANT: WHITE, Barbara
; TITLE OF INVENTION: HUMAN INTERLEUKIN VARIANTS GENERATED BY
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04094
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/224,010
; FILING DATE: 06-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 028754-001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; PCT-US95-04094-3

Query Match 5.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 29;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 113 TTCTGCTCCCACTCTTG 129
Db 1 TTCTGCTCCCACTCTTG 17

RESULT 35
US-08-502-185-9/c
; Sequence 9, Application US/08502185
```



```
; Patent No. 5639736
; GENERAL INFORMATION:
; APPLICANT: Robinson, Gregory S.
; TITLE OF INVENTION: Human VEGF-Specific
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lappin & Kuerner
; STREET: 200 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/502,185
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HYZ-031CPDV1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-330-1300
; TELEFAX: 617-330-1311
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
;
US-08-502-185-9
;
Query Match 5.8%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 27;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 213 CTTCTGTTCTGTCGTC 229
Db 19 CGCTCTGTTCTGTCGTC 3

RESULT 36
US-08-398-945-9/c
; Sequence 9, Application US/08398945
; Patent No. 5639872
; GENERAL INFORMATION:
; APPLICANT: Robinson, Gregory S.
; TITLE OF INVENTION: Human VEGF-Specific
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lappin & Kuerner
; STREET: 200 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/398,945
; FILING DATE:
```

```
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HYZ-031CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-330-1300
; TELEFAX: 617-330-1311
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
;
US-08-398-945-9
;
Query Match 5.8%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 27;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 213 CTTCTGTTCTGTCGTC 229
Db 19 CGCTCTGTTCTGTCGTC 3

RESULT 37
US-08-501-779-9/c
; Sequence 9, Application US/08501779
; Patent No. 5661135
; GENERAL INFORMATION:
; APPLICANT: Robinson, Gregory S.
; TITLE OF INVENTION: Human VEGF-Specific
; TITLE OF INVENTION: Oligonucleotides
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lappin & Kuerner
; STREET: 200 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/501,779
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HYZ-031CPDV2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-330-1300
; TELEFAX: 617-330-1311
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
;
US-08-501-779-9
;
Query Match 5.8%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 27;
```

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 213 CTCTTGTCTGTCTGC 229
| | | | | | | | | | | | | | |
Db 19 CGTCTGTCTGTCTGC 3

RESULT 38
US-08-501-713-9/C
; Sequence 9, Application US/08501713
; Patent No. 5710136
; GENERAL INFORMATION:
; APPLICANT: Robinson, Gregory S.
; APPLICANT: Smith, Lois E.H.
; TITLE OF INVENTION: Inhibition of
; TITLE OF INVENTION: Neovascularization Using
; TITLE OF INVENTION: VEGF-Specific
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Lappin & Kusner
; STREET: 200 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/501,713
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HYZ-031DV2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-330-1300
; TELEFAX: 617-330-1311
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-501-713-9

Query Match 5.8%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 27;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 213 CTCTTGTCTGTCTGC 229
| | | | | | | | | | | | | | |
Db 19 CGTCTGTCTGTCTGC 3

RESULT 39
US-08-378-860-9/C
; Sequence 9, Application US/08378860
; Patent No. 5731294
; GENERAL INFORMATION:
; APPLICANT: Robinson, Gregory S.
; APPLICANT: Smith, Lois E.H.
; TITLE OF INVENTION: Inhibition of
; TITLE OF INVENTION: Neovascularization Using
; TITLE OF INVENTION: VEGF-Specific
; TITLE OF INVENTION: Oligonucleotides

; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lappin & Kusner
; STREET: 200 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,860
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HYZ-031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-330-1300
; TELEFAX: 617-330-1311
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-378-860-9

Query Match 5.8%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 27;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 213 CTCTTGTCTGTCTGC 229
| | | | | | | | | | | | | | |
Db 19 CGTCTGTCTGTCTGC 3

RESULT 40
US-08-501-626-9/C
; Sequence 9, Application US/08501626
; Patent No. 5801156
; GENERAL INFORMATION:
; APPLICANT: Robinson, Gregory S.
; APPLICANT: Smith, Lois E.H.
; TITLE OF INVENTION: Inhibition of
; TITLE OF INVENTION: Neovascularization Using
; TITLE OF INVENTION: VEGF-Specific
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Lappin & Kusner
; STREET: 200 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/501,626
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-031DV4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-330-1300
TELEFAX: 617-330-1311
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-501-626-9

Query Match 5.8%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 27;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 213 CTTCTGTTCTGCTGC 229
Db 19 CGCTCTGTTCTGCTGC 3

RESULT 41
US-08-501-356-9/c
Sequence 9, Application US/08501356
Patent No. 5814620
GENERAL INFORMATION:
APPLICANT: Robinson, Gregory S.
TITLE OF INVENTION: Inhibition of
TITLE OF INVENTION: Neovascularization Using
TITLE OF INVENTION: VEGF-Specific
TITLE OF INVENTION: Oligonucleotides
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lappin & Kusner
STREET: 200 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/501,356
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-031DV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-330-1311
TELEFAX: 617-330-1300
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-501-356-9

Query Match 5.8%; Score 13.8; DB 1; Length 19;

Best Local Similarity 88.2%; Pred. No. 27;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 213 CTTCTGTTCTGCTGC 229
Db 19 CGCTCTGTTCTGCTGC 3

RESULT 42
US-08-270-581-6
Sequence 6, Application US/08270581
Patent No. 5856168
GENERAL INFORMATION:
APPLICANT: Weigel, Paul H.
APPLICANT: Deangelis, Paul L.
TITLE OF INVENTION: Hyaluronate Synthase Gene and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/270,581
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTSG:161\PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
TELEFAX: 713-789-2679
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-270-581-6

Query Match 5.8%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 27;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 32 ATGCTTAGTCCATCC 48
Db 2 ATGCTTAGTCCATCC 18

RESULT 43
US-09-146-893-6
Sequence 6, Application US/09146893
Patent No. 6453504
GENERAL INFORMATION:
APPLICANT: Weigel, Paul H.
APPLICANT: Deangelis, Paul L.
TITLE OF INVENTION: Hyaluronate Synthase Gene and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee

```

; STREET: P. O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/146,893
; FILING DATE: 03-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/270,581
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: USG:161\PAR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-787-1400
; TELEFAX: 713-789-2679
;
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-146-893-6

Query Match      5.8%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 27;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      32 ATGCTTAGTGCATCC 48
Db      2 ATGCTTAGTGCATTC 18

RESULT 44
US-10-117-795-8
; Sequence 8, Application US/10117795
; Patent No. 6852514
; GENERAL INFORMATION:
; APPLICANT: WEIGEL, PAUL E.
; APPLICANT: DEANGELIS, PAUL L.
; APPLICANT: PAPACONSTANTINOU, JOHN
; TITLE OF INVENTION: HYALURONATE SYNTHASE GENES AND USES THEREOF
; FILE REFERENCE: 35541.073
; CURRENT APPLICATION NUMBER: US/10/117,795
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 09/559,793
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 19
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: OLIGONUCLEOTIDE PROBE
US-10-117-795-8

Query Match      5.8%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 27;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      32 ATGCTTAGTGCATCC 48
Db      2 ATGCTTAGTGCATTC 18
```

```

Db      2 ATGCTTAGTGCATTC 18

RESULT 45
US-10-124-222-8
; Sequence 8, Application US/10124222
; Patent No. 6855502
; GENERAL INFORMATION:
; APPLICANT: WEIGEL, PAUL E.
; APPLICANT: DEANGELIS, PAUL L.
; APPLICANT: PAPACONSTANTINOU, JOHN
; TITLE OF INVENTION: HYALURONATE SYNTHASE GENES AND USES THEREOF
; FILE REFERENCE: 35541.069
; CURRENT APPLICATION NUMBER: US/10/124,222
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: 09/146,893
; PRIOR FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 19
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: OLIGONUCLEOTIDE PROBE
US-10-124-222-8

Query Match      5.8%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 27;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      32 ATGCTTAGTGCATCC 48
Db      2 ATGCTTAGTGCATTC 18

RESULT 46
US-11-024-426-8
; Sequence 8, Application US/11024426
; Patent No. 7026159
; GENERAL INFORMATION:
; APPLICANT: WEIGEL, PAUL E.
; APPLICANT: DEANGELIS, PAUL L.
; APPLICANT: PAPACONSTANTINOU, JOHN
; TITLE OF INVENTION: HYALURONATE SYNTHASE GENES AND USES THEREOF
; FILE REFERENCE: 35541.069
; CURRENT APPLICATION NUMBER: US/11/024,426
; CURRENT FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: 09/146,893
; PRIOR FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 19
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: OLIGONUCLEOTIDE PROBE
US-11-024-426-8

Query Match      5.8%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 27;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      32 ATGCTTAGTGCATCC 48
Db      2 ATGCTTAGTGCATTC 18

RESULT 47
US-10-156-306B-6881/C
; Sequence 6881, Application US/10156306B
; Patent No. 7022828
```

```

; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; TITLE OF INVENTION: Levels of IKK-gamma and PKR
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306B
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8014
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 6881
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-10-156-306B-6881

Query Match      5.7%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 35;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      148 CCTTCTCCTTCTGCC 162
Db      16  CCTGCTCCTTCTGCC 2

RESULT 48
US-10-156-306B-6882/C
; Sequence 6882, Application US/10156306B
; Patent No. 7022828
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; TITLE OF INVENTION: Levels of IKK-gamma and PKR
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306B
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8014
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 6882
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-10-156-306B-6882

Query Match      5.7%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 35;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      148 CCTTCTCCTTCTGCC 162
Db      15  CCTGCTCCTTCTGCC 1

RESULT 49
US-09-358-972-204/C
; Sequence 204, Application US/09358972
; Patent No. 6235480
; GENERAL INFORMATION:
; APPLICANT: Shultz, John W
; APPLICANT: Lewis, Martin K.
; APPLICANT: Lieppe, Donna
; APPLICANT: Mandrekar, Michelle
; APPLICANT: Kephardt, Daniel
; APPLICANT: Rhodes, Richard B.
; APPLICANT: Andrews, Christine A.
; APPLICANT: Hartnett, James R.
; APPLICANT: Gu, Trent
; APPLICANT: Olson, Ryan J.
; APPLICANT: Wood, Keith W.
; APPLICANT: Welch, Roy
; TITLE OF INVENTION: Nucleic Acid Detection
; FILE REFERENCE: Pro-103 6868/75528
```

```

; CURRENT APPLICATION NUMBER: US/09/358,972
; CURRENT FILING DATE: 1999-07-22
; EARLIER APPLICATION NUMBER: 09/252,436
; EARLIER FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: 09/042,287
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 204
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CAH reverse
; US-09-358-972-204

Query Match      5.7%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 33;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      51 TTGGTGATGAGTGAG 65
Db      17  TTGGGATGAGTGAG 3

RESULT 50
US-09-406-064-70/C
; Sequence 70, Application US/09406064
; Patent No. 6270973
; GENERAL INFORMATION:
; APPLICANT: Shultz, John W
; APPLICANT: Lewis, Martin K.
; APPLICANT: Leippe, Donna
; APPLICANT: Mandrekar, Michelle
; APPLICANT: Kephardt, Daniel
; APPLICANT: Rhodes, Richard B.
; APPLICANT: Andrews, Christine A.
; APPLICANT: Hartnett, James R.
; APPLICANT: Gu, Trent
; APPLICANT: Wood, Keith W.
; APPLICANT: Welch, Roy
; TITLE OF INVENTION: MULTIPLEX METHOD FOR NUCLEIC ACID DETECTION
; FILE REFERENCE: PRO-107.0 (6868/75532)
; CURRENT APPLICATION NUMBER: US/09/406,064
; CURRENT FILING DATE: 1999-09-27
; EARLIER APPLICATION NUMBER: 09/358,972
; EARLIER FILING DATE: 1999-07-21
; EARLIER APPLICATION NUMBER: 09/252,436
; EARLIER FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: 09/042,287
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 70
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CAH reverse
; US-09-406-064-70

Query Match      5.7%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 33;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      51 TTGGTGATGAGTGAG 65
Db      17  TTGGGATGAGTGAG 3

RESULT 51
```

```
US-09-430-615-40/c
; Sequence 40, Application US/09430615
; Patent No. 627578
; GENERAL INFORMATION:
; APPLICANT: Lewis, Martin K.
; APPLICANT: Leipe, Donna
; APPLICANT: Mandrekas, Michelle
; APPLICANT: Andrews, Christine Ann
; APPLICANT: Hartnett, James Robert
; APPLICANT: Welch, Roy
; APPLICANT: Shultz, John William
; TITLE OF INVENTION: Method for Amplified Nucleic Acid Detection
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/430,615
; CURRENT FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 09/358,972
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 09/252,436
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 09/042,287
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 40
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CAN reverse
US-09-430-615-40

Query Match
Best Local Similarity 5.7%; Score 13.4; DB 1; Length 18;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 51 TTGGTGTAGTGTGAG 65
Db 17 TTGGGATGAGTGTGAG 3

RESULT 52
US-09-406-065-45/c
; Sequence 45, Application US/09406065
; Patent No. 6312902
; GENERAL INFORMATION:
; APPLICANT: Shultz, John W
; APPLICANT: Lewis, Martin K.
; APPLICANT: Leipe, Donna
; APPLICANT: Mandrekas, Michelle
; APPLICANT: Kephart, Daniel
; APPLICANT: Rhodes, Richard B
; APPLICANT: Andrews, Christine A
; APPLICANT: Hartnett, James R
; APPLICANT: Gu, Trent
; APPLICANT: Olson, Ryan J
; APPLICANT: Welch, Roy
; TITLE OF INVENTION: Improved Nucleic Acid Detection
; FILE REFERENCE: Improved Nucleic Acid Detection
; CURRENT APPLICATION NUMBER: US/09/406,065
; CURRENT FILING DATE: 1999-09-27
; EARLIER APPLICATION NUMBER: 09/358,972
; EARLIER FILING DATE: 1999-07-21
; EARLIER APPLICATION NUMBER: 09/252,436
; EARLIER FILING DATE: 1999-02-18
; EARLIER APPLICATION NUMBER: 09/042,287
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 45
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CAN reverse
; OTHER INFORMATION: probe
US-09-406-065-45

Query Match
Best Local Similarity 5.7%; Score 13.4; DB 1; Length 18;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 51 TTGGTGTAGTGTGAG 65
Db 17 TTGGGATGAGTGTGAG 3

RESULT 53
US-09-250-609-48
; Sequence 48, Application US/09250609A
; Patent No. 6458943
; GENERAL INFORMATION:
; APPLICANT: Byrne, Jennifer A.
; TITLE OF INVENTION: Members of the D52 Gene Family
; FILE REFERENCE: 1383.0210002
; CURRENT APPLICATION NUMBER: US/09/250,609A
; CURRENT FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 48
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
US-09-250-609-48

Query Match
Best Local Similarity 5.7%; Score 13.4; DB 1; Length 18;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 51 TTGGTGTAGTGTGAG 65
Db 2 TTGGTGTAGTGTGAG 16

RESULT 54
US-09-250-611-48
; Sequence 48, Application US/09250611
; Patent No. 6528283
; GENERAL INFORMATION:
; APPLICANT: Byrne, Jennifer A.
; APPLICANT: Baaset, Paul
; TITLE OF INVENTION: Members of the D52 Gene Family
; FILE REFERENCE: 1383.0210001
; CURRENT APPLICATION NUMBER: US/09/250,611
; CURRENT FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 48
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
US-09-250-611-48

Query Match
Best Local Similarity 5.7%; Score 13.4; DB 1; Length 18;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 51 TTGGTGTAGTGTGAG 65
Db 2 TTGGTGTAGTGTGAG 16
```

```
RESULT 55
US-09-422-978-11764
; Sequence 11764, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 11764
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: downstream amplification primer 99-889 for SEQ 3899, in complement
US-09-422-978-11764

Query Match          5.7%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 33;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      113 TCCTGCTCCACTCT 127
Db      2 TCCTTCTCCACTCT 16

RESULT 56
US-09-788-847-70/c
; Sequence 70, Application US/09788847
; Patent No. 6653078
; GENERAL INFORMATION:
; APPLICANT: Shultz, John W
; APPLICANT: Lewis, Martin K.
; APPLICANT: Leipe, Donna
; APPLICANT: Mandrekas, Michelle
; APPLICANT: Kephart, Daniel
; APPLICANT: Rhodes, Richard B
; APPLICANT: Andrews, Christine A.
; APPLICANT: Hartnett, James R.
; APPLICANT: Gu, Trent
; APPLICANT: Wood, Keith V.
; APPLICANT: Welch, Roy
; TITLE OF INVENTION: MULTIPLEX METHOD FOR NUCLEIC ACID DETECTION
; FILE REFERENCE: PRO-107.0 (6868/75532)
; CURRENT APPLICATION NUMBER: US/09/788,847
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 09/406,064
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: 09/252,436
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 09/042,287
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 70
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CAH reverse
; OTHER INFORMATION: probe
```

```
US-09-788-847-70

Query Match          5.7%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 33;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      51 TTGGTGATGAGTGG 65
Db      17 TTGGGATGAGTGG 3

RESULT 57
US-09-790-417-204/c
; Sequence 204, Application US/09790417
; Patent No. 6730479
; GENERAL INFORMATION:
; APPLICANT: Shultz, John W
; APPLICANT: Lewis, Martin K.
; APPLICANT: Leipe, Donna
; APPLICANT: Mandrekas, Michelle
; APPLICANT: Kephart, Daniel
; APPLICANT: Rhodes, Richard B.
; APPLICANT: Andrews, Christine A.
; APPLICANT: Hartnett, James R.
; APPLICANT: Gu, Trent
; APPLICANT: Olson, Ryan J.
; APPLICANT: Wood, Keith W.
; APPLICANT: Welch, Roy
; TITLE OF INVENTION: Nucleic Acid Detection
; FILE REFERENCE: PRO-103 6868/75528
; CURRENT APPLICATION NUMBER: US/09/790,417
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 09/358,972
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 09/042,287
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 204
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CAH reverse
; OTHER INFORMATION: probe
US-09-790-417-204

Query Match          5.7%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 33;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      51 TTGGTGATGAGTGG 65
Db      17 TTGGGATGAGTGG 3

RESULT 58
US-09-255-912-14
; Sequence 14, Application US/09255912
; Patent No. 6037142
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowart
; TITLE OF INVENTION: ANTISENSE MODULATION OF SMAD2 EXPRESSION
; FILE REFERENCE: RTS-0044
; CURRENT APPLICATION NUMBER: US/09/255,912
; PRIOR FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 14
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```


OTHER INFORMATION: Antisense Oligonucleotide
US-09-255-912-14

Query Match 5.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 35;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 104 CTCCTCTCTCTCTCTCC 121
Db 1 CTCCTCTCTCTCTCTCC 18

RESULT 59

US-08-413-740A-162
Sequence 162, Application US/08413740A
Patent No. 6171859
GENERAL INFORMATION:
APPLICANT: HERRNSTADT, CORINNA
APPLICANT: PARKER, WILLIAM D.
APPLICANT: DAVIS, ROBERT
APPLICANT: MILLER, SCOTT W.
TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
TITLE OF INVENTION: Animal Models for Diseases Associated with Mitochondrial
NUMBER OF SEQUENCES: 206
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/413, 740A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04063
FILING DATE: 30-MAR-1995
APPLICATION NUMBER: 08/413, 740
FILING DATE: 30-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bonham, David B.
REGISTRATION NUMBER: 34297
REFERENCE/DOCKET NUMBER: 2105/7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-1776
TELEFAX: (202) 429-0796
INFORMATION FOR SEQ ID NO: 162:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-413-740A-162

Query Match 5.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 35;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 106 CTCATCTCTCTCTCTCCA 123
Db 1 CTCCTACTCTCTCTCTCCA 18

RESULT 60

US-08-413-740A-164
Sequence 164, Application US/08413740A
Patent No. 6171859
GENERAL INFORMATION:
APPLICANT: HERRNSTADT, CORINNA
APPLICANT: PARKER, WILLIAM D.
APPLICANT: DAVIS, ROBERT
APPLICANT: MILLER, SCOTT W.
TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
TITLE OF INVENTION: Animal Models for Diseases Associated with Mitochondrial
NUMBER OF SEQUENCES: 206
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/413, 740A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04063
FILING DATE: 30-MAR-1995
APPLICATION NUMBER: 08/413, 740
FILING DATE: 30-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bonham, David B.
REGISTRATION NUMBER: 34297
REFERENCE/DOCKET NUMBER: 2105/7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-1776
TELEFAX: (202) 429-0796
INFORMATION FOR SEQ ID NO: 164:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-413-740A-164

Query Match 5.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 35;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 106 CTCATCTCTCTCTCTCCA 123
Db 1 CTCCTACTCTCTCTCTCCA 18

RESULT 61

US-09-422-978-7274/C
Sequence 7274, Application US/09422978
Patent No. 6537751
GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marla
APPLICANT: Chumakov, Ilya
TITLE OF INVENTION: Biallelic markers for use in constructing a high density...

CURRENT APPLICATION NUMBER: US/09/422,978
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: US 09/298,850
EARLIER FILING DATE: 1999-04-21
EARLIER APPLICATION NUMBER: US 60/109,732
EARLIER FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: US 60/082,614
EARLIER FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 11796
SEQ ID NO 7274
LENGTH: 18
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: primer_bind
LOCATION: 1..18
OTHER INFORMATION: upstream amplification primer 99-3391 for SEQ 3340,
US-09-422-978-7274

Query Match 5.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 35;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 25 CTCATGATGCTTGTG 42
18 CTCATCATGCTGTG 1

RESULT 62
US-09-448-312-162
Sequence 162, Application US/09448312
Patent No. 6867197
GENERAL INFORMATION:
APPLICANT: HERRNSTADT, CORINNA
PARKER, WILLIAM D.
DAVIS, ROBERT
MILLER, SCOTT W.
TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
Animal Models for Diseases Associated with Mitochondrial
Defects
NUMBER OF SEQUENCES: 206
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/448,312
FILING DATE: 23-MAR-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/413,740
FILING DATE: <Unknown>
APPLICATION NUMBER: PCT/US95/04063
FILING DATE: 30-MAR-1995
APPLICATION NUMBER: 08/413,740
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bonham, David B.
REGISTRATION NUMBER: 34297
REFERENCE/DOCKET NUMBER: 2105/7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-1776
TELEFAX: (202) 429-0796
INFORMATION FOR SEQ ID NO: 162:
SEQUENCE CHARACTERISTICS:

LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 162:
US-09-448-312-162

Query Match 5.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 35;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 106 CTCATCTCTGCTGCCA 123
1 CTCCTACTCTGCTGCCA 18

RESULT 63
US-09-448-312-164
Sequence 164, Application US/09448312
Patent No. 6867197
GENERAL INFORMATION:
APPLICANT: HERRNSTADT, CORINNA
PARKER, WILLIAM D.
DAVIS, ROBERT
MILLER, SCOTT W.
TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
Animal Models for Diseases Associated with Mitochondrial
Defects
NUMBER OF SEQUENCES: 206
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/448,312
FILING DATE: 23-MAR-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/413,740
FILING DATE: <Unknown>
APPLICATION NUMBER: PCT/US95/04063
FILING DATE: 30-MAR-1995
APPLICATION NUMBER: 08/413,740
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bonham, David B.
REGISTRATION NUMBER: 34297
REFERENCE/DOCKET NUMBER: 2105/7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-1776
TELEFAX: (202) 429-0796
INFORMATION FOR SEQ ID NO: 164:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 164:
US-09-448-312-164

Query Match 5.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 35;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 106 CTGATTCCTGCTGCCA 123
Db 1 CTCCTACTCCTGCTGCCA 18

RESULT 64
US-09-769-787-365/c
Sequence 365, Application US/09769787
Patent No. 6936252
GENERAL INFORMATION:
APPLICANT: Microbial Techniques Limited
APPLICANT: Gilbert, Christophe FG
APPLICANT: Hansbro, Philip M
TITLE OF INVENTION: Proteins
FILE REFERENCE: PWC/P21129WO
CURRENT APPLICATION NUMBER: US/09/769,787
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: GB 9816337.1
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: US 60/125164
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 388
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 365
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-769-787-365

Query Match 5.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 35;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 CATGGGGCAGATCCCTC 27
Db 18 CATGGTGGCGATCCCGC 1

RESULT 65
PCT-US95-04063-162
Sequence 162, Application PC/TUS9504063
GENERAL INFORMATION:
APPLICANT: HERRNSTADT, CORINNA
APPLICANT: PARKER, WILLIAM D.
APPLICANT: DAVIS, ROBERT W.
APPLICANT: MILLER, SCOTT W.
TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
TITLE OF INVENTION: Animal Models for Diseases Associated with Mitochondrial
TITLE OF INVENTION: Defects
NUMBER OF SEQUENCES: 206
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04063
FILING DATE: 30-MAR-1995
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Bonham, David B.
REGISTRATION NUMBER: 34297
REFERENCE/DOCKET NUMBER: 2105/7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-1776
TELEFAX: (202) 429-0796
INFORMATION FOR SEQ ID NO: 162:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US95-04063-162

Query Match 5.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 35;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 106 CTGATTCCTGCTGCCA 123
Db 1 CTCCTACTCCTGCTGCCA 18

RESULT 66
PCT-US95-04063-164
Sequence 164, Application PC/TUS9504063
GENERAL INFORMATION:
APPLICANT: HERRNSTADT, CORINNA
APPLICANT: PARKER, WILLIAM D.
APPLICANT: DAVIS, ROBERT W.
APPLICANT: MILLER, SCOTT W.
TITLE OF INVENTION: Diagnosis, Therapy and Cellular and
TITLE OF INVENTION: Animal Models for Diseases Associated with Mitochondrial
TITLE OF INVENTION: Defects
NUMBER OF SEQUENCES: 206
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1025 Connecticut Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20036-5405
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04063
FILING DATE: 30-MAR-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Bonham, David B.
REGISTRATION NUMBER: 34297
REFERENCE/DOCKET NUMBER: 2105/7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 429-0796
TELEFAX: (202) 429-1776
INFORMATION FOR SEQ ID NO: 164:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US95-04063-164

Query Match 5.6%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 35;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 106 CTCCTCTCTCTGCTCCCA 123
Db 1 CTCCTACTCTGCTCGCA 18

RESULT 67

US-08-311-760A-343
; Sequence 343, Application US/08311760A
; Patent No. 5599706
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: McSwigen, James
; APPLICANT: Newton, Roger S.
; APPLICANT: Ramharack, Randy
; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF
; TITLE OF INVENTION: PLASMA LIPOPROTEIN (a) [LP(a)] BY
; TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN
; NUMBER OF SEQUENCES: 392
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: California
; ZIP: 90071

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,760A
; FILING DATE: September 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wardburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 343:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-311-760A-343

Query Match 5.4%; Score 12.8; DB 1; Length 16;
Best Local Similarity 62.5%; Pred. No. 46;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 41 TGCCATCCCTTGCTG 56
Db 1 UGCACAGCCCTUGGUG 16

RESULT 68
US-08-311-760A-385
; Sequence 385, Application US/08311760A
; Patent No. 5599706

; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: McSwigen, James
; APPLICANT: Newton, Roger S.
; APPLICANT: Ramharack, Randy
; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF
; TITLE OF INVENTION: PLASMA LIPOPROTEIN (a) [LP(a)] BY
; TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN
; NUMBER OF SEQUENCES: 392
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: California
; ZIP: 90071

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,760A
; FILING DATE: September 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wardburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 385:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-311-760A-385

Query Match 5.4%; Score 12.8; DB 1; Length 16;
Best Local Similarity 62.5%; Pred. No. 46;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 41 TGCCATCCCTTGCTG 56
Db 1 UGCACAGCCCTUGGUG 16

RESULT 69
US-08-486-421-24/C
; Sequence 24, Application US/08486421
; Patent No. 5672479
; GENERAL INFORMATION:
; APPLICANT: Johnson, Edward M.
; APPLICANT: Bergemann, Andrew D.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,421
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470,911
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 6923-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-486-421-24

Query Match 5.4%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 46;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 147 CCCTTCCTCTGCGC 162
DB 16 CCCTTCCTCTGCGC 1

RESULT 70
US-08-470-911-24/C
Sequence 24, Application US/08470911
Patent No. 5756684
GENERAL INFORMATION:
APPLICANT: Johnson, Edward M.
APPLICANT: Bergemann, Andrew D.
TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,911
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 6923-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-470-911-24

Query Match 5.4%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 46;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 147 CCCTTCCTCTGCGC 162
DB 16 CCCTTCCTCTGCGC 1

RESULT 71
US-08-173-489C-168
Sequence 168, Application US/08173489C
Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: MANG, C. -G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10021.

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44MB storage
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: U9518-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (attorney) (212) 708-1880
TELEFAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 168:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 bases
TYPE: nucleic acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: third strand derived from Hepatitis B
DESCRIPTION: isolate ayy sequence region in Seq ID No. 5861244167
HYPOHETICAL: yes
ANTI-SENSE: no
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 168 :FROM 1 TO 16
US-08-173-489C-168

Query Match 5.4%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 46;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 144 TCCCTTCCTCTGCT 159
DB 1 TCCTGCTTCCTCTCT 16

```
RESULT 72
US-08-486-809-24/C
; Sequence 24, Application US/08486809
; Patent No. 5869622
; GENERAL INFORMATION:
; APPLICANT: Johnson, Edward M.
; APPLICANT: Bergemann, Andrew D.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,809
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470,911
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Cornuzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 6923-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; US-08-486-809-24

Query Match          5.4%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 46;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      147 CCCTTCCTCTGCGC 162
Db      16 CCCTTCCTCTGCGC 1

RESULT 73
US-08-774-310-343
; Sequence 343, Application US/08774310
; Patent No. 5877022
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: McSwiggen, James
; APPLICANT: Newton, Roger S.
; APPLICANT: Ramharack, Randy
; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF
; TITLE OF INVENTION: PLASMA LIPOPROTEIN (a) [LP(a)] BY
; TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN
; NUMBER OF SEQUENCES: 392
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
```

```
STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/774,310
; FILING DATE: December 23, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/311,760
; FILING DATE: September 23, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 223/229
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 343:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-774-310-343

Query Match          5.4%; Score 12.8; DB 1; Length 16;
Best Local Similarity 62.5%; Pred. No. 46;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      41 TGCATCCCTTGCGTG 56
Db      1 UGCAGCCCTTGCGTG 16

RESULT 74
US-08-774-310-385
; Sequence 385, Application US/08774310
; Patent No. 5877022
; GENERAL INFORMATION:
; APPLICANT: Stinchcomb, Daniel T.
; APPLICANT: McSwiggen, James
; APPLICANT: Newton, Roger S.
; APPLICANT: Ramharack, Randy
; TITLE OF INVENTION: RIBOZYME TREATMENT OF DISEASES
; TITLE OF INVENTION: OR CONDITIONS RELATED TO LEVELS OF
; TITLE OF INVENTION: PLASMA LIPOPROTEIN (a) [LP(a)] BY
; TITLE OF INVENTION: INHIBITING APOLIPOPROTEIN
; NUMBER OF SEQUENCES: 392
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/08/774,310
FILING DATE: December 23, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/311,760
FILING DATE: September 23, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 223/229
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 385:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-774-310-385

Query Match 5.4%; Score 12.8; DB 1; Length 16;
Best Local Similarity 62.5%; Pred. No. 46;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 41 TGCATCCCTTG 56
1 UGCGACCCCUUG 16

RESULT 75

US-08-290-978A-9
Sequence 9, Application US/08290978A
Patent No. 5624834

GENERAL INFORMATION:

APPLICANT: KUSTERS-VAN SOMEREN, MARGO A.

APPLICANT: MULDER, YVONNE

APPLICANT: KESTER, HERMANUS C.M.

APPLICANT: VISSER, JACOB

APPLICANT: VAN COYEN, ALBERT J.J.

APPLICANT: ROLIN, CLAUDE

TITLE OF INVENTION: CLONING AND EXPRESSION OF THE

TITLE OF INVENTION: EXO-POLYGALACTURONASE GENE FROM ASPERGILLUS

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 2000 Pennsylvania Avenue N.W.

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20006-1812

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/290,978A

FILING DATE: 17-OCT-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MURASHIGE, KATE H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 4615-0044.00

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-0763

TELEFAX: 90-4030

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHEetical: NO
ANTI-SENSE: YES
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: p9ax NcoI antisense
US-08-290-978A-9

Query Match 5.4%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 43;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 39 AGTGCATCCCTTG 54
1 AGTGCATCCATGG 16

RESULT 76
US-08-373-124A-176
Sequence 176, Application US/08373124A
Patent No. 5646042

GENERAL INFORMATION:

APPLICANT: Stinchcomb, Dan T.

APPLICANT: Draper, Kenneth

APPLICANT: McSwiggen, James

APPLICANT: Jarvis, Thale

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR

TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND

NUMBER OF SEQUENCES: 2627

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/373,124A

FILING DATE: January 13, 1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/245,466

FILING DATE: May 18, 1994

APPLICATION NUMBER: 08/192,943

FILING DATE: February 7, 1994

APPLICATION NUMBER: 07/987,132

FILING DATE: December 7, 1992

APPLICATION NUMBER: 07/936,422

FILING DATE: August 26, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 209/035

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 176:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

Query Match 5.4%; Score 12.8; DB 1; Length 17;

Best Local Similarity 50.0%; Pred. No. 43;
Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 144 TCCCTCTCTCTCT 159
Db 2 UCCUCCUCCUCCUCCU 17

RESULT 77

US-08-373-124A-182
Sequence 182, Application US/08373124A
Patent No. 5646042
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwigen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 182:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-373-124A-182

Query Match 5.4%; Score 12.8; DB 1; Length 17;
Best Local Similarity 50.0%; Pred. No. 43;
Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 144 TCCCTCTCTCTCT 159
Db 1 UCCUCCUCCUCCUCCU 16

RESULT 78

US-08-373-124A-184
Sequence 184, Application US/08373124A
Patent No. 5646042

GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwigen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TREATMENT OF RESTENOSIS AND
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373,124A
FILING DATE: January 13, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 184:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-373-124A-184

Query Match 5.4%; Score 12.8; DB 1; Length 17;
Best Local Similarity 50.0%; Pred. No. 43;
Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 106 CTCATCTCTCTCTCC 121
Db 1 CUCCUCCUCCUCCUCC 16

RESULT 79

US-08-435-628-176
Sequence 176, Application US/08435628
Patent No. 5817796

GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwigen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR

```
? TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
? TITLE OF INVENTION: CANCER USING RIBOZYMES
? NUMBER OF SEQUENCES: 2627
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Lyon & Lyon
? STREET: 633 West Fifth Street
? CITY: Los Angeles
? STATE: California
? COUNTRY: U.S.A.
? ZIP: 90071
? COMPUTER READABLE FORM:
? MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
? MEDIUM TYPE: storage
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: IBM P.C. DOS 5.0
? SOFTWARE: Word Perfect 5.1
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/435,628
? FILING DATE: 05-MAY-1995
? CLASSIFICATION: 514
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/373,124
? FILING DATE: January 13, 1995
? APPLICATION NUMBER: 08/245,466
? FILING DATE: May 18, 1994
? APPLICATION NUMBER: 08/192,943
? FILING DATE: February 7, 1994
? APPLICATION NUMBER: 07/987,132
? FILING DATE: December 7, 1992
? APPLICATION NUMBER: 07/936,422
? FILING DATE: August 26, 1992
? ATTORNEY/AGENT INFORMATION:
? NAME: Warburg, Richard
? REGISTRATION NUMBER: 32,327
? REFERENCE/DOCKET NUMBER: 209/035
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (213) 489-1600
? TELEFAX: (213) 955-0440
? TELEX: 67-3510
? INFORMATION FOR SEQ ID NO: 176:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 17 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
?
US-08-435-628-176
?
Query Match 5.4%; Score 12.8; DB 1; Length 17;
Best Local Similarity 50.0%; Pred. No. 43;
Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 144 TCCCCCTTCCTCTCT 159
Db 2 UCCUCCUCCUCCUCCU 17

RESULT 80
US-08-435-628-182
? Sequence 182, Application US/08435628
? Patent No. 5817796
? GENERAL INFORMATION:
? APPLICANT: Stinchcomb, Dan T.
? APPLICANT: Draper, Kenneth
? APPLICANT: McSwigen, James
? APPLICANT: Jarvis, Thale
? TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
? TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
? TITLE OF INVENTION: CANCER USING RIBOZYMES
? NUMBER OF SEQUENCES: 2627
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Lyon & Lyon
? STREET: 633 West Fifth Street
```

```
? STREET: Suite 4700
? CITY: Los Angeles
? STATE: California
? COUNTRY: U.S.A.
? ZIP: 90071
? COMPUTER READABLE FORM:
? MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
? MEDIUM TYPE: storage
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: IBM P.C. DOS 5.0
? SOFTWARE: Word Perfect 5.1
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/435,628
? FILING DATE: 05-MAY-1995
? CLASSIFICATION: 514
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/373,124
? FILING DATE: January 13, 1995
? APPLICATION NUMBER: 08/245,466
? FILING DATE: May 18, 1994
? APPLICATION NUMBER: 08/192,943
? FILING DATE: February 7, 1994
? APPLICATION NUMBER: 07/987,132
? FILING DATE: December 7, 1992
? APPLICATION NUMBER: 07/936,422
? FILING DATE: August 26, 1992
? ATTORNEY/AGENT INFORMATION:
? NAME: Warburg, Richard
? REGISTRATION NUMBER: 32,327
? REFERENCE/DOCKET NUMBER: 209/035
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (213) 489-1600
? TELEFAX: (213) 955-0440
? TELEX: 67-3510
? INFORMATION FOR SEQ ID NO: 182:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 17 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
?
US-08-435-628-182
?
Query Match 5.4%; Score 12.8; DB 1; Length 17;
Best Local Similarity 50.0%; Pred. No. 43;
Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 144 TCCCCCTTCCTCTCT 159
Db 1 UCCUCCUCCUCCUCCU 16

RESULT 81
US-08-435-628-184
? Sequence 184, Application US/08435628
? Patent No. 5817796
? GENERAL INFORMATION:
? APPLICANT: Stinchcomb, Dan T.
? APPLICANT: Draper, Kenneth
? APPLICANT: McSwigen, James
? APPLICANT: Jarvis, Thale
? TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
? TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
? TITLE OF INVENTION: CANCER USING RIBOZYMES
? NUMBER OF SEQUENCES: 2627
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Lyon & Lyon
? STREET: 633 West Fifth Street
? CITY: Los Angeles
? STATE: California
? COUNTRY: U.S.A.
? ZIP: 90071
? COMPUTER READABLE FORM:
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; FILING DATE: 24-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/290,978
; FILING DATE: 17-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 4615-0044.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ANTI-SENSE: YES
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: pgax NcoI antisense
US-08-780-869-9

Query Match 5.4%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 43;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY 39 AGTGCATCCCTTGG 54
|||
Db 1 AGTGCATCTCATGG 16

RESULT 83
US-09-827-998-466/c
; Sequence 466, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MhMOF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acemica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 466
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-466

Query Match 5.4%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 43;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 145 CCCCCTCTCTCTG 160
|||||
Db 17 CCCCCTCTCTCTCAG 2

RESULT 84
US-09-827-998-467/c
; Sequence 467, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:

```

```
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: EPHMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 467
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-467
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```
Query Match          5.4%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 43;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY      145 CCCCCTTCTCTCTG 160
          |||||
Db       16 CCCCCTTCTCTCAG 1
```

RESULT 85

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US-09-866-108A-200/c
; Sequence 200, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 200
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-200
```

```
Query Match          5.4%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 43;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY      109 ATTCTCTGCTCCAC 124
          |||||
Db       17 AATCTCTGCTCCAC 2
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RESULT 86

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US-09-866-108A-201/c
; Sequence 201, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 201
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-201
```

```
Query Match          5.4%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 43;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY      109 ATTCTCTGCTCCAC 124
          |||||
Db       16 AATCTCTGCTCCAC 1
```

```
RESULT 87
US-09-866-108A-2940/c
; Sequence 2940, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
```

```
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
FILE REFERENCE: AECOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aecomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 2940
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108A-2940

Query Match      5.4%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 43;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      55 TGATGAGTGGTTCAC 70
Db      17 TGATGAGTGGACCCAC 2

RESULT 88
US-09-866-108A-2941/c
Sequence 2941. Application US/09866108A
Patent No. 6686188
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
FILE REFERENCE: AECOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aecomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 10395
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
```

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PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aecomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 2941
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-108A-2941

Query Match      5.4%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 43;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      55 TGATGAGTGGTTCAC 70
Db      16 TGATGAGTGGACCCAC 1

RESULT 89
US-09-866-108A-10395
Sequence 10395. Application US/09866108A
Patent No. 6686188
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
APPLICANT: JI, Yonggang
APPLICANT: PENN, Sharon G.
APPLICANT: HANZEL, David K.
APPLICANT: RANK, David R.
APPLICANT: CHEN, Wensheng
APPLICANT: SHANNON, Mark
FILE REFERENCE: AECOMICA-7
CURRENT APPLICATION NUMBER: US/09/866,108A
CURRENT FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 15755
SOFTWARE: Aecomica Sequence Listing Engine
Patent No. 6686188
SEQ ID NO 10395
LENGTH: 17
TYPE: DNA
ORGANISM: Homo sapiens
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CURRENT APPLICATION NUMBER: US/10/156,306B
CURRENT FILING DATE: 2002-05-28
NUMBER OF SEQ ID NOS: 8014
SOFTWARE: Patentin version 3.0
SEQ ID NO 3650
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-10-156-306B-3650

Query Match 5.4%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 43;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 142 GCTCCCTTCCTCCT 157
Db 16 GCTCCGCTTCCTCCT 1

RESULT 94
US-08-684-672-27/c
Sequence 27, Application US/08684672
Patent No. 5700926
GENERAL INFORMATION:
APPLICANT: KERE, Juha
APPLICANT: SCHLESSINGER, David
APPLICANT: de la CHAPELLE, Albert
APPLICANT: SRIVASTAVA, Anand Kumar
TITLE OF INVENTION: MOLECULAR CLONING OF THE ANHIDROTIC
TITLE OF INVENTION: ECTODERMAL DYSPLASIA GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 2213-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/684,672
FILING DATE: 22-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/052,997
FILING DATE: 27-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: O'Shaughnessy, Brian P.
REGISTRATION NUMBER: 32,747
REFERENCE/DOCKET NUMBER: 030956-002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-684-672-27

Query Match 5.4%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 41;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 93 AGCTGGCCCTCTCTC 108
Db 18 AGCTGGCTCTCTCGC 3

RESULT 95
US-08-811-028-26/c
Sequence 26, Application US/08811028C
Patent No. 5691671
GENERAL INFORMATION:
APPLICANT: SUZUKI, Yuji
APPLICANT: MASUDA, Koji
APPLICANT: MASUDA, Toyofumi
TITLE OF INVENTION: METHOD FOR CLEAVING CHIMERIC ENZYME USING PROCESSING
TITLE OF INVENTION: ENZYME
FILE REFERENCE: 001560-234
CURRENT APPLICATION NUMBER: US/08/811,028C
CURRENT FILING DATE: 1987-03-04
EARLIER APPLICATION NUMBER: JP 8-70906
EARLIER FILING DATE: 1996-03-04
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 26
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: primer S12
US-08-811-028-26

Query Match 5.4%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 41;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 208 CCAGCTCTCTCTCT 223
Db 17 CCAGCTCTCTCTCT 2

RESULT 96
US-09-161-244-51
Sequence 51, Application US/09161244
Patent No. 6004814
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
APPLICANT: Coweatt, Lex M.
TITLE OF INVENTION: ANTISENSE MODULATION OF CD71 EXPRESSION
FILE REFERENCE: RTS-0007
CURRENT APPLICATION NUMBER: US/09/161,244
CURRENT FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 91
SEQ ID NO 51
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-161-244-51

Query Match 5.4%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 41;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 19 AGATCCCTCATGATG 34
Db 1 AGATCCCTCACAAATG 16

RESULT 97
US-09-091-219-19
Sequence 19, Application US/09091219
Patent No. 6171592
GENERAL INFORMATION:
APPLICANT: STUDEBERT, Michael J.
APPLICANT: CRABB, Brendan S.
APPLICANT: FENG, Li


```
; TITLE OF INVENTION: EQUINE RHINOVIRUS 1 PROTEINS
; FILE REFERENCE: 040268/0151
; CURRENT APPLICATION NUMBER: US/09/091.219
; CURRENT FILING DATE: 1998-10-05
; EARLIER APPLICATION NUMBER: PCT/AU96/00815
; EARLIER FILING DATE: 1996-12-18
; EARLIER APPLICATION NUMBER: AU PN7201
; EARLIER FILING DATE: 1995-12-18
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 18
; TYPE: DNA
; ORGANISM: equine rhinovirus 1
US-09-091-219-19
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```
Query Match          5.4%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 41;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY      131 ATGAGACCTGCTCC 146
Db       3 AAGAGACCTGCTTC 18
```

```
RESULT 98
US-09-071-433-67/c
; Sequence 67, Application US/09071433A
; Patent No. 6197584
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Cowsett, Lex M
; TITLE OF INVENTION: Antisense Modulation of CD40 Expression
; FILE REFERENCE: RTS-0002
; CURRENT APPLICATION NUMBER: US/09/071.433A
; CURRENT FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-071-433-67
```

```
Query Match          5.4%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 41;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      44 CATCCCTTGCTGATG 59
Db       18 CATCTCTTGCTGCTG 3
```

```
RESULT 99
US-09-920-760-61
; Sequence 61, Application US/09920760
; Patent No. 6492173
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF CYCLIN D2 EXPRESSION
; FILE REFERENCE: RTS-0275
; CURRENT APPLICATION NUMBER: US/09/920.760
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 61
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-920-760-61
```

```
Query Match          5.4%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 41;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      115 CTGCTCCACCTCTTGC 130
Db       3 CTGCTCCACACTTCC 18
```

```
RESULT 100
US-09-660-541-19
; Sequence 19, Application US/09660541
; Patent No. 6531136
; GENERAL INFORMATION:
; APPLICANT: STUDEBERT, Michael J.
; APPLICANT: CRABB, Brendan S.
; APPLICANT: FENG, Li
; TITLE OF INVENTION: EQUINE RHINOVIRUS 1 PROTEINS
; FILE REFERENCE: 040268/0151
; CURRENT APPLICATION NUMBER: US/09/660.541
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/091.219
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: AU PN7201
; PRIOR FILING DATE: EARLIER FILING DATE: 1995-12-18
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 18
; TYPE: DNA
; ORGANISM: equine rhinovirus 1
US-09-660-541-19
```

```
Query Match          5.4%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 41;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      131 ATGAGACCTGCTCC 146
Db       3 AAGAGACCTGCTTC 18
```

```
Search completed: October 2, 2006, 15:37:36
Job time : 0.001 secs
```



```
XX AAV33949;
AC 15-FEB-1999 (first entry)
XX
XX Gibbon interleukin-3 forward primer.
XX
XX Fanconi anaemia complementation group C; FAC; apoptosis; haematopoiesis;
XX bone marrow; chemotherapy; gene therapy; interleukin-3; gibbon;
XX Hls-ILFAC; PCR; primer; ss.
XX
XX Synthetic.
XX Hylobates lar.
XX
XX MO9851792-A1.
XX
XX 19-NOV-1998.
XX
XX 15-MAY-1998; 98WO-US009975.
XX
XX 15-MAY-1997; 97US-0046546P.
XX
XX (BGHM ) BRIGHAM & WOMENS HOSPITAL.
XX
XX Youseoufian H;
XX
XX WPI; 1999-009774/01.
XX
XX New conjugate of Fanconi anaemia molecule and peptide selective for
XX haematopoietic precursor cells - Inhibits apoptosis of these cells, for
XX treating Fanconi anaemia and patients undergoing high-dose chemotherapy
XX for cancer.
XX
XX Example 1; Page 27; 72pp; English.
XX
XX This is the nucleotide sequence of a forward primer for the PCR
XX amplification of gibbon interleukin-3 cDNA (see AAV33946) minus the
XX signal sequence. It includes a 5' BamHI site. The primer was used with a
XX reverse primer (see AAV33950) to amplify the gibbon IL3 mature coding
XX region. The PCR product was utilised in the construction of a prokaryotic
XX expression plasmid encoding a fusion between human Fanconi anaemia
XX complementation group C (FAC) protein (see AAW68546) and gibbon IL3 (see
XX AAW68547). This conjugate, or a nucleic acid encoding it, can be used to
XX deliver FAC to a haematopoietic progenitor cell, specifically to inhibit
XX apoptosis, particularly in patients exposed to high doses of chemotherapy
XX for treatment of non-myeloid cancers, also to treat Fanconi anaemia by
XX complementation of the genetic defect
XX
XX Sequence 27 BP; 7 A; 11 C; 6 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 9.2%; Score 21.8; DB 1; Length 27;
XX Best Local Similarity 92.0%; Pred. No. 6.9;
XX Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 TGTCGGGTCATGGGCGAGATCCC 25
XX 26 TGTCGGGTCATGGGCGAGATCCC 2
XX
XX RESULT 2
XX ACL41022
XX ID ACL41022 standard; RNA; 21 BP.
XX
XX ACL41022;
XX
XX 24-MAR-2005 (first entry)
XX
XX C20orf103 siRNA antisense sequence, SEQ ID 2094.
XX
XX Cyostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss;
XX short interfering RNA; gene silencing.
XX
XX Synthetic.
XX
XX
```

```
XX WO2005001092-A2.
XX
XX 06-JAN-2005.
XX
XX 19-MAY-2004; 2004WO-US015645.
XX
XX 20-MAY-2003; 2003US-0471729P.
XX
XX (AMHP ) WYETH.
XX
XX Be X, Wei L, Slonim DK, Howes SH;
XX
XX WPI; 2005-075568/08.
XX
XX Pharmaceutical composition comprising an agent capable of modulating an
XX expression level or protein activity of a gene, e.g. ABC4, or a T cell
XX activated by the polypeptide or antibody, and a carrier, useful for
XX treating cancer.
XX
XX Claim 3; SEQ ID NO 2094; 113pp; English.
XX
XX The present invention relates to a novel pharmaceutical composition
XX comprising: (a) an agent capable of modulating an expression level or
XX protein activity of a cancer-related transmembrane protein (CRTP) or gene
XX ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and
XX (b) a carrier. The pharmaceutical composition may also comprise a
XX polynucleotide capable of inhibiting or decreasing the expression of the
XX CRTP by RNA interference or an antisense mechanism. The CRTPs of the
XX invention are selected from ABC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
XX FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
XX pharmaceutical composition is useful for treating cancer, e.g. colon
XX cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
XX cancer, stomach cancer, and esophageal cancer. The present sequence is a
XX CRTP short interfering RNAs (siRNA) oligonucleotide. Note: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 21 BP; 2 A; 4 C; 3 G; 0 T; 12 U; 0 Other;
XX
XX Query Match 7.5%; Score 17.8; DB 1; Length 21;
XX Best Local Similarity 38.1%; Pred. No. 21;
XX Matches 8; Conservative 11; Mismatches 2; Indels 0; Gaps 0;
XX
XX 150 TTCTCCTTCGCGCATGATTT 170
XX 1 TUCUUGUUCUGCAUGAUUUU 21
XX
XX RESULT 3
XX ACL40867/C
XX ID ACL40867 standard; DNA; 21 BP.
XX
XX ACL40867;
XX
XX 24-MAR-2005 (first entry)
XX
XX C20orf103 target oligonucleotide, SEQ ID 1939.
XX
XX Cyostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss.
XX Homo sapiens.
XX
XX WO2005001092-A2.
XX
XX 06-JAN-2005.
XX
XX 19-MAY-2004; 2004WO-US015645.
XX
XX 20-MAY-2003; 2003US-0471729P.
XX
XX (AMHP ) WYETH.
XX
XX
```

```
XX Be X, Wei L, Slonim DK, Howes SH;
PI WPI: 2005-075568/08.
XX
XX Pharmaceutical composition comprising an agent capable of modulating an
PT expression level or protein activity of a gene, e.g. ABC4, or a T cell
PT activated by the polypeptide or antibody, and a carrier, useful for
PT treating cancer.
XX
XX Claim 3, SEQ ID NO 1939, 113pp; English.
XX
XX The present invention relates to a novel pharmaceutical composition
CC comprising: (a) an agent capable of modulating an expression level or
CC protein activity of a cancer-related transmembrane protein (CRTP) or gene
CC ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and
CC (b) a carrier. The pharmaceutical composition may also comprise a
CC polynucleotide capable of inhibiting or decreasing the expression of the
CC CRTP by RNA interference or an antisense mechanism. The CRTPs of the
CC invention are selected from ABC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
CC FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
CC pharmaceutical composition is useful for treating cancer, e.g. colon
CC cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
CC cancer, stomach cancer, and esophageal cancer. The present sequence is a
CC target oligonucleotide from one such CRTP for which short interfering
CC RNA (siRNA) were produced. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 21 BP; 11 A; 3 C; 5 G; 2 T; 0 U; 0 Other;
SQ
```

```
Query Match 7.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 21;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 149 CTTCTCTTCTGCGCATGATT 169
DB 21 CTTCTTGTCTGCGCATGATT 1
```

```
RESULT 4
ACLA0869 standard; RNA; 21 BP.
XX
XX AC140869;
AC
XX 24-MAR-2005 (first entry)
DT
XX
XX C20orf103 siRNA antisense sequence, SEQ ID 1941.
DE
XX Cytostatic; Gene therapy; Vaccine; RNA interference; cancer; ss;
KW short interfering RNA; gene silencing.
XX
XX Synthetic.
OS
XX WO2005001092-A2.
EN
XX 06-JAN-2005.
PD
XX 19-MAY-2004; 2004WO-US015645.
XX
XX 20-MAY-2003; 2003US-0471729P.
XX
XX (AMHP ) WYETH.
PA
XX Be X, Wei L, Slonim DK, Howes SH;
PI WPI: 2005-075568/08.
DR
XX
XX Pharmaceutical composition comprising an agent capable of modulating an
PT expression level or protein activity of a gene, e.g. ABC4, or a T cell
PT activated by the polypeptide or antibody, and a carrier, useful for
```

```
PT treating cancer.
XX
XX Claim 3, SEQ ID NO 1941, 113pp; English.
XX
XX The present invention relates to a novel pharmaceutical composition
CC comprising: (a) an agent capable of modulating an expression level or
CC protein activity of a cancer-related transmembrane protein (CRTP) or gene
CC ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and
CC (b) a carrier. The pharmaceutical composition may also comprise a
CC polynucleotide capable of inhibiting or decreasing the expression of the
CC CRTP by RNA interference or an antisense mechanism. The CRTPs of the
CC invention are selected from ABC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
CC FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
CC pharmaceutical composition is useful for treating cancer, e.g. colon
CC cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
CC cancer, stomach cancer, and esophageal cancer. The present sequence is a
CC CRTP short interfering RNA (siRNA) oligonucleotide. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 21 BP; 2 A; 5 C; 3 G; 0 T; 11 U; 0 Other;
SQ
```

```
Query Match 7.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity 42.9%; Pred. No. 21;
Matches 9; Conservative 10; Mismatches 2; Indels 0; Gaps 0;
OY 149 CTTCTCTTCTGCGCATGATT 169
DB 1 CUUCUGUGUGUGCAUGAUUU 21
```

```
RESULT 5
AEC02687 standard; DNA; 21 BP.
XX
XX AEC02687;
AC
XX 03-NOV-2005 (first entry)
DT
XX
XX Human IGE short interfering nucleic acid SEQ ID NO 230.
DE
XX
XX anti-allergic; anti-inflammatory; antiasthmatic; dermatological;
KW immunosuppressive; expression; RNA interference; allergy;
KW atopic dermatitis; urticaria; dermatological disease;
KW immediate type hypersensitivity; immunosuppressive; asthma;
KW antiasthmatic; allergic rhinitis; anti-allergic; anti-inflammatory;
KW ear, nose, throat disease; inflammation; respiratory disease;
KW immune disorder; IGE; short interfering nucleic acid; siRNA;
KW gene silencing; ss.
XX
XX Homo sapiens.
OS
XX WO2005080410-A1.
EN
XX 01-SEP-2005.
PD
XX 21-FEB-2005; 2005WO-NZ000021.
XX
XX 20-FEB-2004; 2004US-0546434P.
XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
PA
XX Watson JD, Murison GJ, Grigor MR, Havukkala JU, Munro G;
PI Abernethy N, Webster G;
XX
XX WPI: 2005-591970/60.
DR
XX
XX New composition comprises small interfering nucleic acid molecule (siRNA)
PT capable of reducing expression of a target gene that is active in a IGE-
PT mediated disorder, useful for treating, e.g. allergic rhinitis or atopic
PT dermatitis.
XX
```

PS Disclosure; SEQ ID NO 290; 178bp; English.
XX
CC The invention describes a composition comprising a small interfering
CC nucleic acid molecule (siNA) capable of reducing expression of a target
CC gene that is active in a IGE-mediated disorder, a genetic construct that
CC expresses the siNA, and a binding agent that specifically binds to a
CC target antigen expressed on the surface of the cell. Also described are:
CC a method for the treatment of an IGE-mediated disorder in a patient;
CC prevention of IGE-mediated disorder in a patient; reduction of
CC eosinophilia in a patient; modulating an IGE-mediated immune response to
CC a specific antigen in a patient; and preventing or reducing the severity
CC of an immune response to a specific antigen in a patient. The composition
CC is useful in the preparation of a medicament useful for the treatment of
CC an IGE-mediated disorder, e.g. allergic rhinitis, asthma, anaphylaxis,
CC urticaria, atopic dermatitis, food allergies, diseases that benefit from
CC the reduction of eosinophilia in the tissues of the respiratory system,
CC or disorders having hypersensitivity immune reaction. This sequence
CC represents a siNA for suppresion of human IGE expression.
XX
SQ Sequence 21 BP; 7 A; 3 C; 6 G; 5 T; 0 U; 0 Other;
XX
Query Match 7.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 21;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 60 AGTGAGTTACAGTGAGAGCTG 80
Db 1 AATGAGTTACATGAGAGCTG 21
XX
RESULT 6
AAH37262/c
ID AAH37262 standard; DNA; 19 BP.
AC AAH37262;
DT 14-AUG-2001 (first entry)
XX
DE SNP specific lower PCR primer SEQ ID 58.
XX
KM Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KM SNEB; genotyping; agammaglobulinemia; diabetes insipidus; cancer;
KM Leech-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KM polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KM acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KM inflammation; forensic investigation; paternity analysis; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200129262-A2.
XX
PD 26-APR-2001.
XX
PF 13-OCT-2000; 2000WO-US028436.
XX
PR 15-OCT-1999; 99US-0160096P.
XX
PA (ORCH-) ORCHID BIOSCIENCES INC.
XX
PI Picoult-Newburg L, Pohl M;
XX
DR WPI; 2001-290930/30.
XX
PT New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.
XX
PS Claim 1; Page 50; 83bp; English.
XX
CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNEP) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the

CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNP primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinemia, diabetes insipidus, Leech-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC diseases of which a component is or may be genetic such as autoimmune
CC diseases, including rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a PCR primer specific
CC for a human SNP containing DNA sequence
XX
SQ Sequence 19 BP; 6 A; 2 C; 9 G; 2 T; 0 U; 0 Other;
XX
Query Match 7.4%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 147 CCCTTCCTTCGCGCATG 165
Db 19 CCCTTCCTTCGCGCATG 1
XX
RESULT 7
AEC36449
ID AEC36449 standard; RNA; 19 BP.
AC AEC36449;
DT 03-NOV-2005 (first entry)
XX
DE VEGF/VEGFR2 multifunctional siNA VEGF target complement sequence #3.
XX
KM short interfering nucleic acid; siNA; short interfering RNA; siRNA;
KM gene silencing; RNA interference; transplant rejection;
KM pulmonary disease; respiratory-gen.; respiratory disease; injury;
KM vulneryary; neurodegenerative disease; neuroprotective;
KM neurological disease; cancer; neoplasm; cytostatic; infection;
KM antimicrobial; ocular disease; ophthalmological; cardiovascular disease;
KM cardiovascular-gen.; prion disease; cerebroprotective; degeneration;
KM inflammation; antiinflammatory; renal disease; nephrotropic;
KM endocrine disease; genitourinary disease; liver disease; hepatotropic;
KM gastrointestinal disease; endocrine-gen.; reproduction disorder; ss;
KM VEGF.
XX
OS Unidentified.
XX
PN WO2005078097-A2.
XX
PD 25-AUG-2005.
XX
PF 09-FEB-2005; 2005WO-US004270.
XX
PR 10-FEB-2004; 2004US-0543480P.
XX
PR 24-MAY-2004; 2004WO-US016390.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Jadhav V, Zinnen S;
XX
DR WPI; 2005-571603/58.
XX
PT New multifunctional short interfering nucleic acid (siNA), useful for
PT modulating RNA function and/or gene expression in a cell or for treating
PT or preventing pulmonary diseases, neurodegenerative conditions, cancers,

PT or ocular diseases.
XX
XX Example 7; SEQ ID NO 114; 168pp; English.
CC The specification describes a multifunctional short interfering nucleic
XX acid (siNA). This multifunctional siNA molecule is of two formulae given
CC in the specification. The multifunctional siNA of the invention is useful
CC for modulating RNA function and/or gene expression in a cell. It can be
CC used for down regulating or inhibiting the expression of one or more
CC target nucleic acid molecules. It is also useful for treating diseases or
CC conditions that responds to modulation of gene expression or actively in
CC a cell, tissue, or organism, e.g. organ or tissue transplant, tissue
CC grafting, or treatment of pulmonary disease (restenosis) or preventing
CC neointimal hyperplasia and atherosclerosis in grafts. It can further be
CC used for treating CNS lesions or injury, including treating
CC neurodegenerative conditions (e.g. Alzheimer's disease, Parkinson's
CC disease, epilepsy, dementia, Huntington's disease, or amyotrophic lateral
CC sclerosis), cancers, infectious diseases, ocular diseases, cardiovascular
CC diseases, prion disease, inflammatory diseases, renal diseases, liver
CC diseases, mitochondrial diseases, endocrine diseases, or reproduction
CC related diseases and conditions. AEC36400-AEC36404 represent target
CC sequences from VEGF, for a multifunctional siNA of the invention which
CC targets VEGF and VEGFR2. AEC36447-AEC36451 represent complementary
CC sequences to the target sequences.
XX
SQ Sequence 19 BP; 1 A; 10 C; 2 G; 0 T; 6 U; 0 Other;
Query Match 7.4%; Score 17.4; DB 1; Length 19;
Best Local Similarity 63.2%; Pred. No. 24;
Matches 12; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
OY 147 CCCTTCCTCTGCGCATG 165
Db 1 CCCUCCUCCUCCGCAUG 19
RESULT 8
AEC36402/C
ID AEC36402 standard; RNA; 19 BP.
XX
AC AEC36402;
XX
XX 03-NOV-2005 (first entry)
DE VEGF/VEGFR2 multifunctional siNA VEGF target sequence #3.
XX
XX Short interfering nucleic acid; siNA; short interfering RNA; siRNA;
KM gene silencing; RNA interference; transplant rejection;
KM pulmonary disease; respiratory-gen.; respiratory disease; injury;
KM vulnerrary; neurodegenerative disease; neuroprotective;
KM neurological disease; cancer; neoplasm; cytostatic; infection;
KM antimicrobial; ocular disease; ophthalmological; cardiovascular disease;
KM cardiovascular-gen.; prion disease; cerebroprotective; degeneration;
KM inflammation; antiinflammatory; renal disease; nephrotoxic;
KM endocrine disease; genitourinary disease; liver disease; hepatocytic;
KM gastrointestinal disease; endocrine-gen.; reproduction disorder; se;
KM VEGF.
XX
XX Unidentified.
OS
XX
XX WO2005078097-A2.
PN
XX
XX 25-AUG-2005.
PD
XX
XX 09-FEB-2005; 2005WO-US004270.
PF
XX
XX 10-FEB-2004; 2004US-0543480P.
PR
XX 24-MAY-2004; 2004WO-US016390.
PR
XX (SIRN-) SIRNA THERAPEUTICS INC.
PA
XX
XX Jadhav V, Zinnen S;
PI

DR WPI; 2005-571603/58.
XX
XX New multifunctional short interfering nucleic acid (siNA), useful for
PT modulating RNA function and/or gene expression in a cell or for treating
PT or preventing pulmonary diseases, neurodegenerative conditions, cancers,
PT or ocular diseases.
XX
XX Example 7; SEQ ID NO 56; 168pp; English.
PS
XX The specification describes a multifunctional short interfering nucleic
CC acid (siNA). This multifunctional siNA molecule is of two formulae given
CC in the specification. The multifunctional siNA of the invention is useful
CC for modulating RNA function and/or gene expression in a cell. It can be
CC used for down regulating or inhibiting the expression of one or more
CC target nucleic acid molecules. It is also useful for treating diseases or
CC conditions that responds to modulation of gene expression or actively in
CC a cell, tissue, or organism, e.g. organ or tissue transplant, tissue
CC grafting, or treatment of pulmonary disease (restenosis) or preventing
CC neointimal hyperplasia and atherosclerosis in grafts. It can further be
CC used for treating CNS lesions or injury, including treating
CC neurodegenerative conditions (e.g. Alzheimer's disease, Parkinson's
CC disease, epilepsy, dementia, Huntington's disease, or amyotrophic lateral
CC sclerosis), cancers, infectious diseases, ocular diseases, cardiovascular
CC diseases, prion disease, inflammatory diseases, renal diseases, liver
CC diseases, mitochondrial diseases, endocrine diseases, or reproduction
CC related diseases and conditions. AEC36400-AEC36404 represent target
CC sequences from VEGF, for a multifunctional siNA of the invention which
CC targets VEGF and VEGFR2. AEC36447-AEC36451 represent complementary
CC sequences to the target sequences.
XX
SQ Sequence 19 BP; 6 A; 2 C; 10 G; 0 T; 1 U; 0 Other;
Query Match 7.4%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 24;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 147 CCCTTCCTCTGCGCATG 165
Db 19 CCCUCCUCCUCCGCAUG 1
RESULT 9
AED05616/C
ID AED05616 standard; RNA; 23 BP.
XX
AC AED05616;
XX
XX 01-DEC-2005 (first entry)
DE Short interfering sense sequence targeting human VEGF 121, seqid 81.
XX
XX vascular endothelial growth factor; RNA interference; gene silencing;
XX macular degeneration; ophthalmological; ocular disease;
XX diabetic retinopathy; antiangiogenic; cardiovascular disease; cancer;
XX cytosstatic; neoplasm; asthma; anasthmatic; immune disorder;
KM inflammation; respiratory disease; angiogenesis disorder; antiangiogenic;
KM ss; short interfering RNA; siRNA.
XX
XX Homo sapiens.
OS
XX
XX WO2005089224-A2.
PN
XX
XX 29-SEP-2005.
PD
XX
XX 11-MAR-2005; 2005WO-US008182.
PF
XX
XX 12-MAR-2004; 2004US-0552620P.
PR
XX 05-APR-2004; 2004US-0559824P.
PR
XX 25-JAN-2005; 2005US-0647191P.
PR
XX (ALNY-) ALNYLAM PHARM INC.
PA
XX
XX De Fougerolles A, Frank-Kamenetsky M, Manoharan M, Rajeev KG;
PI

PI Hadwiger P;
 XX WPI; 2005-658984/67.
 XX
 PT New isolated interfering ribonucleic acid (iRNA) agent comprising a sense
 PT sequence and an antisense sequence, useful for treating a human diagnosed
 PT as having or at risk for having adult macular degeneration.
 XX
 PS Claim 1; SEQ ID NO 81; 200pp; English.
 XX
 CC The present invention relates to the use of siRNA targeting vascular
 CC endothelial growth factor (VEGF). Specifically claimed is an isolated
 CC interfering ribonucleic acid (iRNA) agent comprising a sense sequence and
 CC an antisense sequence, where the sense and the antisense sequences form
 CC an RNA duplex. Also claimed are methods of reducing the amount of VEGF
 CC RNA in a cell, using the iRNA agent; making an iRNA agent by the
 CC synthesis of the iRNA agent, where the sense and antisense strands
 CC comprise at least one modification that stabilizes the iRNA agent against
 CC nucleolytic degradation; a pharmaceutical composition comprising the iRNA
 CC agent; inhibiting VEGF expression; and treating a human diagnosed with
 CC adult macular degeneration (AMD), by administering a therapeutically
 CC effective amount of the iRNA agent. The isolated iRNA agent has the sense
 CC sequence that differs by no more than 1, 2, or 3 nucleotides from a SEQ
 CC ID NO: 2-401, not defined in the specification. The iRNA agent further
 CC comprises a non-nucleotide moiety. The iRNA agent further comprises one
 CC or a second 3'-overhang comprising 1-6 nucleotides. The iRNA agent
 CC further comprises a phosphorothioate at the first internucleotide linkage
 CC at the 5' or 3' end of the antisense and sense sequences. The agent
 CC further comprises a 2'-modified nucleotide. The iRNA agent is useful for
 CC treating adult macular degeneration, diabetic retinopathy, cancer, asthma
 CC and angiogenic disorders. The present sequence is short interfering sense
 CC sequence targeting human VEGF 121.
 XX
 SQ Sequence 23 BP; 7 A; 5 C; 10 G; 0 T; 1 U; 0 Other;
 Query Match 7.4%; Score 17.4; DB 1; Length 23;
 Best Local Similarity 94.7%; Pred. No. 22;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 147 CCCTTCCTTCCTTCGCATG 165
 DB 23 CCCTTCCTTCCTTCGCATG 5
 RESULT 10
 AED05619/c
 ID AED05619 standard; RNA; 23 BP.
 XX
 AC AED05619;
 XX
 DT 01-DEC-2005 (first entry)
 XX
 DE Short interfering sense sequence targeting human VEGF 121, seqid 84.
 XX
 KW vascular endothelial growth factor; RNA interference; gene silencing;
 KW macular degeneration; ophthalmological; ocular disease;
 KW diabetic retinopathy; antidiabetic; cardiovascular disease; cancer;
 KW cytosaratic; neoplasm; asthma; antiasthmatic; immune disorder;
 KW inflammation; respiratory disease; angiogenesis disorder; antiangiogenic;
 KW ss; short interfering RNA; siRNA.
 XX
 OS Homo sapiens.
 OS
 PN WO2005089224-A2.
 PD
 PD 29-SEP-2005.
 PF 11-MAR-2005; 2005WO-US008182.
 XX
 XX 12-MAR-2004; 2004US-0552620P.
 PR 05-APR-2004; 2004US-0559824P.
 PR 25-JAN-2005; 2005US-0647191P.
 XX

PA (ALANY-) ALANYAM PHARM INC.
 XX
 XX De Fougereolles A, Frank-Kamenevsky M, Manoharan M, Rajeev KG;
 PI Hadwiger P;
 XX WPI; 2005-658984/67.
 XX
 PT New isolated interfering ribonucleic acid (iRNA) agent comprising a sense
 PT sequence and an antisense sequence, useful for treating a human diagnosed
 PT as having or at risk for having adult macular degeneration.
 XX
 PS Claim 1; SEQ ID NO 84; 200pp; English.
 XX
 CC The present invention relates to the use of siRNA targeting vascular
 CC endothelial growth factor (VEGF). Specifically claimed is an isolated
 CC interfering ribonucleic acid (iRNA) agent comprising a sense sequence and
 CC an antisense sequence, where the sense and the antisense sequences form
 CC an RNA duplex. Also claimed are methods of reducing the amount of VEGF
 CC RNA in a cell, using the iRNA agent; making an iRNA agent by the
 CC synthesis of the iRNA agent, where the sense and antisense strands
 CC comprise at least one modification that stabilizes the iRNA agent against
 CC nucleolytic degradation; a pharmaceutical composition comprising the iRNA
 CC agent; inhibiting VEGF expression; and treating a human diagnosed with
 CC adult macular degeneration (AMD), by administering a therapeutically
 CC effective amount of the iRNA agent. The isolated iRNA agent has the sense
 CC sequence that differs by no more than 1, 2, or 3 nucleotides from a SEQ
 CC ID NO: 2-401, not defined in the specification. The iRNA agent further
 CC comprises a non-nucleotide moiety. The iRNA agent further comprises one
 CC or a second 3'-overhang comprising 1-6 nucleotides. The iRNA agent
 CC further comprises a phosphorothioate at the first internucleotide linkage
 CC at the 5' or 3' end of the antisense and sense sequences. The agent
 CC further comprises a 2'-modified nucleotide. The iRNA agent is useful for
 CC treating adult macular degeneration, diabetic retinopathy, cancer, asthma
 CC and angiogenic disorders. The present sequence is short interfering sense
 CC sequence targeting human VEGF 121.
 XX
 SQ Sequence 23 BP; 7 A; 4 C; 11 G; 0 T; 1 U; 0 Other;
 Query Match 7.4%; Score 17.4; DB 1; Length 23;
 Best Local Similarity 94.7%; Pred. No. 22;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 147 CCCTTCCTTCCTTCGCATG 165
 DB 20 CCCTTCCTTCCTTCGCATG 2
 RESULT 11
 AED05618/c
 ID AED05618 standard; RNA; 23 BP.
 XX
 AC AED05618;
 XX
 DT 01-DEC-2005 (first entry)
 XX
 DE Short interfering sense sequence targeting human VEGF 121, seqid 83.
 XX
 KW vascular endothelial growth factor; RNA interference; gene silencing;
 KW macular degeneration; ophthalmological; ocular disease;
 KW diabetic retinopathy; antidiabetic; cardiovascular disease; cancer;
 KW cytosaratic; neoplasm; asthma; antiasthmatic; immune disorder;
 KW inflammation; respiratory disease; angiogenesis disorder; antiangiogenic;
 KW ss; short interfering RNA; siRNA.
 XX
 OS Homo sapiens.
 OS
 PN WO2005089224-A2.
 PD
 PD 29-SEP-2005.
 PF 11-MAR-2005; 2005WO-US008182.
 PR 12-MAR-2004; 2004US-0552620P.
 XX

PF	11-MAR-2005; 2005WO-US008182.
XX	
PR	12-MAR-2004; 2004US-0552620P.
PR	05-APR-2004; 2004US-0559824P.
PR	25-JAN-2005; 2005US-0647191P.
XX	
PA	(ALNY-) ALNYLAM PHARM INC.
XX	
P1	De Fougereolles A, Frank-Kamenetsky M, Manoharan M, Rajeev KG,
P1	Hadwiger P;
XX	
DR	WPI; 2005-658984/67.
XX	
PT	New isolated interfering ribonucleic acid (iRNA) agent comprising a sense
PT	sequence and an antisense sequence, useful for treating a human diagnosed
PT	as having or at risk for having adult macular degeneration.
XX	
PS	Claim 1; SEQ ID NO 85; 200dp; English.
XX	
CC	The present invention relates to the use of siRNA targeting vascular
CC	endothelial growth factor (VEGF). Specifically claimed is an isolated
CC	interfering ribonucleic acid (iRNA) agent comprising a sense sequence and
CC	an antisense sequence, where the sense and the antisense sequences form
CC	an RNA duplex. Also claimed are methods of reducing the amount of VEGF
CC	RNA in a cell, using the iRNA agent; making an iRNA agent by the
CC	synthesis of the iRNA agent, where the sense and antisense strands
CC	comprise at least one modification that stabilizes the iRNA agent against
CC	nucleolytic degradation; a pharmaceutical composition comprising the iRNA
CC	agent; inhibiting VEGF expression; and treating a human diagnosed with
CC	adult macular degeneration (AMD), by administering a therapeutically
CC	effective amount of the iRNA agent. The isolated iRNA agent has the sense
CC	sequence that differs by no more than 1, 2, or 3 nucleotides from a SEQ
CC	ID NO: 2-401, not defined in the specification. The iRNA agent further
CC	comprises a non-nucleotide moiety. The iRNA agent further comprises one
CC	or a second 3'-overhang comprising 1-6 nucleotides. The iRNA agent
CC	further comprises a phosphorothioate at the first internucleotide linkage
CC	at the 5' or 3' end of the antisense and sense sequences. The agent
CC	further comprises a 2'-modified nucleotide. The iRNA agent is useful for
CC	treating adult macular degeneration, diabetic retinopathy, cancer, asthma
CC	and angiogenic disorders. The present sequence is short interfering sense
CC	sequence targeting human VEGF 121.
XX	
SQ	Sequence 23 BP; 8 A; 3 C; 11 G; 0 T; 1 U; 0 Other;
	Query Match 7.4%; Score 17.4; DB 1; Length 23;
	Best Local Similarity 94.7%; Pred. No. 22;
	Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0
OY	147 CCCTTCCTCTTGCATG 165
Db	19 CCCCTCCTCTTGCATG 1
RESULT 13	
AC	AED05617/c
XX	ID AED05617 standard; RNA; 23 BP.
XX	
AC	AED05617;
XX	
DT	01-DEC-2005 (first entry)
XX	
DE	Short interfering sense sequence targeting human VEGF 121, seqid 82.
XX	
KM	vascular endothelial growth factor; RNA interference; gene silencing;
KM	macular degeneration; ophthalmological; ocular disease;
KM	diabetic retinopathy; cardiovascular disease; cancer;
KM	cytostatic; neoplasia; asthma; antiasthmatic; immune disorder;
KM	inflammation; respiratory disease; angiogenesis disorder; antiangiogenic;
KM	sar; short interfering RNA; siRNA.
XX	
XX	Homo sapiens.
NN	WO2005089224-A2.


```

XX 29-SEP-2005.
PD
XX
PF 11-MAR-2005; 2005MO-US008182.
XX
XX 12-MAR-2004; 2004US-0552620P.
PR 05-APR-2004; 2004US-0559824P.
PR 25-JAN-2005; 2005US-0647191P.
XX
PA (ALNY-) ALNYLAM PHARM INC.
XX
PI De Fougereolles A, Frank-Kamenetsky M, Manoharan M, Rajeev KG;
PI Hadwiger P;
XX
XX WPI; 2005-658984/67.
XX
XX New isolated interfering ribonucleic acid (iRNA) agent comprising a sense
PT sequence and an antisense sequence, useful for treating a human diagnosed
PT as having or at risk for having adult macular degeneration.
XX
PS Claim 1; SEQ ID NO 82; 200pp; English.
XX
XX The present invention relates to the use of siRNA targeting vascular
CC endothelial growth factor (VEGF). Specifically claimed is an isolated
CC interfering ribonucleic acid (iRNA) agent comprising a sense sequence and
CC an antisense sequence, where the sense and the antisense sequences form
CC an RNA duplex. Also claimed are methods of reducing the amount of VEGF
CC RNA in a cell, using the iRNA agent; making an iRNA agent by the
CC synthesis of the iRNA agent, where the sense and antisense strands
CC comprise at least one modification that stabilizes the iRNA agent against
CC nucleolytic degradation; a pharmaceutical composition comprising the iRNA
CC agent; inhibiting VEGF expression; and treating a human diagnosed with
CC adult macular degeneration (AMD), by administering a therapeutically
CC effective amount of the iRNA agent. The isolated iRNA agent has the sense
CC sequence that differs by no more than 1, 2, or 3 nucleotides from a SEQ
CC ID NO: 2-401, not defined in the specification. The iRNA agent further
CC comprises a non-nucleotide moiety. The iRNA agent further comprises one
CC or a second 3'-overhang comprising 1-6 nucleotides. The iRNA agent
CC further comprises a phosphorothioate at the first internucleotide linkage
CC at the 5' or 3' end of the antisense and sense sequences. The agent
CC further comprises a 2'-modified nucleotide. The iRNA agent is useful for
CC treating adult macular degeneration, diabetic retinopathy, cancer, asthma
CC and angiogenic disorders. The present sequence is short interfering sense
CC sequence targeting human VEGF 121.
XX
SQ Sequence 23 BP; 7 A; 5 C; 10 G; 0 T; 1 U; 0 Other;
Query Match 7.4%; Score 17.4; DB 1; Length 23;
Best Local Similarity 94.7%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 147 CCCTTCCTTCCTTCGCGCATG 165
DB 22 CCCTTCCTTCCTTCGCGCATG 4

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XX 21-MAR-2002; 2002MO-US008614.
XX
XX 21-MAR-2001; 2001US-0277705P.
XX
XX (LEUNG) LEUNG D W.
XX
XX Leung DW, Bergman PA, Lofquist A, Pietz GE, Tompkins CK;
PI Maggoner DW;
XX
XX WPI; 2003-058367/05.
XX
XX Producing monodispersed preparation of polyanionic polymer for therapy,
PT by expressing vector comprising ligation product of oligonucleotides
PT encoding glutamate/aspartate residues in host cell and isolating the
PT product.
XX
PS Disclosure; Fig 5; 74pp; English.
XX
XX The present invention describes a method (M) for producing a
CC monodispersed preparation of a polyanionic polymer (PP) larger than 10
CC kD. (M) involves inserting into an expression vector (EV) a ligation
CC product formed by ligating together oligonucleotides that encode
CC glutamate/aspartate residues, expressing EV in a host cell, and isolating
CC the protein product (P) of EV, where (P) is PP and at least 80% of PP is
CC approximately of the same molecular weight. Also described: (1) a
CC recombinant fusion protein (I) comprising a polyanionic polypeptide and
CC another polypeptide at either one end or at both ends of it; (2) a
CC polyanionic polymer (II) conjugate comprising a polyanionic polymer and
CC leukine, where the polyanionic polymer is polyglutamic acid or
CC polyaspartic acid; (3) a vector (III) comprising a cassette which
CC comprises a nucleotide sequence encoding a polyanionic polymer and at
CC least one other nucleotide sequence, where the polyanionic polymer is
CC polyglutamic acid or polyaspartic acid; (4) production of (I); (5) a cell
CC (IV) comprising (III) or a vector that comprises a nucleotide sequence
CC that encodes a polyanionic polymer that is larger than 10 kDa; and (6) a
CC recombinantly-produced polyanionic polymer (V) that is of any molecular
CC weight or is larger than 10 kD, and is conjugated to another protein. (I)
CC is useful for treating a disease or ailment in an individual by
CC administering (I) to the individual. (I) is also useful for delivering an
CC effective amount of a pharmaceutically active agent, a therapeutic
CC protein or a drug to a patient in need of it, or for diagnostic and
CC testing or research purposes. AB22045 to AB22211 and ABP6374 to
CC ABP6400 represent sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 24 BP; 0 A; 13 C; 0 G; 11 T; 0 U; 0 Other;
Query Match 7.3%; Score 17.2; DB 1; Length 24;
Best Local Similarity 86.4%; Pred. No. 23;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 140 CTGCTCCCTTCCTTCCTTCGCGC 161
DB 1 CTGCTCCCTTCCTTCCTTCGCGC 22

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RESULT 14
AB222095
ID AB222095 standard; DNA, 24 BP.
XX
AC AB222095;
XX
DT 11-MAR-2003 (first entry)
XX
DE Polyanionic polymer related oligonucleotide #49.
XX
XX Polyanionic polymer; bioactivity; water solubility; ss.
XX
OS Synthetic.
XX
PN W0200277036-A2.
XX
PD 03-OCT-2002.

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RESULT 15
AD051553
ID AD051553 standard; DNA, 20 BP.
XX
AC AD051553;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human serine/threonine kinase 16 antisense oligo. ISIS 220645.
XX
XX Serine/threonine kinase 16; PKL12;
XX transforming growth factor-beta-stimulated factor 1; TSP1;
XX myristylated and palmitylated serine/threonine kinase; MPK;
XX hyperproliferative disorder; gene therapy; human; antisense;
XX phosphorothioate backbone; ss.
XX

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OS Homo sapiens.
OS Synthetic.
FH Key
FT modified_base
FT 1..20
FT /tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone in which all cytidine
FT residues are 5-methylcytidines"
FT modified_base
FT 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) bases"
FT modified_base
FT 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) bases"
PN US2004097444-A1.
XX 20-MAY-2004.
XX 16-NOV-2002; 2002US-00298953.
XX 16-NOV-2002; 2002US-00298953.
XX (ISIS-) ISIS PHARM INC.
XX Dobie KM;
XX WPI; 2004-389186/36.
XX
XX New compounds, particularly oligonucleotides targeted to a nucleic acid
XX encoding serine/threonine kinase 16, useful for treating diseases
XX associated with serine/threonine kinase 16, e.g. hyperproliferative
XX disorders.
XX
XX Example 15; SEQ ID NO 44; 36pp; English.
XX
XX The invention relates to compounds, compositions and methods for
XX modulating the expression of serine/threonine kinase 16 (also called
XX PK12, transforming growth factor-beta-stimulated factor 1; TSF1 and
XX myristylated and palmitylated serine/threonine kinase; MSPX). The
XX composition comprise antisense oligonucleotides targeted to PK12 gene.
XX The compound, composition and methods are useful for treating a disease
XX or condition associated with serine/threonine kinase 16, such as a
XX hyperproliferative disorder. They are also useful in research and
XX diagnostics for modulating the expression of serine/threonine kinase 16.
XX The invention is also useful in gene therapy. The present sequence is an
XX antisense oligonucleotide targeted to human serine/threonine kinase 16
XX DNA. This sequence is used to illustrate the method of the invention.
XX
XX Sequence 20 BP; 4 A; 9 C; 1 G; 6 T; 0 U; 0 Other;
SQ
Query Match 7.1%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 106 CTCATTCCTCTGCTCCCACT 125
Db 1 CACATTCCTCTGCTCCCAAT 20
RESULT 16
ACL40112/c
ID ACL40112 standard; RNA; 21 BP.
XX
XX ACL40112;
XX
XX 24-MAR-2005 (first entry)
XX
XX ABCC4 siRNA sense sequence, SEQ ID 1184.
XX
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```
KW Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss;
KW short interfering RNA; gene silencing.
XX Synthetic.
XX
XX WO2005001092-A2.
XX
XX 06-JAN-2005.
XX
XX 19-MAY-2004; 2004WO-US015645.
XX
XX 20-MAY-2003; 2003US-0471729P.
XX
XX (AMHP ) WYETH.
XX
XX Be X, Wei L, Slonim DK, Howes SH;
XX
XX WPI; 2005-075568/08.
XX
XX Pharmaceutical composition comprising an agent capable of modulating an
XX expression level or protein activity of a gene, e.g. ABCC4, or a T cell
XX activated by the polypeptide or antibody, and a carrier, useful for
XX treating cancer.
XX
XX Claim 3; SEQ ID NO 1184; 113pp; English.
XX
XX The present invention relates to a novel pharmaceutical composition
XX comprising: (a) an agent capable of modulating an expression level or
XX protein activity of a cancer-related transmembrane protein (CRTP) or gene
XX ; an antibody specific for a CRTP, or a T cell activated by a CRTP, and
XX (b) a carrier. The pharmaceutical composition may also comprise a
XX polynucleotide capable of inhibiting or decreasing the expression of the
XX CRTP by RNA interference or an antisense mechanism. The CRTPs of the
XX invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
XX FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
XX pharmaceutical composition is useful for treating cancer, e.g. colon
XX cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
XX cancer, stomach cancer, and esophageal cancer. The present sequence is a
XX CRTP short interfering RNA (siRNA) oligonucleotide. Note: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 21 BP; 4 A; 4 C; 6 G; 0 T; 7 U; 0 Other;
SQ
Query Match 7.1%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 171 AAGATTCACGAGGACTTCACA 190
Db 20 AAGATTCACGAGGCTTCACA 1
RESULT 17
ACL41020/c
ID ACL41020 standard; DNA; 21 BP.
XX
XX ACL41020;
XX
XX 24-MAR-2005 (first entry)
XX
XX C20orf103 target oligonucleotide, SEQ ID 2092.
XX
XX Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss.
XX
XX Homo sapiens.
XX
XX WO2005001092-A2.
XX
XX 06-JAN-2005.
XX
XX 19-MAY-2004; 2004WO-US015645.
XX
```

```
XX 20-MAY-2003; 2003US-0471729P.
XX (AMHP ) WYETH.
XX Be X, Wei L, Slonim DK, Howes SH;
XX WPI; 2005-075568/08.
XX
XX Pharmaceutical composition comprising an agent capable of modulating an
XX expression level or protein activity of a gene, e.g. ABCC4, or a T cell
XX PT activated by the polypeptide or antibody, and a carrier, useful for
XX treating cancer.
XX
XX Claim 3; SEQ ID NO 2092; 113pp; English.
XX
XX The present invention relates to a novel pharmaceutical composition
XX comprising: (a) an agent capable of modulating an expression level or
XX protein activity of a cancer-related transmembrane protein (CRTP) or gene
XX ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and
XX (b) a carrier. The pharmaceutical composition may also comprise a
XX polynucleotide capable of inhibiting or decreasing the expression of the
XX CRTP by RNA interference or an antisense mechanism. The CRTPs of the
XX invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
XX FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
XX pharmaceutical composition is useful for treating cancer, e.g. colon
XX cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
XX cancer, stomach cancer, and esophageal cancer. The present invention is a
XX target oligonucleotide from one such CRTP for which short interfering
XX RNAs (siRNA) were produced. Note: The sequence data for this patent did
XX not form part of the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 21 BP; 11 A; 4 C; 4 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 7.1%; Score 16.8; DB 1; Length 21;
XX Best Local Similarity 90.0%; Pred. No. 27;
XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 150 TTCTCCTTCGCGCATGATT 169
XX ||||| ||||| ||||| |||||
XX 21 TTCTGTGTCGCGCATGATT 2
XX
XX RESULT 18
XX ACL40781/c
XX ID ACL40781 standard; RNA; 21 BP.
XX
XX ACL40781;
XX
XX 24-MAR-2005 (first entry)
XX
XX ABCC4 siRNA sense sequence, SEQ ID 1853.
XX
XX Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss;
XX KM short interfering RNA; gene silencing.
XX
XX Synthetic.
XX
XX WO2005001092-A2.
XX
XX 06-JAN-2005.
XX
XX 19-MAY-2004; 2004WO-US015645.
XX
XX 20-MAY-2003; 2003US-0471729P.
XX
XX (AMHP ) WYETH.
XX
XX Be X, Wei L, Slonim DK, Howes SH;
XX
XX WPI; 2005-075568/08.
XX
```

```
XX Pharmaceutical composition comprising an agent capable of modulating an
XX expression level or protein activity of a gene, e.g. ABCC4, or a T cell
XX PT activated by the polypeptide or antibody, and a carrier, useful for
XX treating cancer.
XX
XX Claim 3; SEQ ID NO 1853; 113pp; English.
XX
XX The present invention relates to a novel pharmaceutical composition
XX comprising: (a) an agent capable of modulating an expression level or
XX protein activity of a cancer-related transmembrane protein (CRTP) or gene
XX ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and
XX (b) a carrier. The pharmaceutical composition may also comprise a
XX polynucleotide capable of inhibiting or decreasing the expression of the
XX CRTP by RNA interference or an antisense mechanism. The CRTPs of the
XX invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
XX FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
XX pharmaceutical composition is useful for treating cancer, e.g. colon
XX cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
XX cancer, stomach cancer, and esophageal cancer. The present sequence is a
XX CRTP short interfering RNAs (siRNA) oligonucleotide. Note: The sequence
XX data for this patent did not form part of the printed specification, but
XX was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 21 BP; 4 A; 4 C; 6 G; 0 T; 7 U; 0 Other;
XX
XX Query Match 7.1%; Score 16.8; DB 1; Length 21;
XX Best Local Similarity 90.0%; Pred. No. 27;
XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 171 AAGATTCGAGGAGCTTCACA 190
XX ||||| ||||| ||||| |||||
XX 20 AAGATTCGAGGAGCTTCACA 1
XX
XX RESULT 19
XX ACL40870/c
XX ID ACL40870 standard; DNA; 21 BP.
XX
XX ACL40870;
XX
XX 24-MAR-2005 (first entry)
XX
XX C20orf103 target oligonucleotide, SEQ ID 1942.
XX
XX Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss.
XX KM Homo sapiens.
XX
XX WO2005001092-A2.
XX
XX 06-JAN-2005.
XX
XX 19-MAY-2004; 2004WO-US015645.
XX
XX 20-MAY-2003; 2003US-0471729P.
XX
XX (AMHP ) WYETH.
XX
XX Be X, Wei L, Slonim DK, Howes SH;
XX
XX WPI; 2005-075568/08.
XX
XX Pharmaceutical composition comprising an agent capable of modulating an
XX expression level or protein activity of a gene, e.g. ABCC4, or a T cell
XX PT activated by the polypeptide or antibody, and a carrier, useful for
XX treating cancer.
XX
XX Claim 3; SEQ ID NO 1942; 113pp; English.
XX
XX The present invention relates to a novel pharmaceutical composition
XX comprising: (a) an agent capable of modulating an expression level or
```

CC	proteolytic activity of a cancer-related transmembrane protein (CRTP) or gene
CC	; an antibody specific for a CRTP, or a T cell activated by a CRTP; and
CC	(b) a carrier. The pharmaceutical composition may also comprise a
CC	polynucleotide capable of inhibiting or decreasing the expression of the
CC	CRTP by RNA interference from an antisense mechanism. The CRTPs of the
CC	invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CSR, ENPP3,
CC	FLJ11856, GPR84, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
CC	pharmaceutical composition is useful for treating cancer, e.g. colon
CC	cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
CC	cancer, stomach cancer, and esophageal cancer. The present sequence is a
CC	target oligonucleotide from one such CRTP for which short interfering
CC	RNA (siRNA) were produced. Note: The sequence data for this patent did
CC	not form part of the printed specification, but was obtained in
CC	electronic format directly from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences
CC	
SQ	Sequence 21 BP; 10 A; 3 C; 5 G; 3 T; 0 U; 0 Other;
OY	
Db	Query Match 7.1%; Score 16.8; DB 1; Length 21; Best Local Similarity 90.0%; Pred.No.27; Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0 149 CTCTCCTTGTGCCATGATT 168 20 CTCTCTGTTCGCCATGATT 1
RESULT 20	
ID	ACL40872
XX	ACL40872 standard; RNA; 21 BP.
AC	ACLA0872;
DT	24-MAR-2005 (first entry)
DE	C20orf103 siRNA antisense sequence, SEQ ID 1944.
XX	
KM	Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss;
KW	short interfering RNA; gene silencing.
OS	Synthetic.
XX	
PN	WO2005001092-A2.
XX	
PD	06-JAN-2005.
PF	19-MAY-2004; 2004MO-USO15645.
XX	
PR	20-MAY-2003; 2003US-0471729P.
XX	
PA	(AMHP) WYETH.
XX	
PI	Be X, Wei L, Slonim DK, Howes SH;
DR	WPI; 2005-075568/08.
XX	
PT	Pharmaceutical composition comprising an agent capable of modulating an
PT	expression level or protein activity of a gene, e.g. ABCC4, or a T cell
PT	activated by the polypeptide or antibody, and a carrier, useful for
PT	treating cancer.
XX	
PS	Claim 3; SEQ ID NO 1944; 113pp; English.
XX	
CC	The present invention relates to a novel pharmaceutical composition
CC	comprising: (a) an agent capable of modulating an expression level or
CC	protein activity of a cancer-related transmembrane protein (CRTP) or gene
CC	; an antibody specific for a CRTP, or a T cell activated by a CRTP; and
CC	(b) a carrier. The pharmaceutical composition may also comprise a
CC	polynucleotide capable of inhibiting or decreasing the expression of the
CC	CRTP by RNA interference from an antisense mechanism. The CRTPs of the
CC	invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CSR, ENPP3,
CC	FLJ11856, GPR84, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
CC	pharmaceutical composition is useful for treating cancer, e.g. colon
CC	cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
CC	cancer, stomach cancer, and esophageal cancer. The present sequence is a
CC	target oligonucleotide from one such CRTP for which short interfering
CC	RNA (siRNA) were produced. Note: The sequence data for this patent did
CC	not form part of the printed specification, but was obtained in
CC	electronic format directly from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences
CC	
SQ	Sequence 21 BP; 10 A; 3 C; 5 G; 3 T; 0 U; 0 Other;
OY	
Db	Query Match 7.1%; Score 16.8; DB 1; Length 21; Best Local Similarity 90.0%; Pred.No.27; Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0 149 CTCTCCTTGTGCCATGATT 168 20 CTCTCTGTTCGCCATGATT 1

```

CC cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
CC cancer, stomach cancer, and esophageal cancer. The present sequence is a
CC CRP short interfering RNAs (siRNA) oligonucleotide. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 21 BP; 3 A; 5 C; 3 G; 0 T; 10 U; 0 Other;
Gy Query Match 7.1%; Score 16.8; DB 1; Length 21;
Best Local Similarity 45.0%; Pred. No. 27;
Matches 9; Conservative 9; Mismatches 2; Indels 0; Gaps 0;
Db 149 CTCTCCTTCGCCATGATT 168
2 CUCUCUGUUCGCCAUAU 21
RESULT 21
ABLS8878
ID ABLS8878 standard; DNA; 24 BP.
XX
XX ABL58878;
XX
XX 22-JUL-2002 (first entry)
XX
XX Oligonucleotide 1-T.
DE
KW Marker oligonucleotide; microsatellite; single nucleotide polymorphism;
XX SNP; food production; veterinary; medicine; ss.
OS Synthetic.
XX
XX WO200238804-A1.
XX
XX PD 16-MAY-2002.
XX
XX PF 07-NOV-2001; 2001WO-EP012880.
XX
XX PR 08-NOV-2000; 2000DE-01055368.
XX
XX PA (AGRO-) AGROBIOGEN GMBH BIOTECHNOLOGIE.
PL Brem G;
DR WPI; 2002-435855/46.
PT Marking DNA samples for identifying samples during subsequent analysis by
XX adding microsatellite or single nucleotide polymorphism oligonucleotide.
XX Disclosure; Page 6; 25pp; German.
XX
XX The invention relates to marking DNA-containing samples by treatment with
XX a marker oligonucleotide that is either an artificial microsatellite
XX oligonucleotide or an artificial single nucleotide polymorphism (SNP)
XX oligonucleotide for an analysis. The oligonucleotides are useful as internal
XX markers for identifying samples used for e.g. characterising or typing an
XX animal for monitoring food production and in human or veterinary
XX medicine. The present sequence is that of a artificial oligonucleotide
XX used to exemplify the invention
XX
XX Sequence 24 BP; 0 A; 12 C; 1 G; 11 T; 0 U; 0 Other;
Gy Query Match 7.1%; Score 16.8; DB 1; Length 24;
Best Local Similarity 90.0%; Pred. No. 25;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 140 CTGCTCCCCCTTCTCTCT 159
5 CTTCCTCCCTTCTCTCTCT 24

```

AEC36403/c
 ID AEC36403 standard; RNA, 19 BP.
 XX
 AC AEC36403;
 XX
 DT 03-NOV-2005 (first entry)
 XX
 DE VEGF/VEGFR2 multifunctional siNA VEGF target sequence #4.
 XX
 KM short interfering nucleic acid; siNA; short interfering RNA; siRNA;
 KM gene silencing; RNA interference; transplant rejection;
 KM pulmonary disease; respiratory-gen.; respiratory disease; injury;
 KM vulnerability; neurodegenerative disease; neuroprotective;
 KM neurological disease; cancer; neoplasm; cytostatic; infection;
 KM antimicrobial; ocular disease; ophthalmological; cardiovascular disease;
 KM cardiovascular-gen.; prion disease; cerebroprotective; degeneration;
 KM inflammation; antiinflammatory; renal disease; nephrotropic;
 KM endocrine disease; genitourinary disease; liver disease; hepatotropic;
 KM gastrointestinal disease; endocrine-gen.; reproduction disorder; ss;
 KM VEGF.
 XX
 OS Unidentified.
 XX
 PN WO2005078097-A2.
 XX
 PD 25-AUG-2005.
 XX
 PF 09-FEB-2005; 2005MO-US004270.
 XX
 PR 10-FEB-2004; 2004US-0543480P.
 PR 24-MAY-2004; 2004WO-US016390.
 XX
 XX (SIRN-) SIRNA THERAPEUTICS INC.
 PA
 PI Jadhav V, Zimen S;
 PI WPI; 2005-571603/58.
 DR
 XX
 PT New multifunctional short interfering nucleic acid (siNA), useful for
 PT modulating RNA function and/or gene expression in a cell or for treating
 PT or preventing pulmonary diseases, neurodegenerative conditions, cancers,
 PT or ocular diseases.
 PT
 XX
 PS Example 7; SEQ ID NO 57; 168bp; English.
 XX
 CC The specification describes a multifunctional short interfering nucleic
 CC acid (siNA). This multifunctional siNA molecule is of two formulae given
 CC in the specification. The multifunctional siNA of the invention is useful
 CC for modulating RNA function and/or gene expression in a cell. It can be
 CC used for down regulating or inhibiting the expression of one or more
 CC target nucleic acid molecules. It is also useful for treating diseases or
 CC conditions that responds to modulation of gene expression or activity in
 CC a cell, tissue, or organism, e.g. organ or tissue transplant, tissue
 CC grafting, or treatment of pulmonary disease (restenosis) or preventing
 CC neointimal hyperplasia and atherosclerosis in grafts. It can further be
 CC used for treating CNS lesions or injury, including treating
 CC neurodegenerative conditions (e.g. Alzheimer's disease, Parkinson's
 CC disease, epilepsy, dementia, Huntington's disease, or amyotrophic lateral
 CC sclerosis), cancers, infectious diseases, ocular diseases, cardiovascular
 CC diseases, prion disease, inflammatory diseases, renal diseases, liver
 CC diseases, mitochondrial diseases, endocrine diseases, or reproduction
 CC related diseases and conditions. AEC36400-AEC36404 represent target
 CC sequences from VEGF, for a multifunctional siNA of the invention which
 CC targets VEGF and VEGFR2. AEC36447-AEC36451 represent complementary
 CC sequences to the target sequences.
 CC
 XX
 SQ Sequence 19 BP; 6 A; 2 C; 10 G; 0 T; 1 U; 0 Other;
 Query March 6.9%; Score 16.4; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 31;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 147 CCCTTCCTCTTGCAT 164

Db
 18 CCCTTCCTCTTGCAT 1
 |||||
 RESULT 23
 AEC36450
 ID AEC36450 standard; RNA, 19 BP.
 XX
 AC AEC36450;
 XX
 DT 03-NOV-2005 (first entry)
 XX
 DE VEGF/VEGFR2 multifunctional siNA VEGF target complement sequence #4.
 XX
 KM short interfering nucleic acid; siNA; short interfering RNA; siRNA;
 KM gene silencing; RNA interference; transplant rejection;
 KM pulmonary disease; respiratory-gen.; respiratory disease; injury;
 KM vulnerability; neurodegenerative disease; neuroprotective;
 KM neurological disease; cancer; neoplasm; cytostatic; infection;
 KM antimicrobial; ocular disease; ophthalmological; cardiovascular disease;
 KM cardiovascular-gen.; prion disease; cerebroprotective; degeneration;
 KM inflammation; antiinflammatory; renal disease; nephrotropic;
 KM endocrine disease; genitourinary disease; liver disease; hepatotropic;
 KM gastrointestinal disease; endocrine-gen.; reproduction disorder; ss;
 KM VEGF.
 XX
 OS Unidentified.
 XX
 PN WO2005078097-A2.
 XX
 PD 25-AUG-2005.
 XX
 PF 09-FEB-2005; 2005MO-US004270.
 XX
 PR 10-FEB-2004; 2004US-0543480P.
 PR 24-MAY-2004; 2004WO-US016390.
 XX
 XX (SIRN-) SIRNA THERAPEUTICS INC.
 PA
 PI Jadhav V, Zimen S;
 PI WPI; 2005-571603/58.
 DR
 XX
 PT New multifunctional short interfering nucleic acid (siNA), useful for
 PT modulating RNA function and/or gene expression in a cell or for treating
 PT or preventing pulmonary diseases, neurodegenerative conditions, cancers,
 PT or ocular diseases.
 PT
 XX
 PS Example 7; SEQ ID NO 115; 168bp; English.
 XX
 CC The specification describes a multifunctional short interfering nucleic
 CC acid (siNA). This multifunctional siNA molecule is of two formulae given
 CC in the specification. The multifunctional siNA of the invention is useful
 CC for modulating RNA function and/or gene expression in a cell. It can be
 CC used for down regulating or inhibiting the expression of one or more
 CC target nucleic acid molecules. It is also useful for treating diseases or
 CC conditions that responds to modulation of gene expression or activity in
 CC a cell, tissue, or organism, e.g. organ or tissue transplant, tissue
 CC grafting, or treatment of pulmonary disease (restenosis) or preventing
 CC neointimal hyperplasia and atherosclerosis in grafts. It can further be
 CC used for treating CNS lesions or injury, including treating
 CC neurodegenerative conditions (e.g. Alzheimer's disease, Parkinson's
 CC disease, epilepsy, dementia, Huntington's disease, or amyotrophic lateral
 CC sclerosis), cancers, infectious diseases, ocular diseases, cardiovascular
 CC diseases, prion disease, inflammatory diseases, renal diseases, liver
 CC diseases, mitochondrial diseases, endocrine diseases, or reproduction
 CC related diseases and conditions. AEC36400-AEC36404 represent target
 CC sequences from VEGF, for a multifunctional siNA of the invention which
 CC targets VEGF and VEGFR2. AEC36447-AEC36451 represent complementary
 CC sequences to the target sequences.
 CC
 XX
 SQ Sequence 19 BP; 1 A; 10 C; 2 G; 0 T; 6 U; 0 Other;

PR 05-APR-2004; 2004US-0559824P.
PR 25-JAN-2005; 2005US-0647191P.
XX
XX (ALNY-) ALNYLAM PHARM INC.
XX
XX De Fongereolles A, Frank-Kamenetsky M, Manoharan M, Rajeev KG;
PI Hadwiger P;
XX
XX WPI, 2005-658984/67.
XX
XX New isolated interfering ribonucleic acid (iRNA) agent comprising a sense
PT sequence and an antisense sequence, useful for treating a human diagnosed
PT as having or at risk for having adult macular degeneration.
XX
XX Claim 1; SEQ ID NO 86; 200pp; English.
XX
XX The present invention relates to the use of siRNA targeting vascular
CC endothelial growth factor (VEGF). Specifically claimed is an isolated
CC interfering ribonucleic acid (iRNA) agent comprising a sense sequence and
CC an antisense sequence, where the sense and the antisense sequences form
CC an RNA duplex. Also claimed are methods of reducing the amount of VEGF
CC RNA in a cell, using the iRNA agent; making an iRNA agent by the
CC synthesis of the iRNA agent, where the sense and antisense strands
CC comprise at least one modification that stabilizes the iRNA agent against
CC nucleolytic degradation; a pharmaceutical composition comprising the iRNA
CC agent; inhibiting VEGF expression; and treating a human diagnosed with
CC adult macular degeneration (AMD), by administering a therapeutically
CC effective amount of the iRNA agent. The isolated iRNA agent has the sense
CC sequence that differs by no more than 1', 2', or 3 nucleotides from a SEQ
CC ID NO: 2-401, not defined in the specification. The iRNA agent further
CC comprises a non-nucleotide moiety. The iRNA agent further comprises one
CC or a second 3'-overhang comprising 1-6 nucleotides. The iRNA agent
CC further comprises a phosphorothioate at the first internucleotide linkage
CC at the 5' or 3' end of the antisense and sense sequences. The agent
CC further comprises a 2'-modified nucleotide. The iRNA agent is useful for
CC treating adult macular degeneration, diabetic retinopathy, cancer, asthma
CC and angiogenic disorders. The present sequence is short interfering sense
CC sequence targeting human VEGF 121.
XX
XX Sequence 23 BP; 9 A; 2 C; 11 G; 0 T; 1 U; 0 Other;
SQ
XX
XX Query Match 6.9%; Score 16.4; DB 1; Length 23;
Best Local Similarity 94.4%; Pred. No. 28;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 147 CCTTCTCTCTCTGCGCAT 164
DB 18 CCTCTCTCTCTGCGCAT 1
XX
XX RESULT 29
AED05615/C
ID AED05615 standard; RNA; 23 BP.
XX
XX AED05615;
AC
XX
XX 01-DEC-2005 (first entry)
DT
XX
XX Short interfering sense sequence targeting human VEGF 121, seqid 80.
DE
XX
XX vascular endothelial growth factor; RNA interference; gene silencing;
XX macular degeneration; ophthalmological; ocular disease;
XX diabetic retinopathy; antidiabetic; cardiovascular disease; cancer;
XX cytostatic; neoplasm; asthma; antiasthmatic; immune disorder;
XX inflammation; respiratory disease; angiogenesis disorder; antiangiogenic;
XX ss; short interfering RNA; siRNA.
XX
XX Homo sapiens.
OS
XX
XX WO2005089224-A2.
PN
XX
XX 29-SEP-2005.
PD
XX

PF 11-MAR-2005; 2005WO-US008182.
XX
XX 12-MAR-2004; 2004US-0552620P.
PR
XX 05-APR-2004; 2004US-0559824P.
PR
XX 25-JAN-2005; 2005US-0647191P.
XX
XX (ALNY-) ALNYLAM PHARM INC.
XX
XX De Fongereolles A, Frank-Kamenetsky M, Manoharan M, Rajeev KG;
PI Hadwiger P;
XX
XX WPI, 2005-658984/67.
XX
XX New isolated interfering ribonucleic acid (iRNA) agent comprising a sense
PT sequence and an antisense sequence, useful for treating a human diagnosed
PT as having or at risk for having adult macular degeneration.
XX
XX Claim 1; SEQ ID NO 80; 200pp; English.
XX
XX The present invention relates to the use of siRNA targeting vascular
CC endothelial growth factor (VEGF). Specifically claimed is an isolated
CC interfering ribonucleic acid (iRNA) agent comprising a sense sequence and
CC an antisense sequence, where the sense and the antisense sequences form
CC an RNA duplex. Also claimed are methods of reducing the amount of VEGF
CC RNA in a cell, using the iRNA agent; making an iRNA agent by the
CC synthesis of the iRNA agent, where the sense and antisense strands
CC comprise at least one modification that stabilizes the iRNA agent against
CC nucleolytic degradation; a pharmaceutical composition comprising the iRNA
CC agent; inhibiting VEGF expression; and treating a human diagnosed with
CC adult macular degeneration (AMD), by administering a therapeutically
CC effective amount of the iRNA agent. The isolated iRNA agent has the sense
CC sequence that differs by no more than 1', 2', or 3 nucleotides from a SEQ
CC ID NO: 2-401, not defined in the specification. The iRNA agent further
CC comprises a non-nucleotide moiety. The iRNA agent further comprises one
CC or a second 3'-overhang comprising 1-6 nucleotides. The iRNA agent
CC further comprises a phosphorothioate at the first internucleotide linkage
CC at the 5' or 3' end of the antisense and sense sequences. The agent
CC further comprises a 2'-modified nucleotide. The iRNA agent is useful for
CC treating adult macular degeneration, diabetic retinopathy, cancer, asthma
CC and angiogenic disorders. The present sequence is short interfering sense
CC sequence targeting human VEGF 121.
XX
XX Sequence 23 BP; 7 A; 5 C; 10 G; 0 T; 1 U; 0 Other;
SQ
XX
XX Query Match 6.9%; Score 16.4; DB 1; Length 23;
Best Local Similarity 94.4%; Pred. No. 28;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 148 CCTTCTCTCTGCGCAT 165
DB 23 CCTCTCTCTCTGCGCAT 6
XX
XX RESULT 30
ABX97349
ID ABX97349 standard; DNA; 23 BP.
XX
XX ABX97349;
AC
XX
XX 20-MAY-2003 (first entry)
DT
XX
XX Human NOV-associated probe from primer-probe set Ag3550.
DE
XX
XX NOX; cytostatic; cardiant; antiarteriosclerotic; antiasthmatic; cancer;
XX hypotensive; cardiomyopathy; bronchial asthma; gene therapy; vaccine;
XX human; probe; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200272757-A2.
PN
XX
XX 19-SEP-2002.
PD
XX

PF 08-MAR-2002; 2002W0-US0606308.
XX
PR 08-MAR-2001; 2001US-0274101P.
PR 08-MAR-2001; 2001US-0274194P.
PR 08-MAR-2001; 2001US-0274281P.
PR 08-MAR-2001; 2001US-0274322P.
PR 09-MAR-2001; 2001US-0274849P.
PR 12-MAR-2001; 2001US-0275235P.
PR 13-MAR-2001; 2001US-0275578P.
PR 13-MAR-2001; 2001US-0275579P.
PR 13-MAR-2001; 2001US-0275601P.
PR 14-MAR-2001; 2001US-0276000P.
PR 16-MAR-2001; 2001US-0276776P.
PR 19-MAR-2001; 2001US-0276994P.
PR 20-MAR-2001; 2001US-0277239P.
PR 20-MAR-2001; 2001US-0277321P.
PR 20-MAR-2001; 2001US-0277327P.
PR 21-MAR-2001; 2001US-0277791P.
PR 22-MAR-2001; 2001US-0277833P.
PR 23-MAR-2001; 2001US-0278152P.
PR 26-MAR-2001; 2001US-0278894P.
PR 27-MAR-2001; 2001US-0278999P.
PR 27-MAR-2001; 2001US-0279036P.
PR 28-MAR-2001; 2001US-0279344P.
PR 30-MAR-2001; 2001US-0279389P.
PR 30-MAR-2001; 2001US-0279959P.
PR 30-MAR-2001; 2001US-0280233P.
PR 02-APR-2001; 2001US-0280802P.
PR 02-APR-2001; 2001US-0280822P.
PR 02-APR-2001; 2001US-0280900P.
PR 04-APR-2001; 2001US-0281194P.
PR 13-APR-2001; 2001US-0283675P.
PR 30-APR-2001; 2001US-0287424P.
PR 02-MAY-2001; 2001US-0288066P.
PR 03-MAY-2001; 2001US-0288342P.
PR 03-MAY-2001; 2001US-0288528P.
PR 15-MAY-2001; 2001US-0291190P.
PR 16-MAY-2001; 2001US-0291099P.
PR 16-MAY-2001; 2001US-0291240P.
PR 30-MAY-2001; 2001US-0294485P.
PR 31-MAY-2001; 2001US-0294889P.
PR 31-MAY-2001; 2001US-0294899P.
PR 18-JUN-2001; 2001US-0299027P.
PR 19-JUN-2001; 2001US-0299303P.
PR 19-JUN-2001; 2001US-0299310P.
PR 10-JUL-2001; 2001US-0304354P.
PR 31-JUL-2001; 2001US-0309198P.
PR 16-AUG-2001; 2001US-0312903P.
PR 10-SEP-2001; 2001US-0318462P.
PR 12-SEP-2001; 2001US-0318770P.
PR 27-SEP-2001; 2001US-0325430P.
PR 27-SEP-2001; 2001US-0325681P.
PR 18-OCT-2001; 2001US-0330380P.
PR 31-OCT-2001; 2001US-0335301P.
PR 14-NOV-2001; 2001US-0332172P.
PR 14-NOV-2001; 2001US-0332271P.
PR 14-NOV-2001; 2001US-0332272P.
PR 14-NOV-2001; 2001US-0333184P.
PR 14-NOV-2001; 2001US-0333272P.
PR 21-NOV-2001; 2001US-0332094P.
PR 03-DEC-2001; 2001US-0337426P.
PR 03-DEC-2001; 2001US-0338092P.
PR 04-DEC-2001; 2001US-0337185P.
PR 03-JAN-2002; 2002US-0345705P.
PR 07-MAR-2002; 2002US-00092900.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Padigaru M, Spytek KA, Shenoy SG, Taupier RJ, Pena CE, Li L;
PI Zethuizen BD, Gusev V, Ji W, Gorman L, Miller CE, Kekuda R;
PI Ratuvaajan M, Gangolli E, Verner CM, Guo X, Tchernev V;
PI Fernandes ER, Casman SJ, Malyankar UM, Gerlach V, Liu Y, Anderson D;
PI Spaderna SK, Catterton E, Burgess C, Lette M, Zhong H, Alsbrook JP;

PI Lepley DM, Rieger DK;
XX
DR WPI; 2002-723332/78.
XX
XX NOVX polypeptides and polynucleotides, useful for preventing or treating
PT a disorder associated with aberrant NOVX expression or activity e.g.,
PT cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial
PT asthma.
XX
XX Example C; Page 717; 1103pp; English.
PS
XX This invention describes novel human NOVX polypeptides which have
XX cytostatic, cardiant, antiarteriosclerotic, antiasthmatic and hypotensive
CC activity. Pharmaceutical compositions comprising the NOVX proteins or
CC nucleic acid molecules or NOVX antibodies are useful for preventing or
CC treating a disorder associated with aberrant NOVX expression or activity
CC e.g. cancer, hypertension, atherosclerosis, cardiomyopathy or bronchial
CC asthma. The products of the invention can be used for gene therapy or in
CC a vaccine. ABX13460-ABX13462 and ABX97186-ABX97593 represent PCR primers
CC and probes used in the amplification and isolation of the NOVX
CC polynucleotides represented in ABX97008-ABX97185 which encode the
CC polypeptides represented in ABU55041-ABU5218. The probes described in
CC the invention are modified at the 5'-end by TET and the 3'-end by TAMRA
XX
SQ Sequence 23 BP; 1 A; 13 C; 2 G; 7 T; 0 U; 0 Other;
Query Match 6.9%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 29;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 100 CCCCCTCTCATTCTCCTGCTC 120
Db 2 CCGCCTCTCCTTCTCCGCTC 22
IIIIIIIIII
RESULT 31
ADN62252
ID ADN62252 standard; DNA; 23 BP.
XX AC
XX ADN62252;
XX
XX 01-JUL-2004 (first entry)
XX
XX Human NOV40a RTQ-PCR probe.
XX
XX Human; ss; PCR; NOVX; diabetes; obesity; infectious disease; anorexia;
KW cancer-associated cachexia; cancer; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW hemotopoietic disorder; dyslipidaemia; chronic disease; probe; RTQ-PCR;
KW real time quantitative PCR.
XX
XX OS Homo sapiens.
XX
XX US2004043382-A1.
XX
XX 04-MAR-2004.
XX
XX 07-MAR-2002; 2002US-00092900.
XX
XX 08-MAR-2001; 2001US-0274191P.
XX 08-MAR-2001; 2001US-0274194P.
XX 08-MAR-2001; 2001US-0274281P.
XX 08-MAR-2001; 2001US-0274322P.
XX 09-MAR-2001; 2001US-0274849P.
XX 12-MAR-2001; 2001US-0275235P.
XX 13-MAR-2001; 2001US-0275578P.
XX 13-MAR-2001; 2001US-0275579P.
XX 13-MAR-2001; 2001US-0275601P.
XX 14-MAR-2001; 2001US-0276000P.
XX 16-MAR-2001; 2001US-0276776P.
XX 19-MAR-2001; 2001US-0276994P.
XX 20-MAR-2001; 2001US-0277239P.
XX 20-MAR-2001; 2001US-0277321P.


```
KW antisense oligonucleotide; phosphorothioate; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
XX modified_base 1..20
XX /tag= b
XX /mod_base= OTHER
XX /note= "phosphorothioate backbone"
FT modified_base 1..5
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX US6372492-B1.
XX 16-APR-2002.
XX 30-OCT-2000; 2000US-00702251.
XX 30-OCT-2000; 2000US-00702251.
XX (ISIS-) ISIS PHARM INC.
XX Bennett CF, Cowseert LM;
XX WPI; 2002-470102/50.
XX New antisense compound useful for inhibiting expression of Talin and for
XX preventing or delaying infection, inflammation or tumor formation.
XX Claim 14; Col 42; 46pp; English.
XX The present invention describes an antisense compound (I), 16 to 30 bases
XX in length targeted to specific base regions of a nucleic acid encoding
XX human Talin. Also described: (a) an antisense compound up to 30 bases in
XX length which inhibits the expression of human Talin; (b) a composition
XX (II) comprising (I) or (a); and (c) inhibiting the expression of human
XX Talin in human cells or tissues comprising contacting the cells or
XX tissues in vitro with (I) or (a). (I) has antimicrobial, antiinflammatory
XX and cytostatic activities, and can be used in antisense gene therapy and
XX as a Talin expression inhibitor. (I) can be used to inhibit the
XX expression of human Talin in human cells or tissues; to prevent or delay
XX infection, inflammation or tumor formation; and in diagnostics,
XX therapeutics, prophylaxis, and in research reagents and kits. The present
XX sequence represents a human Talin antisense chimeric phosphorothioate
XX oligonucleotide, having 2'-methoxyethyl (2'-MOE) wings of 5 nucleotides
XX at the 5' and 3' ends and a 10 nucleotide deoxy gap in the middle, which
XX is used in an example from the present invention
XX Sequence 20 BP; 1 A; 7 C; 2 G; 10 T; 0 U; 0 Other;
SQ
Query Match 6.8%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 105 TCTCATTTCTCTGCTC 120
DB 3 TCTCATTTCTCTGCTC 18
```

```
DE Human talin phosphorothioate antisense oligonucleotide, SEQ ID NO:85.
XX Homo sapiens.
XX Key Location/Qualifiers
XX modified_base 1..20
XX /tag= a
XX /mod_base= OTHER
XX /note= "This oligonucleotide has a phosphorothioate
XX backbone and 2'-methoxyethyl (2'-MOE) wings at the 5'
XX and 3' ends, which are 5 nucleotides in length. Also all
XX cytosine nucleotides are 5-methylcytosines"
XX WO200268446-A1.
XX 06-SEP-2002.
XX 30-OCT-2001; 2001WO-US048435.
XX 22-FEB-2001; 2001US-00791942.
XX (ISIS-) ISIS PHARM INC.
XX (BOEH) BOEHRINGER INGELHEIM PHARM INC.
XX Bennett CF, Rothlein R, Kishimoto TK, Cowseert LM;
XX WPI; 2002-691651/74.
XX New antisense oligonucleotides targeted to nucleic acid molecules
XX encoding human Talin, useful for inhibiting the expression of human Talin
XX and for treating a human having a disease or condition associated with
XX Talin.
XX Example 15; SEQ ID NO 85; 114pp; English.
XX Sequences ADG90460-ADG90539 represent phosphorothioate targeted to the
XX human talin gene, which inhibit its expression. The antisense were
XX designed to target different regions of human talin RNA, and were
XX analysed for their effect on talin expression by quantitative real-time
XX PCR. Talin is a cytoplasmic protein which links cytoskeletal proteins
XX such as actin, myosin and vinculin to integrins, thereby linking the
XX extracellular matrix to other cells. It is thought to be involved in the
XX regulation of cellular adhesion and cell morphology. Talin is highly
XX expressed in platelets, and may play a role in platelet adhesion as its
XX subcellular distribution differs between resting non-adhesive platelets
XX and activated adhesive platelets. It could also play a major role in
XX determining muscle strength and cardiac function as it has been found to
XX participate in the transmission of contractile force to the extracellular
XX matrix in cardiomyocytes, and exhibits mechanical loading-dependent
XX expression at myotendinous junctions. The expression of talin is
XX downregulated by androgens in prostate tissues, a phenomenon known to
XX contribute to the development of prostate cancer. The oligonucleotides of
XX the invention are useful for diagnosis, prevention and treatment of talin
XX -related disorders, such as those related to cellular adhesion. The
XX present sequence represents a human c-Ha-ras phosphorothioate antisense
XX oligonucleotide used as a positive control in determining optimal
XX oligonucleotide concentration for a particular cell line.
XX Sequence 20 BP; 1 A; 7 C; 2 G; 10 T; 0 U; 0 Other;
SQ
Query Match 6.8%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 105 TCTCATTTCTCTGCTC 120
DB 3 TCTCATTTCTCTGCTC 18
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RESULT 34

AB084461/c
ID AB084461 standard; DNA; 20 BP.

XX AC AB084461;

XX DT 20-FEB-2003 (first entry)

XX DE DP10 PCR primer #92.

XX DP10; dipeptidyl peptidase; prolyloligopeptidase; enzyme; asthma;
KW antiinflammatory; antiasthmatic; antipsoriatic; antiarthritic;
KW antiinflammatory; vaccine; gene therapy; inflammatory disease;
KW inflammatory bowel disease; atopy; rheumatoid arthritis; psoriasis;
KW chromosome 2q14; PCR primer; ss.

XX OS Homo sapiens.
OS Synthetic.

XX PN WO200286113-A2.

XX PD 31-OCT-2002.

XX PF 24-APR-2002; 2002WO-GB001887.

XX PR 24-APR-2001; 2001GB-00010044.

XX PR 24-APR-2001; 2001GB-00010046.

XX PR 12-OCT-2001; 2001GB-00024575.

XX PR 12-OCT-2001; 2001GB-00024594.

XX PA (ISIS-) ISIS INNOVATIONS LTD.

XX P1 Cookson WOCM, Moffat MF, Allen M, Lench N;

XX DR WPI; 2003-093132/08.

XX PT New nucleic acid sequence comprising DP10 mRNA, useful for the
PT manufacture of a medicament for regulating DP10 protein expression or
PT for preventing or treating inflammatory disease e.g., inflammatory bowel
PT disease.

XX PS Claim 43; Page 314; 321pp; English.

XX CC The present invention describes a new isolated nucleic acid sequence (I)
CC comprising a DP10 mRNA sequence. DP10 is a dipeptidyl peptidase (also
CC known as prolyloligopeptidase). (I) has antiinflammatory, antiasthmatic,
CC antipsoriatic, antiarthritic and antirheumatic activities, and can be
CC used for the manufacture of a medicament for regulating DP10 expression
CC or for preventing or treating inflammatory disease e.g., inflammatory
CC bowel disease, asthma, atopy, rheumatoid arthritis or psoriasis. (I) can
CC also be used in an assay for detecting or measuring DP10 in a sample. A
CC host cell comprising (I) can be used for producing recombinant DP10 gene
CC products, or in drug screening systems to identify agents for diagnosis
CC or treatment of individuals having or susceptible to inflammatory
CC disease. Human DP10 is located on chromosome 2, more specifically
CC chromosome 2q14. AB084254 to AB084612 and ABP55569 to ABP55629 represent
CC sequences used in the exemplification of the present invention

XX SQ Sequence 20 BP; 4 A; 5 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 6.8%; Score 16; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 33;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Gy 191 AGAGCAAACTGCTAAC 206

Db 18 AGAGCAAACTGCTAAC 3

RESULT 35

ADP85740
ID ADP85740 standard; DNA; 20 BP.

XX AC ADP85740;

XX DT 26-AUG-2004 (first entry)

XX DE Human Talin antisense oligonucleotide, ISIS #109184.

XX KW Antisense; Talin; muscular disorder; hematologic disorder;
KW cardiac disorder; hyperproliferative disorder; cancer; human;
KW phosphorothioate; ss.

XX OS Homo sapiens.
XX Synthetic.

XX FH Key Location/Qualifiers

XX FT modified_base 1..20

XX FT /tag= b

XX FT /mod_base= OTHER

XX FT /note= "Phosphorothioate backbone where all cytidine

XX FT residues are 5-methylcytidines"

XX FT modified_base 1..5

XX FT /tag= a

XX FT /mod_base= OTHER

XX FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

XX FT /tag= c

XX FT /mod_base= OTHER

XX FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

XX PN US2004110705-A1.

XX PD 10-JUN-2004.

XX PF 11-SEP-2003; 2003US-00415463.

XX PR 30-OCT-2000; 2000US-00702251.

XX PR 30-OCT-2001; 2001WO-US047585.

XX PA (BENNETT) BENNETT C F.

XX PA (COMS/) COMSERT L M.

XX PI Bennett CF, Cowsett LM;

XX DR WPI; 2004-440384/41.

XX PT New compounds, particularly antisense oligonucleotides targeted to a

XX PT nucleic acid encoding talin, useful for treating muscular, cardiac,

XX PT hematologic, or hyperproliferative disorders.

XX PS Claim 3; SEQ ID NO 85; 48pp; English.

XX CC The invention relates to novel antisense compounds targeted to a nucleic

XX CC acid molecule encoding human Talin to and inhibit its expression. The

XX CC invention is useful for treating a disease or condition associated with

XX CC Talin such as a disease or condition e.g. muscular, hematologic, cardiac

XX CC or hyperproliferative disorder such as cancer. The present sequence is an

XX CC antisense oligonucleotide targeted to human Talin DNA.

XX SQ Sequence 20 BP; 1 A; 7 C; 2 G; 10 T; 0 U; 0 Other;

Query Match 6.8%; Score 16; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 33;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Gy 105 TCTCATTCCTCTGCTC 120

Db 3 TCTCATTCCTCTGCTC 18

RESULT 36

ACT41021/c

```

ID  ACL41021 standard; RNA; 21 BP.
XX
XX  ACL41021;
AC
XX  24-MAR-2005 (first entry)
DT
XX  C20orf103 siRNA sense sequence, SEQ ID 2093.
DE
XX  Cytosratic; Gene therapy; Vaccine; RNA Interference; cancer; ss;
XX  short interfering RNA; gene silencing.
XX
XX  Synthetic.
OS
XX  WO2005001092-A2.
PN
XX  06-JAN-2005.
PD
XX  19-MAY-2004; 2004MO-US015645.
PF
XX  20-MAY-2003; 2003US-0471729P.
PR
XX  (AMHP ) WYETH.
PA
XX  Be X, Wei L, Slonim DK, Howes SH;
PI
XX  WPI; 2005-075568/08.
DR
XX
XX  Pharmaceutical composition comprising an agent capable of modulating an
PT  expression level or protein activity of a gene, e.g. ABCC4, or a T cell
PT  activated by the polypeptide or antibody, and a carrier, useful for
PT  treating cancer.
XX
XX  Claim 3; SEQ ID NO 2093; 113pp; English.
PS
XX
XX  The present invention relates to a novel pharmaceutical composition
CC  comprising: (a) an agent capable of modulating an expression level or
CC  protein activity of a cancer-related transmembrane protein (CRTP) or gene
CC  (b) an antibody specific for a CRTP, or a T cell activated by a CRTP, and
CC  (b) a carrier. The pharmaceutical composition may also comprise a
CC  polynucleotide capable of inhibiting or decreasing the expression of the
CC  CRTP by RNA interference or an antisense mechanism. The CRTPs of the
CC  invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
CC  FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
CC  pharmaceutical composition is useful for treating cancer, e.g. colon
CC  cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
CC  cancer, stomach cancer, and esophageal cancer. The present sequence is a
CC  CRTP short interfering RNAs (siRNA) oligonucleotide. Note: The sequence
CC  data for this patent did not form part of the printed specification, but
CC  was obtained in electronic format directly from WIPO at
CC  ftp.wipo.int/pub/published_pct_sequences
XX
XX  Sequence 21 BP; 10 A; 3 C; 4 G; 0 T; 4 U; 0 Other;
SQ
XX
XX  Query Match 6.7%; Score 15.8; DB 1; Length 21;
XX  Best Local Similarity 89.5%; Pred. No. 34;
XX  Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY
XX  150 TTCTCTTCCGTCATGAT 168
DB  19 TTCTGTGTCGCATGAT 1

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XX  Homo sapiens.
OS
XX  WO2005001092-A2.
PN
XX  06-JAN-2005.
PD
XX  19-MAY-2004; 2004MO-US015645.
PF
XX  20-MAY-2003; 2003US-0471729P.
PR
XX  (AMHP ) WYETH.
PA
XX  Be X, Wei L, Slonim DK, Howes SH;
PI
XX  WPI; 2005-075568/08.
DR
XX
XX  Pharmaceutical composition comprising an agent capable of modulating an
PT  expression level or protein activity of a gene, e.g. ABCC4, or a T cell
PT  activated by the polypeptide or antibody, and a carrier, useful for
PT  treating cancer.
XX
XX  Claim 3; SEQ ID NO 1852; 113pp; English.
PS
XX
XX  The present invention relates to a novel pharmaceutical composition
CC  comprising: (a) an agent capable of modulating an expression level or
CC  protein activity of a cancer-related transmembrane protein (CRTP) or gene
CC  (b) an antibody specific for a CRTP, or a T cell activated by a CRTP, and
CC  (b) a carrier. The pharmaceutical composition may also comprise a
CC  polynucleotide capable of inhibiting or decreasing the expression of the
CC  CRTP by RNA interference or an antisense mechanism. The CRTPs of the
CC  invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
CC  FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
CC  pharmaceutical composition is useful for treating cancer, e.g. colon
CC  cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
CC  cancer, stomach cancer, and esophageal cancer. The present sequence is a
CC  target oligonucleotide from one such CRTP for which short interfering
CC  RNAs (siRNA) were produced. Note: The sequence data for this patent did
CC  not form part of the printed specification, but was obtained in
CC  electronic format directly from WIPO at
CC  ftp.wipo.int/pub/published_pct_sequences
XX
XX  Sequence 21 BP; 5 A; 4 C; 7 G; 5 T; 0 U; 0 Other;
SQ
XX
XX  Query Match 6.7%; Score 15.8; DB 1; Length 21;
XX  Best Local Similarity 89.5%; Pred. No. 34;
XX  Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY
XX  172 AGATTCCAGCGACTTCACA 190
DB  21 AGATTCCAGCGGCTTCACA 3

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RESULT 37
ACLA0780/C
ID  ACLA0780 standard; DNA; 21 BP.
XX
XX  ACLA0780;
AC
XX  24-MAR-2005 (first entry)
DT
XX  ABCC4 target oligonucleotide, SEQ ID 1852.
DE
XX  Cytosratic; Gene therapy; Vaccine; RNA Interference; cancer; ss.
XX

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RESULT 38
ACLA0113
ID  ACLA0113 standard; RNA; 21 BP.
XX
XX  ACLA0113;
AC
XX  24-MAR-2005 (first entry)
DT
XX  ABCC4 siRNA antisense sequence, SEQ ID 1185.
DE
XX  Cytosratic; Gene therapy; Vaccine; RNA Interference; cancer; ss;
XX  short interfering RNA; gene silencing.
XX
XX  Synthetic.
OS
XX  WO2005001092-A2.
PN
XX  06-JAN-2005.
PD
XX  19-MAY-2004; 2004MO-US015645.
PF

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XX 20-MAY-2003; 2003US-0471729P.
XX (AMHP) WYETH.
XX
XX Be X, Wei L, Slonim DK, Howes SH;
XX WPI; 2005-075568/08.
XX
XX Pharmaceutical composition comprising an agent capable of modulating an
XX expression level or protein activity of a gene, e.g. ABCc4, or a T cell
XX activated by the polypeptide or antibody, and a carrier, useful for
XX treating cancer.
XX
XX Claim 3; SEQ ID NO 1185; 113pp; English.

```

Query Match          6.7%; Score 15.8; DB 1; Length 21;
Best Local Similarity 68.4%; Pred.No.34;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0

Oy      172 AGATTCCAGGAGCTTCACA 190
      |||::|||::|||
Db      1 AGAUTCACAGCGCTUCACAC 19

RESULT 39
ACLA0111/c
ID      ACLA0111 standard; DNA; 21 BP.
XX
XX      ACLA0111;
AC
XX
DT      24-MAR-2005 (first entry)
XX
XX      ABCC4 target oligonucleotide, SEQ ID 1183.
DE
XX      Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss.
KM
XX      Homo sapiens.
OS
XX      W02005001092-A2.
FN
XX      06-JAN-2005.
PD
XX      19-MAY-2004; 2004MO-US015645.
PE
XX      20-MAY-2003; 2003US-0471729P.
PR
XX      (AMHP ) WYETH.
PA
XX      Be X, Wei L, Slonim DK, Howes SH;
PI
XX      WPI; 2005-075568/08.
DR
XX
PT      Pharmaceutical composition comprising an agent capable of modulating an

```

PT	expression level or protein activity of a gene, e.g. ABCC4, or a T cell
PT	activated by the polypeptide or antibody, and a carrier, useful for
PT	treating cancer.
XX	
PS	Claim 3; SEQ ID NO 1183; 113pp; English.
XX	
CC	The present invention relates to a novel pharmaceutical composition
CC	comprising: (a) an agent capable of modulating an expression level or
CC	protein activity of a cancer-related transmembrane protein (CRP) or gene
CC	an antibody specific for a CRP, or a T cell activated by a CRP; and
CC	(b) a carrier. The pharmaceutical composition may also comprise a
CC	polynucleotide capable of inhibiting or decreasing the expression of the
CC	CRP by RNA interference or an antisense mechanism. The CRPs of the
CC	invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
CC	FU11866, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
CC	pharmaceutical composition is useful for treating cancer, e.g. colon
CC	cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
CC	cancer, stomach cancer, and esophageal cancer. The present sequence is a
CC	target oligonucleotide from one such CRP for which short interfering
CC	RNAs (siRNA) were produced. Note: The sequence data for this patent did
CC	not form part of the printed specification, but was obtained in
CC	electronic format directly from WIPO at
CC	ftp.wipo.int/pub/published_pot_sequences
SO	
Sequence	21 BP; 5 A; 4 C; 7 G; 5 T; 0 U; 0 Other;
Query Match	6.7%; Score 15.8; DB 1; Length 21;
Best Local Similarity	89.5%; Pred. No. 34;
Matches	17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY	
Db	172 AGATTCAGGGACTTCACA 190 +++++ 21 AGATTCCAGCGCTTCACA 3
RESULT 40	
ACL40868/c	
ID	ACL40868 standard; RNA; 21 BP.
XX	
AC	ACL40868;
XX	
DT	24-MAR-2005 (first entry)
XX	
DE	C20orf103 siRNA sense sequence, SEQ ID 1940.
XX	
KW	Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss;
KW	short interfering RNA; gene silencing.
XX	
OS	Synthetic.
XX	
PN	WO2005001092-A2.
PD	
XX	06-JAN-2005.
PF	
XX	19-MAY-2004; 2004MO-USO15645.
PR	
XX	20-MAY-2003; 2003US-0471729P.
PA	
XX	(AMHP) WTETH.
P1	
XX	Be X, Wei L, Sloniom DK, Howes SH;
DR	
XX	WPI; 2005-075568/08.
FT	
XX	Pharmaceutical composition comprising an agent capable of modulating an
FT	expression level or protein activity of a gene, e.g. ABCC4, or a T cell
FT	activated by the polypeptide or antibody, and a carrier, useful for
FT	treating cancer.
XX	
PS	Claim 3; SEQ ID NO 1940; 113pp; English.
XX	
CC	The present invention relates to a novel pharmaceutical composition
CC	comprising: (a) an agent capable of modulating an expression level or
CC	protein activity of a cancer-related transmembrane protein (CRP) or gene
CC	an antibody specific for a CRP, or a T cell activated by a CRP; and
CC	(b) a carrier. The pharmaceutical composition may also comprise a
CC	polynucleotide capable of inhibiting or decreasing the expression of the
CC	CRP by RNA interference or an antisense mechanism. The CRPs of the
CC	invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
CC	FU11866, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
CC	pharmaceutical composition is useful for treating cancer, e.g. colon
CC	cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
CC	cancer, stomach cancer, and esophageal cancer. The present sequence is a
CC	target oligonucleotide from one such CRP for which short interfering
CC	RNAs (siRNA) were produced. Note: The sequence data for this patent did
CC	not form part of the printed specification, but was obtained in
CC	electronic format directly from WIPO at
CC	ftp.wipo.int/pub/published_pot_sequences

CC protein activity of a cancer-related transmembrane protein (CRTP) or gene
CC : an antibody specific for a CRTP, or a T cell activated by a CRTP; and
CC (b) a carrier. The pharmaceutical composition may also comprise a
CC polynucleotide capable of inhibiting or decreasing the expression of the
CC CRTP by RNA interference or an antisense mechanism. The CRTPs of the
CC invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
CC FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
CC pharmaceutical composition is useful for treating cancer, e.g. colon
CC cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
CC cancer, stomach cancer, and esophageal cancer. The present sequence is a
CC CRTP short interfering RNA (siRNA) oligonucleotide. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
CC
SQ Sequence 21 BP; 9 A; 3 C; 5 G; 0 T; 4 U; 0 Other;

Query Match 6.7%; Score 15.8; DB 1; Length 21;
Best Local Similarity 89.5%; Pred. No. 34;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 149 CTTCTCCTTCGCATGAT 167
Db 19 CTTCTGTTCTGCATGAT 1

RESULT 41

ACLA0782
ID ACLA0782 standard; RNA; 21 BP.

AC ACLA0782;

DT 24-MAR-2005 (first entry)

DE ABCC4 siRNA antisense sequence, SEQ ID 1854.

XX Cytostatic; Gene therapy; Vaccine; RNA interference; cancer; ss;

KW short interfering RNA; gene silencing.

XX Synthetic.

PN W02005001092-A2.

PD 06-JAN-2005.

PE 19-MAY-2004; 2004WO-US015645.

PR 20-MAY-2003; 2003US-0471729P.

PA (AMHP) WYETH.

PI Be X, Wei L, Slonim DK, Howes SH;

DR WPI; 2005-075568/08.

XX Pharmaceutical composition comprising an agent capable of modulating an
PT expression level or protein activity of a gene, e.g. ABCC4, or a T cell
PT activated by the polypeptide or antibody, and a carrier, useful for
PT treating cancer.

XX Claim 3; SEQ ID NO 1854; 113bp; English.

XX The present invention relates to a novel pharmaceutical composition
CC comprising: (a) an agent capable of modulating an expression level or
CC protein activity of a cancer-related transmembrane protein (CRTP) or gene
CC ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and
CC (b) a carrier. The pharmaceutical composition may also comprise a
CC polynucleotide capable of inhibiting or decreasing the expression of the
CC CRTP by RNA interference or an antisense mechanism. The CRTPs of the
CC invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
CC FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
CC pharmaceutical composition is useful for treating cancer, e.g. colon
CC cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney

CC cancer, stomach cancer, and esophageal cancer. The present sequence is a
CC CRTP short interfering RNA (siRNA) oligonucleotide. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
CC
SQ Sequence 21 BP; 5 A; 6 C; 4 G; 0 T; 6 U; 0 Other;

Query Match 6.7%; Score 15.8; DB 1; Length 21;
Best Local Similarity 68.4%; Pred. No. 34;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 172 AGATTCGAGGACTTCACA 190
Db 1 AGAUTCACGCGCUCACA 19

RESULT 42
ACA88981
ID ACA88981 standard; DNA; 22 BP.

AC ACA88981;

DT 08-JUL-2003 (first entry)

DE Selection and amplification of genetic markers PCR related primer #92.

XX Genetic marker selection; multiplex PCR amplification;

KW prenatal diagnostic testing; foetal sex determination;

KW genetic identification; DNA profiling; DNA fingerprinting;

XX forensic analysis; PCR; primer; ss.

OS Homo sapiens.

PN W02003031646-A1.

PD 17-APR-2003.

PE 14-OCT-2002; 2002WO-AU001388.

PR 12-OCT-2001; 2001AU-00008234.

PA (UYQU) UNIV QUEENSLAND.

PI Findlay I, Matthews PL, Mulcahy BK;

DR WPI; 2003-381725/36.

XX Selecting genetic markers as targets for nucleic acid sequence
PT amplification, useful for improving genetic testing, e.g. fetal sex
PT determination, comprises selecting each of the genetic markers according
PT to a heterozygosity index.

XX Claim 36; Page 40; 64pp; English.

XX The invention describes a method of selecting genetic markers as targets
CC for nucleic acid sequence amplification comprising selecting each of the
CC genetic markers according to a heterozygosity index of 0.5 or greater.
CC Selecting and amplification of genetic markers are useful as targets for
CC nucleic acid sequence amplification, for genetic testing or facilitating
CC multiplex PCR amplification from limiting amounts of target nucleic acid.
CC The methods are also useful for improving genetic diagnostic and
CC screening methods, such as prenatal diagnostic testing, foetal sex
CC determination or genetic identification, e.g. DNA profiling or DNA
CC fingerprinting. The nucleic acid sequence amplification is also useful in
CC forensic analysis of degraded, old, ancient and difficult samples that
CC are difficult to amplify and identify. This sequence represents a PCR
CC primer used in the selection and amplification of genetic markers
XX
SQ Sequence 22 BP; 2 A; 8 C; 2 G; 10 T; 0 U; 0 Other;

Query Match 6.6%; Score 15.6; DB 1; Length 22;

Best Local Similarity 81.8%; Pred. No. 34;
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 144 TCCCTCTCTCTCTGCGCATG 165
 DB 1 TTTCTCTTCACCTTCTGCGCATG 22

RESULT 43
 ADU84382
 ID ADU84382 standard; DNA; 17 BP.
 AC ADU84382;
 DT 10-FEB-2005 (first entry)
 DE Human MetAP-2 hammerhead ribozyme substrate sequence #391.
 XX Enzymatic nucleic acid molecule; gene expression; down regulation;
 KW protea-tyrosine-phosphatase-1b; PTB-1b; methionine aminopeptidase;
 KW MetAP-2; human telomerase; hTERT; protein kinase C alpha; PKC alpha;
 KW beta-secretase; BACE; human epidermal growth factor receptor-2; HER2;
 KW c-erb2; neu; phospholamban; PLN; presenilin-1; ps-1; presenilin-2; ps-2;
 KW hepatitis B virus; HBV; hammerhead; HH; hairpin; NCH; inozyme; G-cleaver;
 KW amberzyme; zinzyme; DNAzyme; cancer; breast cancer; Alzheimer's disease;
 KW diabetes; obesity; cardiac disease; heart disease; age-related disease;
 KW hepatitis B infection; hepatocellular carcinoma; genetic drift; human;
 KW db.
 XX Homo sapiens.
 OS
 AC WO200116312-A2.
 DT 08-MAR-2001.
 DE 30-AUG-2000; 2000WO-US02398.
 XX 31-AUG-1999; 99US-0151713P.
 PR 27-SEP-1999; 99US-0040664J.
 PR 27-SEP-1999; 99US-0156236P.
 PR 27-SEP-1999; 99US-0156467P.
 PR 08-NOV-1999; 99US-00436430.
 PR 06-DEC-1999; 99US-0169100P.
 PR 29-DEC-1999; 99US-0047443Z.
 PR 29-DEC-1999; 99US-0173612E.
 PR 30-DEC-1999; 99US-00476387.
 PR 04-FEB-2000; 2000US-00498824.
 PR 20-MAR-2000; 2000US-0053102S.
 PR 14-APR-2000; 2000US-0197769P.
 PR 23-MAY-2000; 2000US-00578823.
 PR 09-AUG-2000; 2000US-00636385.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX Mcswiggen J, Usman N, Blatt L, Beigelman L, Burgin A;
 PI Karpelsky A, Matulic-Adamic J, Svedler D, Draper K, Chowrira B;
 PI Stinchcomb D, Beaudry A, Zinnen S, Ludwig J, Sproat BS;
 XX WPI/ 2001-244406/25.
 DR
 XX Enzymatic nucleic acid molecules able to cleave separate RNA molecules
 PT are used for treating cancer, Alzheimer's disease, hepatitis, diabetes,
 PT obesity and heart disease.
 XX
 XX Example 3; Page 249; 717pp; English.
 XX
 XX The present invention relates to the use of enzymatic nucleic acid
 CC molecules (e.g. ribozymes) to modulate gene expression. The invention
 CC also methods for their use to down regulate or inhibit the expression of
 CC genes encoding protein-tyrosine-phosphatase-1b (PTB-1b), methionine
 CC aminopeptidase (MetAP-2), human telomerase (hTERT), protein kinase C
 CC alpha (PKC alpha), beta-secretase (BACE), human epidermal growth factor
 CC receptor-2 (HER2/c-erb2/neu), phospholamban (PLN), presenilin-1 (ps-1),

CC presenilin-2 (ps-2), and hepatitis B virus (HBV) proteins. The enzymatic
 CC nucleic acid molecules used to inhibit the expression of the said genes
 CC include hammerhead (HH), hairpin, NCH (inozyme), G-cleaver, amberzyme,
 CC zinzyme, and/or DNAzyme motifs. The methods of the invention are useful
 CC for treating cancer, in particular breast cancer, Alzheimer's disease,
 CC diabetes, obesity, cardiac diseases e.g. heart disease, age-related
 CC diseases, hepatitis B infections, and hepatitis and hepatocellular
 CC carcinoma. The enzymatic nucleic acid molecules can also be used as
 CC diagnostic tools to examine genetic drift and mutations within diseased
 CC cells and to detect the presence of specific RNA in a cell. The present
 CC sequence represents a substrate/target sequence for a ribozyme used in
 CC the examples of the present invention. Note: Some SEQ ID Nos are repeated
 CC more than once in the specification, but these have different sequences
 CC associated with them.
 XX
 XX Sequence 17 BP; 4 A; 1 C; 5 G; 7 T; 0 U; 0 Other;
 SQ

Query Match 6.5%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 41;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 75 GAGCTGGTTGTTGAAA 91
 DB 1 GAGCTGGTTTGTGAAA 17

RESULT 44
 ACN08391
 ID ACN08391 standard; RNA; 17 BP.
 AC ACN08391;
 DT 22-APR-2004 (first entry)
 DE
 XX MNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 8394.
 XX
 KW MNV; West Nile Virus; antiinflammatory; cytosolic; hepatotropic;
 KW virucide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; inozyme; DNAzyme;
 KW Amberzyme; Zinzyme; ss.
 XX
 OS West Nile Virus.
 FN
 XX WO200268637-A2.
 PD 06-SEP-2002.
 XX 19-OCT-2001; 2001WO-US048350.
 PF 20-OCT-2000; 2000US-0242411P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 XX Blatt L, Mcswiggen JA;
 PI
 XX WPI/ 2002-706994/76.
 DR
 XX New nucleic acid molecule that modulates replication of West Nile Virus
 PT (MNV), useful for treating a condition related to MNV infection e.g.
 PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
 XX
 XX Claim 23; SEQ ID NO 8394; 495pp; English.
 XX
 XX The invention relates to nucleic acid molecules that modulate replication
 CC of the West Nile Virus (MNV). The nucleic acid molecules are useful for
 CC treating a condition related to MNV infection e.g. pancreatitis,
 CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
 CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
 CC molecule is selected from the group of ribozymes consisting of
 CC Hammerhead, inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The

CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention

XX
SQ Sequence 17 BP; 0 A; 9 C; 0 G; 0 T; 8 U; 0 Other;

Query Match 6.5%; Score 15.4; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 41;
Matches 9; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Qy 143 CTCGCCCTTCCTCTCT 159
|:|||||:|:|:|:|:|:|:
Db 1 CUCUCCUCCUCCUCCU 17

RESULT 45
ACN06460/c
ID ACN06460 standard; RNA; 17 BP.
XX
ACN06460;
XX
XX
DT 22-APR-2004 (first entry)
XX
DE MNV Amberzyme substrate SEQ ID NO 6463.
XX
XX MNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX virucide; neuroprotective; antibacterial; replication; pancreatitis;
XX encephalitis; myocarditis; meningitis; infection; hepatitis;
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
XX Amberzyme; Zinzyme; ss.
XX
XX West Nile Virus.
XX
XX WO200268637-A2.
XX
XX 06-SEP-2002.
XX
XX 19-OCT-2001; 2001WO-US048350.
XX
XX 20-OCT-2000; 2000US-0242411P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGEN J A.
XX
XX Blatt L, Mcswiggen JA;
XX
XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
XX (MNV), useful for treating a condition related to MNV infection e.g.
XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX Claim 23; SEQ ID NO 6463; 495bp; English.

XX
XX The invention relates to nucleic acid molecules that modulate replication
XX of the West Nile Virus (MNV). The nucleic acid molecules are useful for
XX treating a condition related to MNV infection e.g. pancreatitis,
XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
XX molecule is selected from the group of ribozymes consisting of
XX Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
XX nucleic acid molecules further comprise at least five ribose residues, at
XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at
XX least three of the 5' terminal nucleotides and a 3' end modification of a
XX 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
XX in the specification. The present sequence is that of a nucleic acid
XX molecule of the invention

XX
SQ Sequence 17 BP; 8 A; 1 C; 8 G; 0 T; 0 U; 0 Other;

Query Match 6.5%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 41;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 144 TCCGCCCTTCCTCTCTG 160
|:|||||:|:|:|:|:|:|:
Db 17 TCTCCCTTCCTCTCTG 1

RESULT 46
ACN08392
ID ACN08392 standard; RNA; 17 BP.
XX
ACN08392;
XX
XX
DT 22-APR-2004 (first entry)
XX
XX MNV minus strand Hammerhead Ribozyme substrate SEQ ID NO 8395.
XX
XX MNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX virucide; neuroprotective; antibacterial; replication; pancreatitis;
XX encephalitis; myocarditis; meningitis; infection; hepatitis;
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
XX Amberzyme; Zinzyme; ss.
XX
XX West Nile Virus.
XX
XX WO200268637-A2.
XX
XX 06-SEP-2002.
XX
XX 19-OCT-2001; 2001WO-US048350.
XX
XX 20-OCT-2000; 2000US-0242411P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGEN J A.
XX
XX Blatt L, Mcswiggen JA;
XX
XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
XX (MNV), useful for treating a condition related to MNV infection e.g.
XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX Claim 23; SEQ ID NO 8395; 495bp; English.

XX
XX The invention relates to nucleic acid molecules that modulate replication
XX of the West Nile Virus (MNV). The nucleic acid molecules are useful for
XX treating a condition related to MNV infection e.g. pancreatitis,
XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
XX molecule is selected from the group of ribozymes consisting of
XX Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
XX nucleic acid molecules further comprise at least five ribose residues, at
XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at
XX least three of the 5' terminal nucleotides and a 3' end modification of a
XX 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
XX in the specification. The present sequence is that of a nucleic acid
XX molecule of the invention

XX
SQ Sequence 17 BP; 0 A; 8 C; 1 G; 0 T; 8 U; 0 Other;

Query Match 6.5%; Score 15.4; DB 1; Length 17;
Best Local Similarity 52.9%; Pred. No. 41;
Matches 9; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

```
Qy      144 TCCCCCTTCTCCTTCTG 160
          :| |||::|::|::|
Db      1 UCUCCCUUCUCCUUCUG 17
```

RESULT 47
AAD12693/c
ID AAD12693 standard; DNA; 20 BP.

De	Human α phae/ α phan-chimeric cDNA sequencing primer, FVR1479F.
XX	
KM	Human, ANC_2H01 protein; catenin-binding protein; signal transduction.
KM	gene regulation; zinc finger protein; α phan-catenin; drug screening;
KM	therapy; cancer; neurological disorder; cytostatic; neuroprotective;
KM	α phae/ α phan-chimera; primer; ss.

PT Novel recombinant nucleic acids useful for diagnosing, prognosing and/or treating cancer and neurological disorders, corresponds to a protein binding to alpha-catenin protein and with signal transduction function.

The invention relates to human catenin-binding proteins and their corresponding cDNA molecules which functions in signal transduction and gene regulatory pathways. The invention also provides an isolated and/or recombinant nucleic acid or its functional fragment, homologue or derivative, corresponding to a alpha-catenin binding protein. The invention also relates to a novel human zinc finger protein binding with a member of the a-catenin/vinculin family, preferably with a human isoform of alpha N-catenin (neural form). The invention also relates to the field of drug discovery, diagnosis, prognosis and treatment of cancer and neurological disorders. The present sequence is a PCR primer which is used for sequencing and cloning human alpha6/alpha9-chimeras in pGB7 two hybrid vector

```

Query Match      6.5%;   Score 15.4;   DB 1;   length 20;
Best Local Similarity 94.1%;   Pred. No. 38;
Matches 16;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0

```

RESULT	46
ABZ31192/c	
ID	ABZ31192 standard; DNA; 20 BP
XX	
AC	ABZ31192;
XX	
DT	30-JAN-2003 (first entry)

XX DE	Candida albicans GRACE strain PCR primer SEQ ID NO 5411.

KW Fungus; yeast; tetracycline; promoter; GRACE strain; biosynthesis;
KW signal transduction; DNA replication; cell division; growth;
KW proliferation; *Candida albicans*; fungicide; antifungal; PCR; primer; ss.

OS *Candida albicans*.

PN WO200253728-A2.

PD 11-JUL-2002

PF 26-DEC-2001; 2001WO-US049486.

PR 29-DEC-2000; 2000US-0259128P.
PR 20-FEB-2001; 2001US-00792024.
PR 22-AUG-2001; 2001US-0314050P.

PA (ELIT-) ELITRA PHARM INC.

PI Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL; and

DR WPI; 2002-566694/60.

PT Constructing strains for identifying gene products as effective targets
PT for therapeutic intervention, by inactivating in the strain one allele of
PT a gene and placing other allele of the gene under conditional expression.

PS Claim 36; SEQ ID NO 5411; 167pp + Sequence Listing; English.

CC The invention relates to constructing (M1) a strain of diploid fungal
CC cells in which both alleles of a gene are modified, comprising modifying
CC one allele by insertion or replacement by a cassette having an
CC expressible selectable marker and modifying other allele by
CC recombination, of a promoter replacement fragment with a heterologous
CC promoter, so that expression of the second allele is regulated by the
CC promoter. (M1) is useful for constructing a strain of diploid fungal
CC cells in which both alleles of a gene are modified. The diploid fungal
CC cells having both alleles modified are useful for identifying a gene that
CC is essential to the survival or growth of a fungus, a gene that
CC contributes to the virulence and/or pathogenicity of a fungus, a gene
CC that contributes to the resistance of a diploid fungus to an antifungal
CC agent, an antifungal agent that inhibits the growth of a diploid fungus
CC and for identifying a therapeutic agent for treatment of a mammalian
CC disease. (M1) is useful for identifying a compound which modulates the
CC activity of a gene product, preferably enzymatic activity, carbon
CC compound catabolism, biosynthetic, transporter, transcriptional,
CC translational, signal transduction, DNA replication and cell division
CC activity. The method is useful for identifying a compound having the
CC ability to inhibit growth or proliferation of *C. albicans* cells and for
CC treating infection by *C. albicans*. The present sequence is that of a PCR
CC primer used in the method of the invention. Note: The sequence data for
CC this patent is not represented in the printed specification but is based
CC on sequence information supplied to Derwent by the European Patent Office

Query March Similarity 6.5%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. NO. 38;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0

RESULT	49
ID	AEF40118/C
XX	AEF40118 standard; DNA; 22 BP.
AC	AEF40118;

```

DT 23-MAR-2006 (first entry)
XX
XX Human hepatocarcinoma-associated VEGF PCR primer 1.
XX
XX Protein production; protein purification; tumor marker; hepatocarcinoma;
XX cytostatic; diagnosis; vascular endothelial cell growth factor; VEGF;
XX PCR; primer; ss.
XX
XX Homo sapiens.
XX
XX CN1629304-A.
XX
XX 22-JUN-2005.
XX
XX 02-DEC-2003; 2003CN-01116861.
XX
XX 02-DEC-2003; 2003CN-01116861.
XX
XX (HUJ/) HU J.
XX
XX Hu J, Yang J;
XX
XX WPI; 2005-726682/75.
XX
XX Chinese Han nationality vascular endothelial growth factor recombinant
XX gene, useful in hepatic carcinoma clinical diagnosis and treatment.
XX
XX Claim 2; Page 3; 10pp; Chinese.
XX
XX The invention relates to a method for the recombinant production and
XX purification of a human vascular endothelial growth factor (VEGF) protein
XX encoded by a polynucleotide originally obtained from human
XX hepatocarcinoma tissue. The method involves the inducible expression of
XX the VEGF protein in Escherichia coli, followed by protein extraction and
XX affinity chromatography to yield high purity VEGF protein. The invention
XX also relates to the isolation and cloning of the hepatocarcinoma-
XX associated VEGF polynucleotide, and to the use of the recombinantly
XX expressed VEGF protein or variants and derivatives thereof in the
XX diagnosis or treatment of hepatocarcinoma. Sequences AEP40118-AEP40119
XX represent human VEGF PCR primers which are specifically claimed for
XX isolating the hepatocarcinoma-associated VEGF polynucleotide.
XX
XX Sequence 22 BP; 7 A; 5 C; 9 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 6.5%; Score 15.4; DB 1; Length 22;
XX Best Local Similarity 94.1%; Pred. No. 36;
XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 149 CTCTCTCTCTGCGCATG 165
XX |||||
XX 22 CTCCTCTCTGCGCATG 6
XX
XX RESULT 50
XX AA248049/C
XX ID AA248049 standard; DNA; 20 BP.
XX
XX AA248049;
XX
XX 08-MAR-2000 (first entry)
XX
XX Human foetal 5'-UTR IGF-II antisense oligonucleotide GT14009.
XX
XX Human; IGF-II; insulin-like growth factor II; cell growth modulation;
XX tumour inhibition; antisense oligonucleotide; phosphorothioate;
XX metastasis; antitumour; antiproliferative; angiogenesis; apoptosis;
XX tumour cell migration; proliferative disease; atherosclerosis; psoriasis;
XX ss.
XX
XX Synthetic.
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX

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```

FT modified_base 1..20
FT /*tag= a
FT /mod_base
FT /note="phosphorothioate linkages"
XX
XX WO955854-A2.
XX
XX 04-NOV-1999.
XX
XX 23-APR-1999; 99WO-CA000323.
XX
XX 23-APR-1998; 98US-0082791P.
XX
XX (GENE-) GENSENSE TECHNOLOGIES INC.
XX
XX Wright JA, Young AH, Lee YS;
XX
XX WPI; 2000-062027/05.
XX
XX Antisense oligonucleotides against mRNA of insulin-like growth factor II,
XX for treating tumors and other proliferative diseases.
XX
XX Claim 4; Page 18; 72pp; English.
XX
XX AA248041 to AA248070 represent specifically claimed antisense
XX oligonucleotides (I) complementary to the mRNA of human insulin-like
XX growth factor II (IGF-II). The present invention also describes a method
XX for inhibiting growth or metastasis of mammalian tumours by administering
XX (I). (I) have antitumour and antiproliferative activity, and inhibits
XX (i) the autocrine and paracrine functions of IGF-II which promote tumour-
XX induced angiogenesis and tumour cell migration; and (ii) autocrine growth
XX of tumour cells, possibly including induction of apoptosis. (I) may also
XX function as ribozymes. (I) are used for inhibiting growth and metastasis
XX of mammalian tumours, also: (i) for treatment of other proliferative
XX diseases; e.g. atherosclerosis and psoriasis; (ii) when labeled, as
XX probes for detecting IGF-II mRNA; and (iii) as molecular weight markers.
XX (I) that bind to the 5'-untranslated region of the foetal transcript (the
XX form present in tumour cells) should not affect the adult transcript.
XX They are effective against drug-resistant tumours
XX
XX Sequence 20 BP; 5 A; 4 C; 11 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 6.4%; Score 15.2; DB 1; Length 20;
XX Best Local Similarity 85.0%; Pred. No. 40;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 98 GGGCCCTCTCATTTCTCTG 117
XX |||||
XX 20 GGCCCGCGCTCTTCTCCG 1
XX
XX RESULT 51
XX AA71802/C
XX ID AA71802 standard; DNA; 20 BP.
XX
XX AA71802;
XX
XX 08-JAN-2001 (first entry)
XX
XX FFA FANCIPI1 interactor PCR primer FANCIPI1-SPI.
XX
XX FFA: FANCIPI1; Fanconi anemia protein of complementation group A;
XX interactor; antitumor; ancytopenia; defective DNA repair; gene therapy;
XX cell-cycle aberration; tumorigenesis; tumor progression; PCR primer; ss.
XX
XX Unidentified.
XX
XX WO200046244-A1.
XX
XX 10-AUG-2000.
XX
XX 24-JAN-2000; 2000WO-EP000506.
XX

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PR 05-FEB-1999; 99DE-01004650.
XX
XX (MULT-) MULTIGENE BIOTECH GMBH.
XX
XX Gross HJ, Reuter T, Hoehn H, Henterich S;
XX
XX MPI, 2000-524414/47.
XX
XX New nucleic acid encoding Fanconi anemia protein interactor, useful e.g.
XX for diagnosis, treatment and prevention of tumors and cytopenia.
XX
XX Discloure; Fig 4; 33pp; German.
XX
XX This invention describes a novel nucleic acid (I) encoding an interactor
XX of the Fanconi anemia protein of complementation group A (FAA), described
XX as FANCIPI. The products of the invention have antitumor and
XX anticypopenia activity. The protein encoded by (I) interacts with FAA,
XX and becomes part of the complex or signal transduction cascade that, when
XX defective, results in Fanconi anemia. (I) is used to express the
XX corresponding polypeptide (II) and this is used to raise specific
XX antibodies (Ab), or to identify compounds (A) that react with and/or
XX alter regions of (II). Compositions containing (I), vectors or cells that
XX contain (I), (II), Ab or (A) are used for diagnosis of disease associated
XX with defective DNA repair, cell-cycle aberrations, cytopenia,
XX tumorigenesis and/or tumor progression, or predisposition to the
XX disorders, and to treat or prevent the diagnosed disease, e.g. by gene
XX therapy. Modified forms of (I) are useful as antisense sequences and
XX ribozymes. This sequence represents a PCR primer used in the isolation of
XX the FAA interactor protein FANCIPI which is described in the method of
XX the invention
XX
SQ Sequence 20 BP; 6 A; 1 C; 11 G; 2 T; 0 U; 0 Other;
XX
Query Match 6.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 40;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
Qy 103 CCTCTCATTCCTCTCTCC 122
Db 20 CCTCTCATTCCTCTCTCC 1
XX
RESULT 52
AAK95233/C
ID AAK95232 standard; DNA; 20 BP.
XX
XX AAK95232;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human cDNA clone-specific primer, SEQ ID NO: 4477.
XX
XX Human; full length cDNA; cDNA synthesis; oligo-capping; PCR primer; ss.
XX
XX Homo sapiens.
XX
XX EP1130094-A2.
XX
XX 05-SEP-2001.
XX
XX 07-JUL-2000; 2000EP-00114089.
XX
XX 08-JUL-1999; 99JP-00194486.
XX
XX 11-JAN-2000; 2000JP-00118774.
XX
XX 02-MAY-2000; 2000JP-00183765.
XX
XX (HELI-) HELIX RES INST.
XX
XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
XX Wakematsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX MPI, 2001-524255/58.
XX

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```

PT 830 Primers useful for synthesizing full length cDNA clones and their use
XX in genetic manipulation.
XX
XX Example 18; Page 134; 1380pp + Sequence Listing; English.
XX
XX The invention relates to primers for synthesizing full length cDNA
XX clones. 830 cDNA molecules encoding a human protein have been isolated
XX and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
XX been determined. Primers for synthesizing the full length cDNA are useful
XX for clarifying the function of the protein encoded by the cDNA. The full
XX length clones were obtained by construction of full length enriched cDNA
XX libraries that were synthesised by the oligo-capping method. The primers
XX enable the production of the full length cDNA easily without any special
XX methods. The present sequence is a primer used to amplify a human cDNA
XX clone provided in the invention
XX
SQ Sequence 20 BP; 9 A; 4 C; 7 G; 0 T; 0 U; 0 Other;
XX
Query Match 6.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 40;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
Qy 141 TGCTCCCTCTCTCTCTG 160
Db 20 TGCTCCCTCTCTCTCTG 1
XX
RESULT 53
ABL45325/C
ID ABL45325 standard; DNA; 20 BP.
XX
XX ABL45325;
XX
XX 11-APR-2002 (first entry)
XX
XX Human chromosome 21q22.1 PCR primer SEQ ID NO:2369.
XX
XX Human chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
XX PCR primer; ss.
XX
XX Homo sapiens.
XX
XX JP2001321190-A.
XX
XX 20-NOV-2001.
XX
XX 12-MAR-2001; 2001JP-00068285.
XX
XX 10-MAR-2000; 2000JP-00066716.
XX
XX (RIKA ) RIKAGAKU KENKYUSHO.
XX (GENO-) GENOTEX YG.
XX
XX MPI, 2002-144136/19.
XX
XX Arraying genome clones.
XX
XX Claim 6; Page 52; 528pp; Japanese.
XX
XX The present invention describes a method of arraying genome clones. The
XX method comprises: (a) clones of the genomic libraries contained in
XX multiwell plates numbered for discrimination are mixed in each of the
XX multiwell plates; (b) a primer designed based on the chromosome marker
XX sequence is added to the mixture to carry out an amplification reaction;
XX (c) a signal corresponding to the marker is detected from the resultant
XX amplified product to specify the discrimination Nos. of the multiwell
XX plates containing the clones having said marker sequence; (d) the order
XX of the markers is changed so that the same discrimination Nos. succeed to
XX the maximum in the specified discrimination Nos. to array the multiwell
XX plates; (e) the clones in the multiwell plates of the specified
XX discrimination Nos. are mixed respectively in each wells of longitudinal
XX and lateral directions; (f) the mixed clones are cultured and the
XX resultant cultures are amplified by using the above primer; (g) signals
XX

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CC are detected from the amplified products; (h) the clones in the multiwell
 CC plates are specified from the detected result; and (i) the clones are
 CC reconstituted as the positions on the chromosome and arrayed. The
 CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent
 CC PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
 CC represent PCR primers for human chromosome 21q22.1, which are
 CC specifically claimed for use in the present invention
 XX
 SQ Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 U; 0 Other;
 Query Match 6.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 40;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 16 GGAGATCCCTCATGATCG 35
 Db 20 GGAGAGTCTCTCATGATCG 1
 RESULT 54
 ABV72231/c
 ID ABV72231 standard; DNA; 20 BP.
 XX
 AC ABV72231;
 XX
 DT 05-DEC-2002 (first entry)
 XX
 DB Antisense oligonucleotide targeting human IGF-II foetal mRNA.
 XX
 KW Antisense oligonucleotide; insulin-like growth factor II; IGF-II;
 KW tumour growth; proliferative disorder; cancer; psoriasis;
 KW atherosclerosis; ss.
 XX
 OS Homo sapiens.
 XX
 PN US6417169-B1.
 XX
 PD 09-JUL-2002.
 XX
 PF 22-APR-1999; 99US-002955593.
 XX
 PR 23-APR-1998; 98US-0082791P.
 XX
 PA (GENE-) GENESENSE TECHNOLOGIES INC.
 XX
 PI Wright JA, Young AH, Lee YS;
 XX
 DR WPI; 2002-634739/68.
 XX
 PT Novel antisense compounds targeted to insulin-like growth factor mRNA,
 PT useful for inhibiting tumor growth and metastasis in mammals.
 XX
 PS Claim 4; Col 10; 40pp; English.
 XX
 CC ABV7223-37 represent antisense oligonucleotides which are targeted to
 CC human insulin-like growth factor II (IGF-II) foetal mRNA. The
 CC oligonucleotides are complementary to the 5' untranslated region
 CC consisting of exons 4, 5 or 6 of human fetal IGF-II mRNA. The antisense
 CC oligonucleotides of the invention are useful for inhibiting the growth of
 CC human tumor, where a chemotherapeutic agent is also administered. They
 CC are also useful for treating proliferative disorders including various
 CC forms of cancer, psoriasis, and atherosclerosis, as hybridisation probes
 CC to detect the presence of IGF-II mRNA in mammalian cells, and as
 CC molecular weight markers
 XX
 SQ Sequence 20 BP; 5 A; 4 C; 11 G; 0 T; 0 U; 0 Other;
 Query Match 6.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 40;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 98 GGCCCTCTCATCTTCCTG 117
 ||||||| ||| |||||||

Db 20 GGCCCTCTCTTCTCCG 1
 RESULT 55
 ABL94297
 ID ABL94297 standard; DNA; 20 BP.
 XX
 AC ABL94297;
 XX
 DT 29-JUL-2002 (first entry)
 XX
 DE Human/mouse C/EBP beta antisense oligonucleotide, SEQ ID:63.
 XX
 KW Human; murine; C/EBP beta; CCAAT/enhancer-binding protein beta; C/EBP2;
 KW human; LAP; TCF5; CRP2; NF16; IL6BP; NF-M; AGP/EBP; Apc/EBP;
 KW transcription factor; tissue development; cellular function;
 KW proliferation; differentiation; hormone responsiveness;
 KW oxidative stress response; IL-6 signalling mediator; interleukin-6;
 KW carbohydrate metabolism; immunity; Th1 response; female fertility;
 KW glucocorticoids; ovarian; cancer; tumour formation; type II diabetes;
 KW infection; inflammation; expression inhibition; phosphorothioate;
 KW antisense oligonucleotide; ss.
 XX
 OS Homo sapiens.
 OS Mus musculus.
 XX
 FH Key
 FT modified_base 1..20 Location/Qualifiers
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate linkages"
 FT modified_base 1..5
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE
 FT cytosines are 5-methylcytosine"
 FT modified_base 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE
 FT cytosines are 5-methylcytosine"
 XX
 PN US6271030-B1.
 XX
 PD 07-AUG-2001.
 XX
 PF 14-JUN-2000; 2000US-00593711.
 XX
 PR 14-JUN-2000; 2000US-00593711.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Monia BP, Butler MM, Wyatt J;
 XX
 DR WPI; 2002-214451/27.
 XX
 PT Novel antisense compound targeted to nucleic acids encoding human or
 PT mouse CCAAT/enhancer binding protein (C/EBP) beta, useful in vitro for
 PT inhibiting expression of human or mouse C/EBP beta in cells/tissues.
 XX
 PS Claim 1; Col 43-44; 69pp; English.
 XX
 CC Sequences ABL94252-ABL94476 represent antisense oligonucleotides targeted
 CC to the human or mouse CCAAT/enhancer-binding protein alpha (C/EBP alpha)
 CC gene, which inhibit its expression. The antisense oligonucleotides were
 CC designed to target different regions of the human and/or mouse C/EBP
 CC alpha RNA, and were analysed for their effect on C/EBP alpha mRNA levels
 CC by quantitative real-time PCR. The C/EBP family of proteins are a family
 CC of transcription factors which regulate the expression of a wide range of
 CC genes that control normal tissue development, cellular function, cellular
 CC proliferation and functional differentiation. C/EBP beta (also known as
 CC C/EBP2, LAP, TCF5, CRP2, NF16, IL6BP, NF-M, AGP/EBP and Apc/EBP)
 CC primarily regulates hormone responsiveness and oxidative stress responses

CC and is a mediator of IL-6 (interleukin-6) signalling. C/EBP beta is
 CC thought to be involved in carbohydrate metabolism, immunity, the Th1
 CC response, female fertility and gluconeogenic pathways. C/EBP beta is
 CC expressed in the liver, lung, spleen, kidney, brain, and testis, with the
 CC highest expression found in the lung. It is also expressed at a higher
 CC level in malignant ovarian tissue compared with normal ovarian tissue,
 CC and its expression in pancreas is upregulated in response to chronically
 CC elevated levels of glucose, indicating that it is involved in the
 CC impairment of insulin secretion in type II diabetes. The oligonucleotides
 CC of the invention are useful for diagnosis, prevention and treatment of
 CC conditions associated with C/EBP beta expression, such as cancer
 CC (particularly ovarian cancer), tumour formation, diabetes (particularly
 CC type II diabetes), infection, or inflammation

SO Sequence 20 BP; 3 A; 9 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 6.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 40;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 133 GAGACAGCTGCTCCCTTC 152
 Db 1 GCGACAGCTGCTCCACCTTC 20

RESULT 56
 ABL94414
 ID ABL94414 standard; DNA; 20 BP.

AC ABL94414;
 XX
 XX 29-JUN-2002 (first entry)

DE Mouse C/EBP beta phosphorothioate antisense oligonucleotide, SEQ ID:180.

XX
 XX Mouse; murine; C/EBP beta; CCAAT/enhancer-binding protein beta; C/EBP2;
 KM LAP; TCF5; CRP2; NFIL6; IL6BP; NF-M; AGP/EBP; Apc/EBP;
 KM transcription factor; tissue development; cellular function;
 KM proliferation; differentiation; hormone responsiveness;
 KM oxidative stress response; IL-6 signalling mediator; interleukin-6;
 KM carbohydrate metabolism; immunity; Th1 response; female fertility;
 KM gluconeogenesis; ovarian cancer; tumour formation; type II diabetes;
 KM infection; inflammation; expression inhibition; phosphorothioate;
 KM antisense oligonucleotide; ss.

OS Mus musculus.

XX
 XX Key Location/Qualifiers
 FH modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate linkages"
 FT modified_base 1..5
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE
 FT cytosines are 5-methylcytosine"
 FT modified_base 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides. All 2' MOE
 FT cytosines are 5-methylcytosine"

XX
 XX US6271030-B1.
 XX
 XX 07-AUG-2001.
 XX
 XX 14-JUN-2000; 2000US-00593711.
 XX
 XX 14-JUN-2000; 2000US-00593711.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX

PI Monica BP, Butler MM, Wyatt J;
 XX
 XX WPI; 2002-214451/27.

DR
 XX
 XX Novel antisense compound targeted to nucleic acids encoding human or
 PT mouse CCAAT/enhancer binding protein (C/EBP) beta, useful in vitro for
 PT inhibiting expression of human or mouse C/EBP beta in cells/tissues.

XX
 XX Example 17; Col 51-52; 69pp; English.

PS
 XX
 XX Sequences ABL94252-ABL94476 represent antisense oligonucleotides targeted
 CC to the human or mouse CCAAT/enhancer-binding protein alpha (C/EBP alpha)
 CC gene, which inhibit its expression. The antisense oligonucleotides were
 CC designed to target different regions of the human and/or mouse C/EBP
 CC alpha RNA, and were analysed for their effect on C/EBP alpha mRNA levels
 CC by quantitative real-time PCR. The C/EBP family of proteins are a family
 CC of transcription factors which regulate the expression of a wide range of
 CC genes that control normal tissue development, cellular function, cellular
 CC proliferation and functional differentiation. C/EBP beta (also known as
 CC C/EBP2, LAP, TCF5, CRP2, NFIL6, IL6BP, NF-M, AGP/EBP and Apc/EBP)
 CC primarily regulates hormone responsiveness and oxidative stress responses
 CC and is a mediator of IL-6 (interleukin-6) signalling. C/EBP beta is
 CC thought to be involved in carbohydrate metabolism, immunity, the Th1
 CC response, female fertility and gluconeogenic pathways. C/EBP beta is
 CC expressed in the liver, lung, spleen, kidney, brain, and testis, with the
 CC highest expression found in the lung. It is also expressed at a higher
 CC level in malignant ovarian tissue compared with normal ovarian tissue,
 CC and its expression in pancreas is upregulated in response to chronically
 CC elevated levels of glucose, indicating that it is involved in the
 CC impairment of insulin secretion in type II diabetes. The oligonucleotides
 CC of the invention are useful for diagnosis, prevention and treatment of
 CC conditions associated with C/EBP beta expression, such as cancer
 CC (particularly ovarian cancer), tumour formation, diabetes (particularly
 CC type II diabetes), infection, or inflammation

SO Sequence 20 BP; 3 A; 9 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 6.4%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 40;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 136 ACACCTGCTCCCTTC 155
 Db 1 ACACCTGCTCCACCTTC 20

RESULT 57
 ABZ59163/C
 ID ABZ59163 standard; DNA; 20 BP.

AC ABZ59163;
 XX
 XX 28-APR-2003 (first entry)

DE Nucleotide sequence of antisense oligo r-invent102.

XX
 XX AChE; acetylcholinesterase; neuroprotective; relaxant; vasotropic;
 KM anticonvulsant; neuroleptic; gene therapy; antisense; rat; ss.

OS Synthetic.
 OS Rattus sp.

XX
 XX WO2003002739-A1.
 XX
 XX 09-JAN-2003.
 XX
 XX 23-MAY-2002; 2002WO-IL000411.
 XX
 XX 24-MAY-2001; 2001IL-00143379.
 XX
 XX (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
 XX
 XX Soreq H;
 XX

```

XX WPI; 2003-210276/20.
DR
XX
XX New composition comprising an the antisense oligodeoxynucleotide hEN101,
PT useful for treating or preventing a progressive neuromuscular disorder,
PT e.g. myasthenia gravis, Eaton-Lambert disease, muscular dystrophy or
PT sclerosis.
XX
XX Example; Page 37; 84pp; English.
PS
XX The invention relates to a pharmaceutical composition, which comprises an
CC antisense oligonucleotide hEN101 that inhibits the human AChE
CC (acetylcholinesterase) mRNA. The composition is for the treatment and/or
CC prevention of a progressive neuromuscular disorder, for improving
CC straining, and/or for use in chronic muscle fatigue. This composition
CC facilitates the passage of compounds through the blood-brain barrier
CC (BBB). It is useful for treating and/or preventing a progressive
CC neuromuscular disorder, particularly a disorder associated with an excess
CC of AChE mRNA or protein, an excess of acetylcholinesterase 'readthrough',
CC variant or isoform (AChE-R) mRNA, or impairment of cholinergic
CC transmission. The composition is also useful for treating and/or
CC preventing a progressive neuromuscular disorder involving muscle
CC distortion, muscle re-innervation or neuromuscular junction (NMJ)
CC abnormalities, e.g. myasthenia gravis, Eaton-Lambert disease, muscular
CC dystrophy, amyotrophic lateral sclerosis, post-traumatic stress disorder
CC (PTSD), multiple sclerosis, dystonia, post-stroke sclerosis, post-injury
CC muscle damage, excessive re-innervation, post-surgery paralysis of
CC unknown origin, or post-exposure to AChE inhibitors. The composition is
CC also useful for improving straining in physical exercise or in decreasing the
CC muscle fatigue. This is also useful for treating conditions affecting the
CC central nervous system, where the BBB would normally impede their
CC delivery, e.g. ischaemia, brain tumours, hypoxia, epilepsy, anxiety or
CC schizophrenia. The present sequence represents a rat AChE mRNA inhibiting
CC antisense oligo
XX
SQ Sequence 20 BP; 7 A; 0 C; 13 G; 0 T; 0 U; 0 Other;
Query Match 6.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 40;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 102 CCTCTCATTTCTCTGCTCC 121
Db 20 CCTCTCTCTCTCTCTCTCC 1
RESULT 58
ACCA4831/c
ID ACC4831 standard; DNA; 20 BP.
XX
XX ACC4831;
AC
XX 11-AUG-2003 (first entry)
DT
XX
DE Campylobacter jejuni wlaK gene PCR primer LS16.
XX
XX Infection; classification; glycosylation; wlaK gene; antibacterial; PCR;
KM primer; ss.
XX
XX Campylobacter jejuni.
OS
XX WO2003020958-A2.
PN
XX 13-MAR-2003.
PD
XX
XX 03-SEP-2002; 2002WO-EP009857.
PF
XX
XX 04-SEP-2001; 2001EP-00307499.
PR
XX
XX (EXPO-) EXPONENTIAL BIOTHERAPIES INC.
PA
XX Carleton RM, Wren BW;
PI
XX

```

```

DR WPI; 2003-300898/29.
XX
XX Producing progeny of bacteriophages having genes encoding proteinaceous
PT molecules allowing binding of the phage to Campylobacter spp, by
PT contacting phage with Campylobacter mutant devoid of component present in
PT wild-type.
XX
XX Example 1; Page 26; 66pp; English.
PS
XX The present sequence is PCR primer LS16 for the Campylobacter jejuni wlaK
CC gene. LS16 was used in the construction of an insertional knockout mutant
CC of the wlaK gene of C. jejuni NCTC 11168. Mutagenesis of the gene was
CC shown to disrupt binding by SBA lectin, and a role in protein
CC glycosylation was indicated. The invention relates to methods for the
CC detection, diagnosis and treatment or prevention of Campylobacter
CC infections, especially in poultry. A method is provided for producing or
CC selecting for progeny of phage comprising a nucleic acid encoding a
CC protein allowing targeting or binding of the phage to Campylobacter spp.
CC This involves contacting a phage library with a Campylobacter spp. mutant
CC devoid of a surface component present in the wild-type, e.g. a
CC glycosylated component. The phage can be used in the classification of a
CC C. jejuni variant, and in a pharmaceutical composition for treating a
CC Campylobacter infection
XX
SQ Sequence 20 BP; 3 A; 3 C; 8 G; 6 T; 0 U; 0 Other;
Query Match 6.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 40;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 117 GCTCCCACTTGTGATGAGA 136
Db 20 GCTCCCACTTGTGATGAGA 1
RESULT 59
ADG47261/c
ID ADG47261 standard; DNA; 20 BP.
XX
XX ADG47261;
AC
XX 11-MAR-2004 (first entry)
DT
XX
DE Human IGF-II antisense oligonucleotide #GRI4009.
XX
XX Insulin like growth factor II; IGF-II; tumour; metastasis; cytostatic;
KM gene therapy; antisense; human; ss.
XX
XX Homo sapiens.
OS
XX US2002187954-A1.
PN
XX 12-DEC-2002.
PD
XX
XX 17-APR-2002; 2002US-00125181.
PF
XX
XX 23-APR-1998; 98US-0082791P.
PR
XX 22-APR-1999; 99US-00295593.
XX
XX (GENE-) GENESENSE TECHNOLOGIES INC.
PA
XX Wright JA, Young AH, Lee YS;
PI
XX
XX WPI; 2004-040950/04.
DR
XX
XX Inhibiting the growth of a human tumor by administering a cytostatic
PT antisense oligonucleotide of twenty to one hundred nucleotides.
XX
XX Claim 7; SEQ ID NO 9; 41pp; English.
PS
XX The present invention relates to oligonucleotides complementary to
CC insulin like growth factor II (IGF-II) genes which modulate tumour cell
CC growth in mammals. The invention is useful for inhibiting the growth or

```


Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 110 TTCTCTGCTCCCACTCTG 129
 |||||
 Db 1 TTCTCTGCTCCCAATTGG 20

RESULT 62
 ID ADP12005/c
 ADP12005 standard; DNA; 20 BP.

AC ADP12005;
 DT 12-AUG-2004 (first entry)
 XX

DE Set 2 right PCR primer for marker probe #111.

XX transplant rejection; immune system; rheumatoid arthritis; lupus;
 KM inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss; primer.

XX Homo sapiens.

OS WO2004042346-A2.

PN 21-MAY-2004.

PD 24-APR-2003; 2003WO-US012346.

PF 24-APR-2002; 2002US-00131831.

PR 20-DEC-2002; 2002US-00325899.

XX (EXPR-) EXPRESSION DIAGNOSTICS INC.

XX Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
 PI Rosenberg S;

XX WPI; 2004-400724/37.

XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
 PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
 PT rejection, in an individual, comprises detecting the expression level of
 the genes.

PS Claim 58; SEQ ID NO 2014; 1762pp; English.

XX The present invention relates to diagnosing or monitoring transplant
 CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
 CC comprising detecting the expression level of one or more genes. The
 CC methods, system and kits are useful in diagnosing or monitoring
 CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
 CC islet, lung, bone marrow or stem cell transplant rejection,
 CC xenotransplant rejection or mechanical organ replacement rejection, in an
 CC individual. The method is also useful in assessing the immune status of
 CC an individual. The methods are also useful in diagnosing and monitoring
 CC diseases that involve the immune system, e.g. rheumatoid arthritis,
 CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
 CC viral, bacterial or fungal infection. The present sequence represents a
 CC primer for a 50 mer oligonucleotide marker for diagnosis and monitoring
 CC of allograft rejection and other disorders.

XX Sequence 20 BP; 6 A; 1 C; 11 G; 2 T; 0 U; 0 Other;

Query Match 6.4%; Score 15.2; DB 1; Length 20;

Best Local Similarity 85.0%; Pred. No. 40;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 134 AGACACCTGCTCCCTTCT 153
 |||||
 Db 20 AGACCCCTCTTCCCTTCT 1

RESULT 63
 ADP82177/c

ID ADP82177 standard; DNA; 20 BP.
 XX
 AC ADP82177;
 XX
 DT 26-AUG-2004 (first entry)
 XX

DE Human DRI-associated protein 1 target oligonucleotide #9.

XX DRI-associated protein 1; DRAP1; negative cofactor 2 alpha; NC2-alpha;
 KM developmental disorder; therapy; human; ss.

XX Homo sapiens.

OS US2004110703-A1.

PN 10-JUN-2004.

PD 10-DEC-2002; 2002US-00317279.

PF 10-DEC-2002; 2002US-00317279.

PR 10-DEC-2002; 2002US-00317279.

XX (ISIS-) ISIS PHARM INC.

XX Chiang M, Dobie KW;

PI WPI; 2004-440383/41.

XX New compounds, particularly oligonucleotides targeted to a nucleic acid
 PT encoding DRI-associated protein 1, useful for treating diseases
 PT associated with DRI-associated protein 1, e.g. developmental disorders.
 XX Example 15; SEQ ID NO 56; 33pp; English.

XX The present sequence is directed to antisense oligonucleotides targeted
 CC to DRI-associated protein 1 (also known as DRAP1 and negative cofactor 2
 CC alpha (NC2-alpha)) and which modulates to the expression of DRI-
 CC associated protein 1. The invention is useful for treating a disease or
 CC condition associated with DRI-associated protein 1 such as a
 CC developmental disorder. The present sequence is human DRI-associated
 CC protein 1 target oligonucleotide. This sequence is used in the
 CC exemplification of the invention.

PS Sequence 20 BP; 6 A; 3 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 6.4%; Score 15.2; DB 1; Length 20;

Best Local Similarity 85.0%; Pred. No. 40;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 108 CATTCTCTGCTCCCACTCT 127
 |||||
 Db 20 CATCTCTGCTCCGACTCT 1

RESULT 64
 ID ADP82163
 ADP82163 standard; DNA; 20 BP.

AC ADP82163;

XX 26-AUG-2004 (first entry)

DE Human DRI-associated protein 1 antisense oligonucleotide ISIS #171311.

XX DRI-associated protein 1; DRAP1; negative cofactor 2 alpha; NC2-alpha;

KM developmental disorder; therapy; human; antisense;

XX phosphorothioate backbone; ss.

OS Homo sapiens.

OS Synthetic.

Key Location/Qualifiers
 modified_base 1..20
 /*tag= b

FT	/mod_base= OTHER
FT	/note= "Phosphorothioate backbone where all cytidines are
FT	5-methyl cytidines"
FT	modified_base
FT	1..5
FT	/*tag= a
FT	/mod_base= OTHER
FT	/note= "2' -methoxyethyl nucleotides"
FT	16..20
FT	/*tag= c
FT	/mod_base= OTHER
FT	/note= "2' -methoxyethyl nucleotides"
PX	
PN	US2004110703-A1.
PD	10-JUN-2004.
PX	
PF	10-DEC-2002; 2002US-00317279.
PX	
PR	10-DEC-2002; 2002US-00317279.
PX	
PA	(ISIS-) ISIS PHARM INC.
PX	
PI	Chiang M, Doble KW;
PX	
DR	WPI; 2004-440383/41.
PX	
PT	New compound, particularly oligonucleotides targeted to a nucleic acid
PT	encoding DRI-associated protein 1, useful for treating diseases
PT	associated with DRI-associated protein 1, e.g. developmental disorders.
PX	
PS	Example 15; SEQ-ID NO 42; 33pp; English.
PX	
CC	The present sequence is directed to antisense oligonucleotides targeted
CC	to DRI-associated protein 1 [also known as DRAP1 and negative cofactor 2
CC	alpha (NC-alpha)] and which modulates to the expression of DRI-
CC	associated protein 1. The invention is useful for treating a disease or
CC	condition associated with DRI-associated protein 1 such as a
CC	developmental disorder. The present sequence is human DRI-associated
CC	protein 1 antisense oligonucleotide. This sequence is used in the
XX	exemplification of the invention.
SQ	
Sequence	20 BP; 2 A; 9 C; 3 G; 6 T; 0 U; 0 Other;
Query Match	6.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity	85.0%; Pred.No. 40;
Matches	17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY	
108	CATTCTCCTGCTCCACTCT 127
DB	
1	CATCTCCTGTGCAGTCT 20
ID	AEC34439/C
RESULT 65	
AEC34439/C	
ID	AEC34439 standard; DNA; 20 BP.
AC	AEC34439;
DT	17-NOV-2005 (first entry)
DE	Human EGFR regulatory region SNP detection primer SEQ ID NO:10.
KM	SS; primer; PCR; Epidermal growth factor receptor; EGFR; cancer;
KM	cystostatic; neoplasm; polymorphism; diagnostic.
OS	Homo sapiens.
PN	WO2005085473-A2.
PD	15-SEP-2005.
PF	01-MAR-2005; 2005WO-US006559.

PR	01-MAR-2004; 2004US-0549069P.
XX	(UTCH-) UNIV CHICAGO.
PA	
XX	
PI	Ratain MJ, Liu W, Innocenti F;
XX	
DR	WPI, 2005-630736/64.
XX	
PT	Evaluating potential efficacy of epidermal growth factor receptor (EGFR) -
PT	targeting therapeutic agent for treating cancer or disease associated
PI	with dysregulation of EGFR, by determining sequence of polymorphism in
XX	EGFR genes in patient.
XX	
PS	Example 1; SEQ ID NO 10; 66bp; English.
XX	
CC	The invention relates to a method of evaluating (M1) the potential
CC	efficacy of an epidermal growth factor receptor (EGFR)-targeting
CC	therapeutic agent for treating cancer or a disease associated with the
CC	regulation of EGFR in a patient, comprising determining the sequence of a
CC	polymorphism in one or both EGFR genes in the patient. Also included are:
CC	predicting (M2) the clinical prognosis for a cancer patient, comprising
CC	determining the sequence of a polymorphism in one or both EGFR genes in
CC	the patient; evaluating (M3) a patient's risk of toxicity to an EGFR-
CC	targeting therapeutic agent, comprising determining the sequence of a
CC	polymorphism in one or both EGFR genes in the patient; predicting the
CC	expression level of EGFR in a cell, comprising determining the sequence
CC	at position 216 in one or both alleles of the EGFR gene in the cell,
CC	where thymine at position 216 in one or both alleles is indicative of a
CC	higher expression level; and a kit for performing (M1), comprising a
CC	nucleic acid, or restriction enzyme for determining the sequence of a
CC	polymorphism in an EGFR gene locus. (M1) is useful for evaluating the
CC	potential efficacy of EGFR-targeting therapeutic agent, where the EGFR-
CC	targeting therapeutic agent is an EGFR-tyrosine kinase inhibitor or
CC	monoclonal antibody. The present sequence represents a PCR primer used to
CC	detect single nucleotide polymorphisms (SNPs) in the human EGFR
CC	regulatory region.
XX	
SEQ	Sequence 20 BP; 7 A; 1 C; 11 G; 1 T; 0 U; 0 Other;
XX	
Query Match	6.4%; Score 15.2; DB 1; Length 20;
Best Local Similarity	85.0%; Pred. No. 40;
Matches	17; Conservative 0; Mismatches 3; Indels 0; Gaps 0.
QY	101 CCCCTTCATCTCTCTGCTC 120
DB	20 CTCCTCGCATCTCTCTCTC 1
RESULT 66	
AAQ08505/C	
ID	AAQ08505 standard; DNA; 21 BP.
XX	
AC	AAQ08505;
XX	
DT	25-MAR-2003 (revised)
DT	29-MAR-1992 (first entry)
XX	
DE	Sequence of 5' probe, complementary to a sequence encoding part of the
DE	human interleukin-3 (huIL-3) leader.
XX	
KW	Lymphokine; bone marrow proliferation; cytopenia therapy; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO9001039-A.
XX	
PD	08-FEB-1990.
XX	
PF	14-JUN-1989; 89WO-US002599.
XX	
FR	20-JUL-1988; 88US-00221699.
XX	
PA	(IMMV) IMMUNEX CORP.

```

XX Anderson DM, Cosman DJ, Price VL;
PI WPI; 1990-067162/09.
XX
XX Compens. contg. recombinant non-glycosylated human interleukin-3 - has
PT increased biological activity and binding affinity, for treating
PT cytopenias.
XX
XX Example; Page 10; 23pp; English.
XX
XX The inventors claim a pharmaceutical compsn. which contains an effective
CC amt. of a recombinant human interleukin-3 protein analogue, rhIL-3,
CC (Asp15, Asp70). The rhIL-3 analogue has AA SQ in AAR09326. The compsn.
CC may also comprise the N-terminal octapeptide in AAR09327, and a diluent
CC and 1 or more than 1 biological response modifier. The compsn. has a
CC biological specific activity of equal to or more than 4.0 x 10 to the 7
CC mcg/mg in a human bone marrow proliferation assay, and a binding affinity
CC for human monocyte IL-3 receptors of equal to or more than 4.0 x 10 to
CC the 10 (M to the minus 1). (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 21 BP; 6 A; 3 C; 10 G; 2 T; 0 U; 0 Other;

Query Match      6.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 107 TCATTCCTCCGCTCCCACTC 126
Db 20 TCCTGCTCTGCTCCCACTC 1

RESULT 67
AAQ10344/C
ID AAQ10344 standard; DNA; 21 BP.
XX
XX AAQ10344;
XX
XX 25-MAR-2003 (revised)
DT 10-APR-1991 (first entry)
XX
XX Probe to the human interleukin-3 gene.
XX
XX huIL-3; urticaria; granulopoesis; erythropoesis; thrompoeosis;
KM neutropaenia; anaemia; thrombocytopenia; ss.
XX
XX Homo sapiens.
OS
XX
XX WO9100350-A.
PN
XX
XX 10-JAN-1991.
PD
XX
XX 30-JUN-1989; 89US-00374667.
PF
XX
XX 30-JUN-1989; 89US-00374667.
PR
XX
XX (IMMV ) IMMUNEX CORP.
PA
XX
XX Urdal DL, Sassenfeld H;
PI
XX
XX WPI; 1991-036745/05.
XX
XX Non-glycosylated human interleukin-3 analog proteins - expressed by
PT transformed yeast of Saccharomyces cerevisiae which do not give
PT detectable urticaria.
XX
XX Example A; Page 7; 18pp; English.
XX
XX Probes were used in the isolation of human IL-3, which was then expressed
CC in a modified form, with a mutation in the N-glycosylation sites. The
CC modified IL-3 does not result in urticaria or infiltration of mast cells
CC and lymphocytes into the dermis. It stimulates granulopoesis,
CC erythropoesis and thrompoeosis in vivo and may used to treat

```

```

CC neutropaenia, anaemia and thrombocytopenia. (Updated on 25-MAR-2003 to
CC correct PA field.)
XX
XX Sequence 21 BP; 6 A; 3 C; 10 G; 2 T; 0 U; 0 Other;
SQ

Query Match      6.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 107 TCATTCCTCCGCTCCCACTC 126
Db 20 TCCTGCTCTGCTCCCACTC 1

RESULT 68
AAQ42803/C
ID AAQ42803 standard; cDNA; 21 BP.
XX
XX AAQ42803;
XX
XX 25-MAR-2003 (revised)
DT 15-SEP-1993 (first entry)
XX
XX Human IL-3 probe.
DE
XX
XX Mast cell growth factor; interleukin; haematopoietic progenitor cell;
KM bone marrow cell; proliferation; differentiation; functional activation;
KW peripheral blood leukocyte; circulating granulocyte; ss.
XX
XX Synthetic.
XX
XX WO9310229-A1.
PN
XX
XX 27-MAY-1993.
PD
XX
XX 19-NOV-1992; 92WO-US009848.
PF
XX
XX 22-NOV-1991; 91US-00797553.
PR
XX
XX (IMMV ) IMMUNEX CORP.
PA
XX
XX Williams DE;
PI
XX
XX WPI; 1993-182546/22.
XX
XX MGF-Interleukin-3 fusion proteins having enhanced activity - used for
PT regulating immune and inflammatory responses.
PT
XX
XX Example 1; Page 17; 41pp; English.
XX
XX Two oligonucleotides were synthesised, with sequences complementary to
CC selected 5' and 3' sequences of the huIL-3 gene. The 5' probe, has the
CC complementary to a sequence encoding part of the huIL-3 leader, has the
CC sequence given in AAQ42803. The 3' probe, corresp. to a region encoding
CC amino acids 123-130 of the mature protein, has the sequence given in
CC AAQ42804. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 21 BP; 6 A; 3 C; 10 G; 2 T; 0 U; 0 Other;

Query Match      6.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 107 TCATTCCTCCGCTCCCACTC 126
Db 20 TCCTGCTCTGCTCCCACTC 1

RESULT 69
AAZ61533/C
ID AAZ61533 standard; DNA; 21 BP.
XX
XX AAZ61533;
AC

```

XX	19-JUN-2000	(first entry)
DT		
XX		
DE	Primer 6U for a human 5'-OT EST (oxytocin expressed sequence tag).	
KM	Oxytocin expressed sequence tag; 5'-OT EST; obesity; fertility; male;	
KM	transgenic animal; human late onset obesity; late onset visceral obesity;	
KM	male infertility; wasting; anorexia; cachexia; malabsorptive state;	
KM	catabolic state; inflammatory condition; Crohn's disease; AIDS wasting;	
KM	burn; cancer; bone disease; PCR primer; probe; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200009686-A1.	
PD		
XX	24-FEB-2000.	
PF	12-AUG-1999; 99WO-GB002658.	
PR	12-AUG-1998; 98GB-00017566.	
PR	06-MAY-1999; 99GB-00010522.	
XX		
PA	(MED1-) MEDICAL RES COUNCIL.	
XX		
PI	Robinson ICAF, Stoye JP, Flavell D, Wells SE, Le Tissier P;	
DR	WPI; 2000-224331/19.	
PT	New anti-obesity polypeptide useful for treating obesity or infertility	
PT	in mammals.	
XX		
PS	Disclosure; Page 26; 162pp; English.	
XX		
CC	PCR primers and probes AAZ61533-34 are used to amplify and identify human	
CC	5'-OT-EST (oxytocin expressed sequence tag) cDNA sequences. The 5'-OT EST	
CC	gene is involved in the control of obesity and fertility in males. 5'-OT	
CC	EST nucleic acids are useful for producing transgenic animals. The	
CC	transgenic animals created serve as a model for human late onset obesity	
CC	and other related disorders and are also used for identifying the genetic	
CC	cause of obesity. Compounds which modulate 5'-OT EST expression or	
CC	activity are useful in the treatment or modulation of late onset visceral	
CC	obesity or male infertility particularly in the disorders related to	
CC	these conditions such as wasting, or anorexia, or cachexia associated	
CC	with prolonged illness, or malabsorptive states or catabolic states	
CC	associated with other diseases such as inflammatory conditions, Crohn's	
CC	disease or AIDS wasting, or burns, or cancer, or bone disease	
XX		
SO	Sequence 21 BP; 6 A; 3 C; 12 G; 0 T; 0 U; 0 Other;	
	Query Match 6.4%; Score 15.2; DB 1; Length 21;	
	Best Local Similarity 85.0%; Pred. No. 39;	
	Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0	
OY	139 CCTGCTCCCGCTTCCTTC 158	
DB	20 CCTGCTCCCGCTTCCTTC 1	
	RESULT 70	
	ADP29145	
ID	ADP29145 standard; DNA; 21 BP.	
XX		
AC	ADP29145;	
XX		
DT	12-AUG-2004 (first entry)	
XX		
DE	Human secreted protein encoding sequence SEQ ID #1143.	
XX		
KM	Cycostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;	
KM	cancer; Inflammatory; Immune; ds; human secreted protein.	
XX		
OS	Homo sapiens.	
XX		

PN	W02.004.035732-A2.
PD	
XX	29-APR-2004.
PF	28-AUG-2003; 2003WO-US026780.
XX	
PR	29-AUG-2002; 2002ZUS-04065676P
PR	29-AUG-2002; 2002ZUS-0406579P
PR	29-AUG-2002; 2002ZUS-0406585P
PR	29-AUG-2002; 2002ZUS-0406588P
PR	29-AUG-2002; 2002ZUS-0406608P
PR	29-AUG-2002; 2002ZUS-0406611P
PR	29-AUG-2002; 2002ZUS-0406612P
PR	29-AUG-2002; 2002ZUS-0406616P
PR	29-AUG-2002; 2002ZUS-0406640P
PR	29-AUG-2002; 2002ZUS-0406642P
PR	29-AUG-2002; 2002ZUS-0406646P
PR	29-AUG-2002; 2002ZUS-0406653P
PR	29-AUG-2002; 2002ZUS-0406655P
PR	29-AUG-2002; 2002ZUS-0406666P
PR	17-SEP-2002; 2002ZUS-0410946P
PR	17-SEP-2002; 2002ZUS-0410947P
PR	17-SEP-2002; 2002ZUS-0410958P
PR	17-SEP-2002; 2002ZUS-0410959P
PR	17-SEP-2002; 2002ZUS-0410960P
PR	17-SEP-2002; 2002ZUS-0410962P
PR	17-SEP-2002; 2002ZUS-0411019P
PR	17-SEP-2002; 2002ZUS-0411022P
PR	17-SEP-2002; 2002ZUS-0411023P
PR	17-SEP-2002; 2002ZUS-0411032P
PR	17-SEP-2002; 2002ZUS-0411035P
PR	17-SEP-2002; 2002ZUS-0411037P
PR	17-SEP-2002; 2002ZUS-0411041P
PR	17-SEP-2002; 2002ZUS-0411045P
PR	17-SEP-2002; 2002ZUS-0411046P
PR	17-SEP-2002; 2002ZUS-0411048P
PR	17-SEP-2002; 2002ZUS-0411052P
PR	17-SEP-2002; 2002ZUS-0411055P
PR	17-SEP-2002; 2002ZUS-0411073P
PR	17-SEP-2002; 2002ZUS-0411082P
PR	17-SEP-2002; 2002ZUS-0411101P
PR	17-SEP-2002; 2002ZUS-0411111P
PR	18-APR-2003; 2003ZUS-0463700P
PR	18-APR-2003; 2003ZUS-0463708P
PR	18-APR-2003; 2003ZUS-0463716P
PR	18-APR-2003; 2003ZUS-0463719P
PR	02-MAY-2003; 2003ZUS-0467201P
PR	02-MAY-2003; 2003ZUS-0467203P
PR	02-MAY-2003; 2003ZUS-0467230P
PR	19-MAY-2003; 2003ZUS-0471336P
PR	19-MAY-2003; 2003ZUS-0471336P
PR	22-MAY-2003; 2003ZUS-0472420P
PR	02-JUN-2003; 2003ZUS-0472430P
PR	09-JUN-2003; 2003ZUS-0476609P
PR	09-JUN-2003; 2003ZUS-0476641P
PR	08-JUL-2003; 2003ZUS-0485218P
PR	08-JUL-2003; 2003ZUS-0485223P
PR	08-JUL-2003; 2003ZUS-0485224P
PR	08-JUL-2003; 2003ZUS-0485252P
PR	14-JUL-2003; 2003ZUS-0486446P
PR	14-JUL-2003; 2003ZUS-0486480P
PR	15-JUL-2003; 2003ZUS-0486691P
PR	08-AUG-2003; 2003ZUS-0486660P
PR	08-AUG-2003; 2003ZUS-0493341P
PR	08-AUG-2003; 2003ZUS-0493370P
PR	08-AUG-2003; 2003ZUS-0493373P

PR 08-AUG-2003; 2003US-0493577P.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
PI Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D,
PI Halenbeck RF, Huang WM, Kochakota S, Halshan L, Linnemann T,
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
DR WPI; 2004-348438/32.
XX
XX
XX New nucleic acid molecule for diagnosing, preventing or treating diseases
PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,
PT genetic, bacterial and viral diseases.
XX
XX
XX Claim 1; SEQ ID NO 1143; 428bp; English.
XX
XX The present invention relates to an isolated nucleic acid molecule
CC encoding a polypeptide which is believed to be cytostatic,
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The
CC composition and methods are useful for diagnosing, preventing and
CC treating diseases such as proliferative (e.g. cancer), inflammatory,
CC immune, metabolic, genetic, bacterial and viral diseases. The present
CC sequence represents a human secreted protein encoding sequence. The
CC present sequence is available on WIPOMED and is not in the specification.
XX
XX
SQ Sequence 21 BP; 1 A; 13 C; 0 G; 7 T; 0 U; 0 Other;
Query Match 6.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 139 CCTGCTCCCTCTCTCTTC 158
Db 1 CCTCTCTCTCTCTCTTC 20
RESULT 71
ADU26666
ID ADU26666 standard; DNA; 21 BP.
XX
XX
XX ADU26666;
XX
XX 27-JAN-2005 (first entry)
XX
XX Knock-down target sequence #64.
XX
XX de; RNA production; protein production; drug development;
XX knock-down target.
XX
XX Unidentified.
XX
XX
XX WO2004094636-A1.
XX
XX 04-NOV-2004.
XX
XX 24-APR-2003; 2003WO-EP004362.
XX
XX 24-APR-2003; 2003WO-EP004362.
XX
XX 24-APR-2003; 2003WO-EP004362.
XX
XX (GALA-) GALAPAGOS GENOMICS NV.
XX PA (VSCH/) VAN DER SCHUREN J.
XX
XX Arts GJF, Lambrecht WJ, Djokic K, Clasen RJ, Meisic E;
PI Griffioen S, Berge CUI;
XX
XX WPI; 2004-775940/76.
XX
XX
XX New knockdown sequences, useful in lowering the amount of RNA and/or
PT protein production in cells used in drug development process.
XX
XX
XX Claim 11; SEQ ID NO 67; 402bp; English.
XX
XX The invention relates to a polynucleotide comprising an RNA sequence. The

CC polynucleotides, vector, libraries, and method are useful in lowering the
CC amount of RNA and/or protein production in cells used in drug development
CC process. The present sequence represents a knock-down target sequence.
XX
XX
SQ Sequence 21 BP; 5 A; 3 C; 7 G; 6 T; 0 U; 0 Other;
Query Match 6.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 24 CCTCATGATGGTTTACTGC 43
Db 2 CATCATGACGGTTTACTGC 21
RESULT 72
ACT41023/c
ID ACT41023 standard; DNA; 21 BP.
XX
XX
XX ACT41023;
XX
XX 24-MAR-2005 (first entry)
XX
XX
XX C20orf103 target oligonucleotide, SEQ ID 2095.
XX
XX
XX Cytostatic; Gene therapy; Vaccine; RNA Interference; cancer; ss.
XX
XX
XX Homo sapiens.
XX
XX WO200501092-A2.
XX
XX 06-JAN-2005.
XX
XX 19-MAY-2004; 2004WO-US015645.
XX
XX 20-MAY-2003; 2003US-0471729P.
XX
XX (AMHP) WYETH.
XX
XX Be X, Wei L, Slonim DK, Howes SH;
XX
XX WPI; 2005-075568/08.
XX
XX
XX Pharmaceutical composition comprising an agent capable of modulating an
PT expression level or protein activity of a gene, e.g. ABCC4, or a T cell
PT activated by the polypeptide or antibody, and a carrier, useful for
PT treating cancer.
XX
XX
XX Claim 3; SEQ ID NO 2095; 113bp; English.
XX
XX
XX The present invention relates to a novel pharmaceutical composition
CC comprising: (a) an agent capable of modulating an expression level or
CC protein activity of a cancer-related transmembrane protein (CRTP) or gene
CC ; an antibody specific for a CRTP, or a T cell activated by a CRTP; and
CC (b) a carrier. The pharmaceutical composition may also comprise a
CC polynucleotide capable of inhibiting or decreasing the expression of the
CC CRTP by RNA interference or an antisense mechanism. The CRTPs of the
CC invention are selected from ABCC4, C20orf103, CACNA1D, CDH6, CST, ENPP3,
CC FLJ11856, GPR54, HAVCR1, SLC6A3, SLC30A4, TRG, and TRPM4. The
CC pharmaceutical composition is useful for treating cancer, e.g. colon
CC cancer, lung cancer, breast cancer, prostate cancer, liver cancer, kidney
CC cancer, stomach cancer, and esophageal cancer. The present sequence is a
CC target oligonucleotide from one such CRTP for which short interfering
CC RNAs (siRNA) were produced. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX
SQ Sequence 21 BP; 9 A; 3 C; 7 G; 2 T; 0 U; 0 Other;
Query Match 6.4%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 39;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 146 CCCCTTCCTCTGCATG 165
 |||||
 DB 20 CCACCTTCCTCTGCATG 1

RESULT 73

AD219613
 ID AD219613 standard; RNA; 21 BP.

AC AD219613;

DT 16-JUN-2005 (first entry)

DE Human siRNA targeted against the human PIK3CB gene Seq 497.

XX screening; synthetic lethal interaction; RNA interference;
 KW gene silencing; siRNA; short interfering RNA; tumor suppressor; cancer;
 KW cytostatic; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT misc_feature 20..21

FT /*tag= a /note= "dtrr dinucleotide to enhance siRNA binding"

XX WO2005031002-A2.

XX 07-APR-2005.

XX 22-SEP-2004; 2004WO-US031629.

XX 22-SEP-2003; 2003US-0505229P.

XX 27-FEB-2004; 2004US-0546568P.

XX 17-MAR-2004; 2004US-0554284P.

XX (ROSE-) ROSETTA INPHARMATICS LLC.

XX (MERI) MERCK & CO INC.

XX Lineley PS, Mao M, Kim AS, Friend SH, Bartz SR, Cleary MA;

XX WPI; 2005-273396/28.

XX Example 3; SEQ ID NO 497; 284bp; English.

CC This invention relates to a novel screening method for identifying a gene
 CC whose product modulates the effect of an agent on a cell of a cell type.
 CC Specifically, it refers to identifying lethal/ synthetic lethal
 CC interactions between a gene (or its product) and an agent such as a drug,
 CC using RNA interference. The present invention describes screening of an
 CC siRNA library for genes that interact with inhibitors of the KSP gene
 CC (kinesin-like motor protein gene). In particular it illustrates STX6 and
 CC TP53 as two genes that each independently exhibit synthetic lethal
 CC interactions with KSP such that they can be used therapeutically to
 CC inhibit tumor cell growth and hence for the treatment of cancer. The
 CC invention further describes RNAi-mediated silencing of the CHEK1 and TP53
 CC genes that leads to synthetic lethality in human tumor cells. It also
 CC provides semi-automated siRNA screens for the identification of cellular
 CC response genes that enhance or reduce cell killing by DNA damaging
 CC agents. Accordingly, compositions derived thereof be used therapeutically
 CC such that they exhibit cytostatic activity. This oligonucleotide sequence
 CC is an siRNA oligo that was used to identify a human gene that enhances
 CC cell killing by DNA damaging agents (doxorubicin screen), given in an
 CC exemplification of the invention.

XX Sequence 21 BP; 4 A; 3 C; 7 G; 2 T; 5 U; 0 Other;

Query Match 6.4%; Score 15.2; DB 1; Length 21;
 Best Local Similarity 65.0%; Pred. No. 39;

Matches 13; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 OY 64 AGTTACCTGAGAGCTGTT 83
 |||||
 DB 2 AGUUCAGUCAGAGCUGCTT 21

RESULT 74

AEC02602
 ID AEC02602 standard; DNA; 21 BP.

AC AEC02602;

DT 03-NOV-2005 (first entry)

DE Human IGE short interfering nucleic acid SEQ ID NO 205.

XX antiallergic; antiinflammatory; antiasthmatic; dermatological;
 KW immunosuppressive; expression; RNA interference; allergy;
 KW atopic dermatitis; urticaria; dermatological; dermatological disease;
 KW immediate type hypersensitivity; immunosuppressive; asthma;
 KW antiasthmatic; allergic rhinitis; antiallergic; antiinflammatory;
 KW ear, nose, throat disease; inflammation; respiratory disease;
 KW immune disorder; IGE; short interfering nucleic acid; siNA;
 KW gene silencing; ss.

XX Homo sapiens.

XX WO2005080410-A1.

XX 01-SEP-2005.

XX 21-FEB-2005; 2005WO-NZ000021.

XX 20-FEB-2004; 2004US-0546434P.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX Watson JD, Morrison GJ, Grigor MR, Havukkala IU, Munro G;

XX Abernethy N, Webster G;

XX WPI; 2005-591970/60.

XX New composition comprises small interfering nucleic acid molecule (siNA)
 PT capable of reducing expression of a target gene that is active in a IGE-
 PT mediated disorder, useful for treating, e.g. allergic rhinitis or atopic
 PT dermatitis.

XX Disclosure; SEQ ID NO 205; 178bp; English.

XX The invention describes a composition comprising a small interfering
 CC nucleic acid molecule (siNA) capable of reducing expression of a target
 CC gene that is active in a IGE-mediated disorder, a genetic construct that
 CC expresses the siNA, and a binding agent that specifically binds to a
 CC target antigen expressed on the surface of the cell. Also described are:
 CC a method for the treatment of an IGE-mediated disorder in a patient;
 CC prevention of IGE-mediated disorder in a patient; reduction of
 CC eosinophilia in a patient; modulating an IGE-mediated immune response to
 CC a specific antigen in a patient; and preventing or reducing the severity
 CC of an immune response to a specific antigen in a patient. The composition
 CC is useful in the preparation of a medicament useful for the treatment of
 CC an IGE-mediated disorder, e.g. allergic rhinitis, asthma, anaphylaxis,
 CC urticaria, atopic dermatitis, food allergies, diseases that benefit from
 CC the reduction of eosinophilia in the tissues of the respiratory system,
 CC or disorders having hypersensitivity immune reaction. This sequence
 CC represents a siNA for suppression of human IGE expression.

XX Sequence 21 BP; 3 A; 7 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 6.4%; Score 15.2; DB 1; Length 21;
 Best Local Similarity 85.0%; Pred. No. 39;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 31 AATGGTTAGTGCATCCCC 50
 CC ||||| ||||| ||||| |||||
 Db 2 AATGGCTTGCTCCTCC 21

RESULT 75
 ID AEC30534 standard; DNA; 21 BP.
 XX AEC30534;
 AC AEC30534;
 DT 17-NOV-2005 (first entry)
 XX
 DE Human locus-specific oligonucleotide #1822.
 XX
 KM Haploctype mapping; genetic marker; single nucleotide polymorphism; SNP;
 KM major histocompatibility complex; MHC; HLA; human leukocyte antigen;
 KM immune disorder; inflammation; inflammatory bowel disease;
 KM ulcerative colitis; Crohn's disease; rheumatoid arthritis; diabetes;
 KM diabetes mellitus; myasthenia gravis; vitiligo; Graves disease;
 KM Hashimoto's disease; Addison's disease; gastritis; autoimmune hepatitis;
 KM rheumatism; systemic lupus erythematosus; scleroderma; polymyositis;
 KM dermatomyositis; pernicious anemia; primary biliary cirrhosis;
 KM idiopathic thrombocytopenia purpura; Sjogrens syndrome;
 KM multiple sclerosis; Reiter's syndrome; psoriasis; anti-inflammatory;
 KM galectinase-1-gen.; anticancer; immunomodulator; immunosuppressive;
 KM antiarthritic; antirheumatic; antidiabetic; muscular-gen.;
 KM neuroprotective; dermatological; antihypertic; hepatotropic; anti-anemic;
 KM hemostatic; ophthalmological; uropathic; antipsoriatic; ss;
 KM SNP detection.
 XX
 OS Homo sapiens.
 XX
 PN WO2005082110-A2.
 XX
 PD 09-SEP-2005.
 XX
 PF 28-FEB-2005; 2005WO-US006628.
 XX
 PR 26-FEB-2004; 2004US-0547823P.
 XX
 PA (ILLU-) ILLUMINA INC.
 XX
 PI Oliphant A, Murray S;
 XX
 DR WPI; 2005-638856/65.
 XX
 PT Identifying single nucleotide polymorphism (SNP) haplotype that
 PT correlates with the HLA type, useful for diagnosing an immunological or
 PT inflammatory condition, comprises providing SNPs in the major
 PT histocompatibility complex region.
 XX
 PS Example 1; SEQ ID NO 6554; 175bp; English.
 XX
 CC The invention relates to a method of identifying the nucleotide for each
 CC of a set of single nucleotide polymorphisms (SNPs) in the major
 CC histocompatibility complex (MHC) region in a population of individuals,
 CC comprising providing the HLA type for the individuals and identifying an
 CC SNP haplotype in the population that correlates with the HLA type, where
 CC the SNP haplotype comprises the SNPs in the MHC region. The invention
 CC also relates to a method of predicting the HLA type of an individual, a
 CC method of determining the presence or absence of an allelic variant of an
 CC MHC gene in an individual, a method of identifying an SNP haplotype that
 CC correlates with susceptibility to a disease or condition, and a method of
 CC determining the susceptibility of an individual to a disease or
 CC condition. The disease or condition is an immune disorder or inflammatory
 CC condition selected from inflammatory bowel disease, ulcerative colitis,
 CC Crohn's disease, rheumatoid arthritis, diabetes, diabetes mellitus,
 CC myasthenia gravis, vitiligo, Graves disease, Hashimoto's disease,
 CC Addison's disease, gastritis, autoimmune hepatitis, rheumatism, systemic
 CC lupus erythematosus, systemic sclerosis, polymyositis, dermatomyositis,
 CC pernicious anemia, primary biliary cirrhosis, idiopathic thrombocytopenia
 CC purpura, Sjogren's syndrome, multiple sclerosis, Reiter's syndrome and

CC psoriasis. This sequence represents a human locus-specific
 CC oligonucleotide used in the scope of the invention.
 XX
 SQ Sequence 21 BP; 8 A; 6 C; 3 G; 4 T; 0 U; 0 Other;
 CC
 CC Query Match 6.4%; Score 15.2; DB 1; Length 21;
 CC Best Local Similarity 85.0%; Pred. No. 39;
 CC Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 CC

Oy 174 ATTCCAGGAGCTTCACAGA 193
 CC ||||| ||||| ||||| |||||
 Db 1 ATTCCAGAGCTTCACAGA 20

RESULT 76
 ID AAT72472/C
 XX AAT72472 standard; DNA; 20 BP.
 XX
 AC AAT72472;
 XX
 DT 29-SEP-1997 (first entry)
 XX
 DE Human CII-3 gene exon A primer HuPS1.Forw1.
 XX
 KM Mammalian artificial chromosome; MAC; selectable marker; CII-3;
 KM mitochondrial electron transport chain complex II; transgenic animal;
 KM polymerase chain reaction; PCR; primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO9716533-A1.
 XX
 PD 09-MAY-1997.
 XX
 PF 29-OCT-1996; 96WO-US017476.
 XX
 PR 31-OCT-1995; 95US-00550717.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Scheffler IE;
 XX
 DR WPI; 1997-272103/24.
 XX
 PT New mammalian artificial chromosomes - comprising a mammalian centromere
 PT and a unique cloning site, used for stable expression of large fragments
 PT of DNA.
 XX
 PS Example 2; Page 45; 71bp; English.
 XX
 CC Primers HuPS1.Forw1 (AAT72472) and pUOS2.T7 (AAT72473) are respectively
 CC complementary to exon A (see also AAT72462) and subunit Y (see also
 CC AAT72465) of the human CII-3 gene that encodes a subunit (AAW21674) of
 CC complex II of the human mitochondrial electron transport chain. They were
 CC used to amplify genomic DNA from HeLa cells, hamster B9 cells, hamster
 CC XHMS.1.1(+) cells containing a complete human chromosome 1, XHMS.1.1(-)
 CC cells, and hamster XHMS.2.3 cells congt. mammalian artificial chromosome
 CC MAC8.2.3. A PCR product of expected size (1.05 bp) was obtd. from HeLa,
 CC XHMS.1.1(+) and XHMS.2.3 cell DNA, indicating that cloned human genomic
 CC CII-3 sequences are present on chromosome 1, including the portion of
 CC chromosome 1 comprising MAC8.2.3
 CC

SQ Sequence 20 BP; 3 A; 5 C; 5 G; 7 T; 0 U; 0 Other;
 CC
 CC Query Match 6.4%; Score 15; DB 1; Length 20;
 CC Best Local Similarity 100.0%; Pred. No. 42;
 CC Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC

Oy 178 CAGGAGCTTCACAG 192
 CC ||||| ||||| ||||| |||||
 Db 16 CAGGAGCTTCACAG 2

```

RESULT 77
ADK96774/c
ID ADK96774 standard; DNA; 20 BP.
XX
XX
AC ADK96774;
XX
XX
DT 06-MAY-2004 (first entry)
XX
DE Primer of the invention #2494.
XX
XX human; single nucleotide polymorphism; SNP; ss; primer.
XX
XX Synthetic.
XX
XX JP2003259875-A.
XX
XX 16-SEP-2003.
XX
XX 08-MAR-2002; 2002JP-00064373.
XX
XX 08-MAR-2002; 2002JP-00064373.
XX
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
XX WPI; 2004-093977/10.
XX
XX Novel polynucleotide useful for PCR amplification along with two DNA
XX fragment from another set of sequences, or for detecting single
XX nucleotide polymorphism in human gene.
XX
XX Claim 2; SEQ ID NO 5803; 2627bp; Japanese.
XX
CC The present invention relates to a polynucleotide isolated from a human
CC gene and is useful for detecting a single nucleotide polymorphism in a
CC human gene or for diagnosing of disease. The invention enables the
CC detection of a single nucleotide polymorphism in a human gene. The
CC present sequence represents a primer of the invention.
XX
SQ Sequence 20 BP; 7 A; 3 C; 8 G; 2 T; 0 U; 0 Other;
Query Match 6.4%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 103 CCTCTCATTCCTCTG 117
Db 19 CCTCTCATTCCTCTG 5
XX
RESULT 78
ADS73903/c
ID ADS73903 standard; RNA; 19 BP.
XX
XX
AC ADS73903;
XX
XX
DT 16-DEC-2004 (first entry)
XX
DE DMD gene specific antisense oligonucleotide h59A0N2.
XX
XX DMD; Duchenne muscular dystrophy; collagen VI alpha 1; COL6A1;
XX myotubular myopathy 1; MTM1; dysferlin; DYSF; laminin-alpha 2; LAMA2;
XX emery-dreifus muscular dystrophy; EMD; calpain 3; CAPN3; antisense; ss.
XX Synthetic.
XX
XX WO2004083446-A2.
XX
XX 30-SEP-2004.
XX
XX 22-MAR-2004; 2004WO-NL000196.
XX
XX 21-MAR-2003; 2003WO-NL000214.
XX

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PA (ZIEK-) ACAD ZIEKENHUIS LEIDEN.
XX
XX
PI Van Ommereen GB, Van Deutekom JCT, Den Dunnen JT, Aartsma-Rus A;
XX
XX WPI; 2004-691060/67.
XX
XX
DR WPI; 2004-691060/67.
XX
XX
PT Generating an oligonucleotide for treating diseases, comprises
XX determining a structure of RNA from an exon, a region that assumes a
XX structure hybridized to another part of the RNA and a region that is not
XX hybridized in the structure.
XX
XX Example 1; Page 89; 117bp; English.
XX
XX
CC The invention relates to generating an oligonucleotide and involves
CC determining from a secondary structure of RNA from an exon, a region that
CC assumes a structure that is hybridized to another part of the RNA (closed
CC structure), and a region that is not hybridized in the structure (open
CC structure), and subsequently generating an oligonucleotide, where at
CC least a part of the oligonucleotide is complementary to the closed
CC structure and at least another part of the oligonucleotide is
CC complementary to the open structure. In generating an oligonucleotide,
CC the open and closed structures are adjacent to each other. The
CC oligonucleotide is complementary to a consecutive part of 14-50
CC nucleotides of the RNA. It also comprises RNA, where the RNA contains a
CC modification, preferably a 2'-O-methyl modified ribose (RNA) or
CC deoxyribose (DNA) modification. The pre-mRNA comprising the exon exhibits
CC undesired splicing in a subject. The absence of the exon from mRNA
CC produced from the pre-mRNA generates a coding region for a protein. The
CC gene from which the RNA comprising the exon is transcribed encodes an
CC aberrant Duchenne muscular dystrophy gene (DMD), a collagen VI alpha 1
CC gene (COL6A1), a myotubular myopathy 1 gene (MTM1), a dysferlin gene
CC (DYSF), a laminin-alpha 2 gene (LAMA2), an emery-dreifus muscular
CC dystrophy gene (EMD), and/or a calpain 3 gene (CAPN3). Preferably, the
CC gene is the DMD gene. The oligonucleotide, its equivalent, or the
CC compound is useful for at least in part altering recognition of the exon
CC or exons in a pre-mRNA; for the preparation of a medicament for the
CC treatment of an inherited disease; for inducing exon skipping in a pre-
CC mRNA; for altering exon-recognition in a pre-mRNA; for altering the
CC efficiency with which a splice donor or splice acceptor sequence is used
CC by a splicing machinery; for inducing exon-skipping of two, three, or
CC more exons in a pre-mRNA; or for inducing skipping of the at least two
CC exons and a sequence located between the at least two exons (intervening
CC sequence) on the pre-mRNA, where intervening sequence further comprises
CC exon or exons. Sequences ADS73865-ADS73903 represent antisense
CC oligonucleotides (AONs) used to study targeted skipping of 15 different
CC DMD exons.
XX
SQ Sequence 19 BP; 3 A; 3 C; 5 G; 0 T; 8 U; 0 Other;
Query Match 6.3%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 171 AAGATTCAGGACTTCA 188
Db 19 AAGACTCCAGGACTTCA 2
XX
RESULT 79
AEB93316/c
ID AEB93316 standard; DNA; 19 BP.
XX
XX
AC AEB93316;
XX
XX
DT 03-NOV-2005 (first entry)
XX
DE Human siRNA transcribed in the inventive optimized system, SEQ ID 79.
XX
XX Short interfering RNA; ds; gene silencing; RNA interference;
XX pharmaceutical; siRNA.
XX
XX Homo sapiens.
XX

```



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PN WO2005078089-A1.
XX
PD 25-AUG-2005.
XX
PF 03-FEB-2005; 2005WO-EP001079.
XX
PR 11-FEB-2004; 2004EP-00003079.
PR 03-AUG-2004; 2004EP-00018376.
XX
PA (UYBE-) UNIV BERLIN CHARITE.
XX
PI Trusa M, Hagemeyer C;
XX
PI WPI; 2005-582876/59.
XX
PT Small interfering RNA molecule useful for generating transgenic non-human
PT animal, comprises 5 prime-protruding end that corresponds to consensus
PT sequence of nucleotides of natural promoter of DNA-dependent RNA-
PT polymerase.
XX
PS Example 1; SEQ ID NO 79; 56bp; English.
XX
CC The invention relates to a small interfering (siRNA) molecule (I),
CC comprising a 5'-protruding end that corresponds to the consensus sequence
CC of the nucleotides 0 to +5 of the natural promoter of a DNA-dependent RNA
CC -polymerase (e.g. T7, T3 or SP6 polymerase). Also included are a DNA
CC molecule encoding the siRNA, an expression vector comprising the DNA, a
CC host cell transfected/infected with the vector, a transgene comprising
CC the DNA and/or vector, a transgenic non-human animal (one or more of its
CC cells comprising the transgene, where the transgene is expressed in one
CC or more cells of the transgenic animal resulting in the animal exhibiting
CC ribonucleic acid interference (RNAi) of the target gene by the expressed
CC siRNA), a cell derived from the transgenic animal and producing an siRNA
CC by in vitro-method (involving providing the expression vector, admixing
CC the vector with a recombinant DNA-dependent RNA-polymerase,
CC ribonucleotides, suitable buffers and RNase inhibitor, incubating the
CC mixture at a suitable temperature for 30 minutes-24 hours for
CC transcription, optionally inactivating the DNA template, and purifying
CC expressed siRNA). The siRNA is useful for generating a non-human
CC transgenic animal. The vector is useful for in vitro production of the
CC siRNA. The siRNA is useful for the transient application in cell culture
CC and animal models. The siRNA enables high-throughput projects in genomic
CC research, in target gene validation, in pharmaceutical industry,
CC biological interference with vector-based siRNA systems. The siRNA is
CC biocompatible, cost effective, easy to use and suitable for
CC automatization. The present sequence is a human siRNA produced by the
CC method of the invention. NOTE: The present sequence is described as an
CC siRNA but is clearly a DNA molecule.
XX
SQ Sequence 19 BP; 8 A; 1 C; 9 G; 1 T; 0 U; 0 Other;
Oy
Oy 109 ATTCTCCTGCTCCACTC 126
Db 19 ATTCTCCTGCTCTTCTC 2

```

Query Match 6.3%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

109 ATTCTCCTGCTCCACTC 126
|||||
19 ATTCTCCTGCTCTTCTC 2

RESULT 80
AAS45831
ID AAS45831 standard; DNA; 20 BP.
XX
AC AAS45831;
XX
DT 18-DEC-2001 (first entry)
XX
DE Mouse PARP-2 antisense inhibitor ISIS #110297.
XX
KW Mouse; 89; PARP; Poly (ADP-ribose) polymerase; antisense oligonucleotide;
KW cytoskeletal; neurotrophic; neuroprotective; antiinflammatory; antidiabetic;
KW immunosuppressant; hyperproliferative disorder; cancer; cellular injury;

```

KW oxidative stress; neurological disorder; parkinsonism; apoptosis;
KW meningitis-associated intracranial complication; ischemia; probe;
KW inflammatory disorder; autoimmune disorder; arthritis; diabetes.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note="Phosphorothioate backbone"
FT modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note="All cytidine residues are 5-methyl cytidine"
FT modified_base 1..5
FT /*tag= c
FT /mod_base= OTHER
FT /note="2'-methoxyethyl nucleotides"
FT modified_base 16..20
FT /*tag= d
FT /mod_base= OTHER
FT /note="2' methoxyethyl nucleotides"
XX
XX WO200164955-A1.
XX
XX 07-SEP-2001.
XX
XX 01-MAR-2001; 2001WO-US006572.
XX
XX 02-MAR-2000; 2000US-00517467.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Popoff I, Cowseert LM;
XX
XX WPI; 2001-602570/68.
XX
PT Antisense compound useful for treating hyperproliferative, neurological,
PT inflammatory and autoimmune disorders and diabetes inhibits human PARP.
XX
XX Example 17; Page 89; 168bp; English.
XX
CC The invention relates to antisense oligonucleotides targeted to human
CC PARP nucleic acid and inhibiting expression of human PARP. PARP (Poly
CC (ADP-ribose) polymerase plays an important role in chromatin
CC decondensation, DNA replication, DNA repair, gene expression, malignant
CC transformation, cellular differentiation and apoptosis. The antisense
CC oligonucleotide inhibitors are useful for inhibiting the expression of
CC PARP in human cells or tissues. They are also useful for treating a human
CC with a disease associated with PARP especially hyperproliferative
CC disorders (e.g. cancer), cellular injury resulting from oxidative stress,
CC neurological (e.g. parkinsonism, meningitis-associated intracranial
CC complications and ischemia), inflammatory and autoimmune disorders (e.g
CC arthritis) and diabetes. The present sequence is an antisense
CC oligonucleotide of the invention
XX
SQ Sequence 20 BP; 2 A; 8 C; 3 G; 7 T; 0 U; 0 Other;
Oy
Oy 41 TGGCATCCCTTGATGAT 58
Db 1 TCCCATCCCTTGATGCT 18

```

Query Match 6.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 44;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

41 TGGCATCCCTTGATGAT 58
|||||
1 TCCCATCCCTTGATGCT 18

RESULT 81
ADE43868/c
ID ADE43868 standard; DNA; 20 BP.
XX
AC ADE43868;

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XX 29-JAN-2004 (first entry)
DT
XX
DE Human eotaxin gene SSCP PCR primer #1.
XX
XX Human; ss; primer; eotaxin; SNP; single nucleotide polymorphism;
XX antiasthmatic; antiinflammatory; antiallergic; gene therapy; asthma;
XX rhinitis; inflammatory condition; eosinophil accumulation;
XX respiratory tract; single-strand conformation polymorphism; SSCP;
XX amplification refractory mutation system; ARMS; PCR.
OS Homo sapiens.
XX
XX US6548245-B1.
XX
XX 15-APR-2003.
XX
XX 12-MAY-1998; 98US-00076259.
XX
XX 16-MAY-1997; 97US-0046720P.
XX
XX (BGM ) BRIGHAM & WOMENS HOSPITAL INC.
XX
XX Lilly CM, Luster AD, Drazen JM;
XX
XX WPI; 2003-605370/57.
XX
XX Diagnosing, predicting or treating asthma or other inflammatory
XX conditions of respiratory tract and other tissues, comprises identifying
XX a nucleic acid sequence that exhibits a polymorphism in an eotaxin gene.
XX
XX Claim 12; SEQ ID NO 2; 12pp; English.
XX
XX The invention relates to diagnosing or predicting asthma or an
XX inflammatory condition of respiratory tissues that is associated with
XX tissue accumulation of eosinophils, comprising identifying a nucleic acid
XX sequence that exhibits a polymorphism in an eotaxin gene, where the
XX polymorphism comprises a substitution of adenine for guanine 67 base
XX pairs following the ATG initiation codon of the gene, and where counting
XX is initiated at the A in that codon. The method uses a single-strand
XX conformation polymorphism (SSCP) technique or by amplification refractory
XX mutation system (ARMS) technique. The method is useful in diagnosing,
XX predicting and treating asthma, rhinitis and other inflammatory
XX conditions associated with eosinophil accumulation in respiratory tract
XX and other tissues. The present sequence is an SSCP primer used in the
XX method of the invention to detect the polymorphism.
XX
XX Sequence 20 BP; 7 A; 9 C; 2 G; 2 T; 0 U; 0 Other;
SQ
Query Match 6.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 44;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 70 CGTGAGAGCTGTTGTTT 87
DB 20 CGTGAGAGCTGTTGTTT 3

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KM PCR; primer; ss.
XX
XX Homo sapiens.
XX
XX US2003165980-A1.
XX
XX 04-SEP-2003.
XX
XX 14-APR-2003; 2003US-00413255.
XX
XX 16-MAY-1997; 97US-0046720P.
XX
XX 12-MAY-1998; 98US-00076259.
XX
XX (BGM ) BRIGHAM & WOMENS HOSPITAL INC.
XX
XX Lilly CM, Luster AD, Drazen JM;
XX
XX WPI; 2003-898062/82.
XX
XX Diagnosing, predicting and/or treating asthma or other inflammatory
XX conditions associated with eosinophil accumulation in respiratory and
XX other tissues, such as rhinitis and atopy, using an eotaxin coding
XX sequence polymorphism.
XX
XX Claim 8; SEQ ID NO 2; 12pp; English.
XX
XX The present invention relates to a method for diagnosing and/or
XX predicting asthma. The method comprises identifying a nucleic acid
XX sequence exhibiting a polymorphism in an eotaxin gene, where the
XX polymorphism comprises a substitution of adenine for guanine 67 bp
XX following the ATG initiation codon of the gene, where counting is
XX initiated at the A in that codon. The method involves amplifying the
XX nucleic acid by PCR, and testing the nucleic acid by a single-strand
XX conformation polymorphism (SSCP) or by an amplification refractory
XX mutation system (ARMS) technique. The method of the invention is useful
XX for diagnosing, predicting and/or treating asthma or an inflammatory
XX condition associated with eosinophil accumulation in respiratory and
XX other tissues, including rhinitis and atopy. The present sequence
XX represents a PCR primer used in the method of the present invention.
XX
XX Sequence 20 BP; 7 A; 9 C; 2 G; 2 T; 0 U; 0 Other;
SQ
Query Match 6.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 44;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 70 CGTGAGAGCTGTTGTTT 87
DB 20 CGTGAGAGCTGTTGTTT 3

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RESULT 82
ADF77306/C
ID ADF77306 standard; DNA; 20 BP.
XX
XX ADF77306;
XX
XX 26-FEB-2004 (first entry)
XX
XX PCR primer #1 for human eotaxin gene.
XX
XX Asthma; polymorphism detection; eotaxin;
XX single-strand conformation polymorphism; SSCP;
XX amplification refractory mutation system; ARMS; inflammatory condition;
XX eosinophil accumulation; respiratory tissue; rhinitis; atopy;
XX antiasthmatic; antiallergic; antiinflammatory; dermatological; human;

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RESULT 83
ADG43900/C
ID ADG43900 standard; DNA; 20 BP.
XX
XX ADG43900;
XX
XX 26-FEB-2004 (first entry)
XX
XX Human DYRK4 antisense oligonucleotide ISIS 206819.
XX
XX ss; dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4;
XX DYRK4; Down syndrome; mental retardation; cancer; infection;
XX inflammation; tumour; antisense.
XX
XX Synthetic.
XX
XX US2003211606-A1.
XX
XX 13-NOV-2003.
XX
XX 10-MAY-2002; 2002US-00144140.
XX

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```
PR 10-MAY-2002; 2002US-00144140.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Dobie KW, Freier SM;
XX WPI; 2003-901593/82.
XX
XX New compound that hybridizes with nucleic acid molecules encoding dual-
PT specificity tyrosine-(Y)-phosphorylation regulated kinase 4 (DYRK4) and
PT inhibits expression of DYRK4, useful for treating e.g. cancer or Down
PT syndrome.
XX
XX Example 15; SEQ ID NO 28; 46bp; English.
XX
XX The invention relates to a compound targeted to a nucleic acid molecule
CC encoding dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4
CC (DYRK4). The compound is useful for inhibiting the expression of DYRK4 in
CC cells or tissues. It can also be used for treating a disease or condition
CC associated with DYRK4, preferably Down syndrome, mental retardation or
CC cancer. The antisense compounds can also be used as research agents, in
CC diagnostics, or as prophylaxis to prevent or delay infection, in
CC inflammation or tumor formation. The present sequence represents a human
CC dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4, DYRK4,
CC antisense oligonucleotide.
XX
XX Sequence 20 BP; 3 A; 3 C; 8 G; 6 T; 0 U; 0 Other;
SQ
Query Match 6.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 44;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 172 AGATTCCAGGACTTCAC 189
DB 18 AGATTCCAGGACTTCAC 1
RESULT 84
ADJ96199
ID ADJ96199 standard; DNA; 20 BP.
XX
XX ADJ96199;
XX
XX 06-MAY-2004 (first entry)
DE Human TNFR-6alpha amplifying RT-PCR primer #1.
XX
XX Tumour necrosis factor receptor; TNFR; inflammation;
XX inflammatory bowel disease; encephalitis; atherosclerosis; psoriasis;
XX autoimmune disorder; systemic lupus erythematosus; arthritis;
XX multiple sclerosis; Crohn's disease; autoimmune encephalitis;
XX graft vs. host disease; GVHD; allergy; asthma; gene therapy; human;
XX RT-PCR; reverse-transcriptase; primer; 88.
XX
XX Homo sapiens.
OS
XX US2004013664-A1.
XX
XX 22-JAN-2004.
XX
XX 18-APR-2003; 2003US-00418242.
XX
XX 14-JAN-1997; 97US-0035496P.
XX 13-JAN-1998; 98US-00006352.
XX 04-MAR-1999; 99US-0121774P.
XX 12-MAR-1999; 99US-0124092P.
XX 27-APR-1999; 99US-0131279P.
XX 30-APR-1999; 99US-0131964P.
XX 02-AUG-1999; 99US-0146371P.
XX 01-DEC-1999; 99US-0168235P.
XX 03-MAR-2000; 2000US-00518931.
XX 25-AUG-2000; 2000US-0227598P.
XX 21-NOV-2000; 2000US-0252131P.
XX
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```
PR 06-JUL-2001; 2001US-0303224P.
PR 24-AUG-2001; 2001US-00935727.
PR 19-APR-2002; 2002US-0373604P.
XX
XX (GENTZ/) GENTZ R L.
XX (YUGG/) YU G.
XX (NIJ/) NI J.
XX (EBNER/) EBNER R.
XX (FENG/) FENG P.
XX (RUBEN/) RUBEN S M.
XX
XX Gentz RL, Yu G, Ni J, Ebner R, Feng P, Ruben SM;
XX WPI; 2004-121528/12.
XX
XX Treating or preventing an inflammatory or autoimmune disorder, graft vs
PT host disease (GVHD), allergy or asthma comprises administering to an
PT animal Tumor Necrosis Factor Receptor protein.
XX
XX Example 28; SEQ ID NO 50; 165bp; English.
XX
XX The present invention relates to novel tumour necrosis factor receptors
CC (TNFR) proteins and their encoding nucleic acids. The invention is useful
CC for treating and preventing inflammatory disorders such as inflammatory
CC bowel disease, encephalitis, atherosclerosis and psoriasis, autoimmune
CC disorders such as systemic lupus erythematosus, arthritis, multiple
CC sclerosis, Crohn's disease and autoimmune encephalitis, graft vs. host
CC disease (GVHD), allergy and asthma. The invention is also useful in gene
CC therapy. The present sequence is human TNFR-6alpha amplifying RT-PCR
CC primer. The primer is used in the exemplification of the invention.
XX
XX Sequence 20 BP; 2 A; 9 C; 3 G; 6 T; 0 U; 0 Other;
SQ
Query Match 6.3%; Score 14.8; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 44;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 92 GAGCCTGGCCCCCTCA 109
DB 3 GATCTGGCCCCCTCTTA 20
RESULT 85
AEC22797/C
ID AEC22797 standard; DNA; 20 BP.
XX
XX AEC22797;
XX
XX 20-OCT-2005 (first entry)
DE Human myocardial infarction (MI) gene marker PCR primer SEQ ID NO 7.
XX
XX cardiant; C-reactive-protein-reducer; leukotriene-synthesis-antagonist;
XX 5-lipoxygenase activating protein; primer; genetic marker.
XX
XX Homo sapiens.
OS
XX WO2005075022-A2.
XX
XX 18-AUG-2005.
XX
XX 31-JAN-2005; 2005WO-US003312.
XX
XX 30-JAN-2004; 2004US-00769542.
XX 30-JAN-2004; 2004US-00769744.
XX 22-APR-2004; 2004US-00829674.
XX 22-APR-2004; 2004US-00830477.
XX 10-JAN-2005; 2005US-0642909P.
XX
XX (DECO-) DECODE GENETICS EHF.
XX
XX Helgadottir A, Hakonarson H, Gulcher JR, Gurney ME;
XX
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[illegible]

	The invention comprises a method of prophylaxis therapy for myocardial infarction. The method involves selecting a human subject susceptible to myocardial infarction by screening for a genetic variation in either the 5-lipoxygenase activating protein (FLAP) gene or the leukotriene A ₄ hydroxylase (LTAH) gene. The method further involves administration of a therapeutic agent and monitoring at least one inflammatory marker in the subject before and during the prophylaxis treatment. The method of the invention is useful for prophylaxis therapy for myocardial infarction.
	The present DNA sequence represents a PCR primer that was used to amplify a microsatellite marker from within the human FLAP gene.
SQ	Sequence 20 BP; 4 A; 5 C; 6 G; 5 T; 0 U; 0 Other;
Query Match	6.3%; Score 14.8; DB I; Length 20;
Best Local Similarity	88.9%; Pred. No. 44;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0	
OY	18 CAGATCCCTCATGAAATGG 35
Dd	18 CAGCTCCTCATGTATTGG 1
RESULT 87	
AAQ82294/c	
ID	AAQ82294 standard; DNA; 21 BP.
XX	
AC	AAQ82294;
XX	
DT	25-MAR-2003 (revised)
DT	07-SEP-1995 (first entry)
XD	
DE	Chromosome 11 (locus DIS11J1) STS primer CSRL-4e3-tZ.
XX	
KM	sequence sampled mapping; genomic analysis; complex genome mapping; cosmid library; chromosome 11; sequence tagged site; STS analysis; ss.
KW	
XK	Synthetic.
OS	
NN	WO9429486-AI.
PB	22-DEC-1994.
XX	
PF	15-JUN-1994; 94WO-USO06810.
PR	15-JUN-1993; 93US-O0078471. 07-SEP-1993; 93US-O0117952.
PA	(SALK) SALK INST BIOLOGICAL STUDIES.
PI	Evens GA, Smith MW;
DR	WP1, 1995-036508/05.
PT	Sequencing complex genomes, present as fragments in a cosmid library - by sequencing end-specific nucleic acids of each clone then correlating with spatial relationship of cosmid, esp. for mammalian chromosomes.
PS	Example 4; Page 75; 128pp; English.
XX	
CC	Sequences were determined from the ends of chromosome 11-specific cosmids
CC	by automated sequencing without intermediate subcloning. A sample of 371
CC	DNA sequence fragments were determined and of these, 277 were suitable
CC	for STS primer prediction by computer analysis (using the "Primer"
CC	program available from E.Lander, MIT). The STSs and cosmids were mapped
CC	by in situ hybridisation, somatic cell hybrid analysis or both. Using
CC	this method, 370 STSs specific for human chromosome 11 were generated and
CC	most of them were regionally mapped. This procedure illustrates a novel
CC	method for sequencing complex genomes, designated "sequence sampled
CC	mapping". The sequence sampled mapping method is useful for the
CC	completion of high density sequence-based maps, and ultimately, for the
CC	detailed sequencing of genomic DNA directly from cosmid clones. See
CC	AAQ82001-Q82706 for STS primers. (Updated on 25-MAR-2003 to correct PN

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CC field.)
XX
SQ Sequence 21 BP; 8 A; 5 C; 1 G; 7 T; 0 U; 0 Other;

Query Match      6.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 42;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      74 AGACGTGTTGTTGAAA 91
Db      18 AAGCTGTTTGTGAAA 1

RESULT 88
ADG77905
ID ADG77905 standard; DNA; 21 BP.
AC ADG77905;
DT 11-MAR-2004 (first entry)
XX
DE Canine disease marker-related PCR primer 749.
XX
KM genetic disease; genetic trait; dog; carrier of recessive disease;
KM copper toxicosis; CT; canine genome map; breed-specific profile;
KM DNA fingerprint; dog identification; PCR; primer; ss.
XX
OS Canis familiaris.
XX
PN WO9731011-A1.
XX
PD 28-AUG-1997.
XX
PF 18-FEB-1997; 97WO-US002396.
XX
PR 22-FEB-1996; 96US-0012060P.
XX
PA (UNMI ) UNIV MICHIGAN.
XX (UNMS ) UNIV MICHIGAN STATE.
XX
PI Brewer GJ, Venta PJ, Yuzbasiyan-Gurkan V;
XX
DR WPI; 1997-435082/40.
XX
PT New oligonucleotide primers for diagnosis of genetic diseases and traits
PT in dogs - amplify specific regions of the genome containing
PT microsatellite repeats, especially for diagnosing copper toxicosis and
PT carriers.
XX
PS Claim 1; Page 18; 40pp; English.
XX
CC This invention relates to novel oligonucleotide PCR primers which may be
CC used to identify markers associated with genetic diseases and traits in
CC dogs, in particular to diagnose genetic diseases that are not
CC phenotypically visible and to identify carriers of recessive diseases. A
CC specific application is diagnosis of copper toxicosis (CT). The invention
CC can also be used to create a genetic map of the canine genome; to
CC generate breed-specific profiles; to establish paternity and to identify
CC dogs from DNA fingerprints. The method provides rapid analysis of the
CC target sequences from only a small sample of DNA. Diagnosis can be done
CC at any time in the dog's life. The present sequence is that of a PCR
CC primer of the invention.
XX
SQ Sequence 21 BP; 0 A; 9 C; 3 G; 9 T; 0 U; 0 Other;

Query Match      6.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 42;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      145 CCCCCTTCTCTCTGCC 162
Db      1 CCTGCTTCTCTCTGCC 18

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RESULT 89
AAS43670
ID AAS43670 standard; DNA; 21 BP.
XX
AC AAS43670;
XX
DT 18-DEC-2001 (first entry)
XX
DE Corneodesmosin PCR primer #140.
XX
KM Human; single nucleotide polymorphism; SNP; PCR primer; antiinflammatory;
KM antipsoriatic; corneodesmosin; inflammatory disease; psoriasis; ss.
XX
OS Homo sapiens.
XX
PN WO200162788-A2.
XX
PD 30-AUG-2001.
XX
PF 23-FEB-2001; 2001WO-GB000795.
XX
PR 23-FEB-2000; 2000GB-00004312.
XX
PA (OXAG-) OXAGEN LTD.
XX
PI Olaveson M, Lench N, Allen M, Tazi-Ahmini R;
XX
DR WPI; 2001-570627/64.
XX
PT Corneodesmosin protein and polynucleotide encoding it, having one or more
PT polymorphisms useful in treating, diagnosing or determining
PT susceptibility to corneodesmosin-mediated diseases, for e.g. inflammatory
PT diseases.
XX
PS Disclosure; Page 38; 60pp; English.
XX
CC The invention relates to corneodesmosin protein (I) and nucleic acid (II)
CC encoding the corneodesmosin gene, where the gene comprises a base
CC substitution, deletion or insertion at one or more positions. (I) and
CC (II) are useful for screening for agents for use in prognosis, diagnosis
CC and treatment of individuals having or being susceptible to
CC corneodesmosin-mediated disease, by monitoring the reaction between the
CC molecules and the agents. The nucleotide and amino acid polymorphisms are
CC useful for diagnosing or determining susceptibility to corneodesmosin-
CC mediated disease, which facilitates subsequent treatment of the disease
CC for e.g. inflammatory diseases, in particular psoriasis. Fragments of (I)
CC are useful in diagnostic, prognostic or therapeutic methods and as
CC research tools for e.g. in drug screening. (II) is useful as probes or
CC primers for detecting an allele of the polymorphism or in the regulation
CC of corneodesmosin gene. Antibodies which binds to (I) are useful for
CC screening DNA clone libraries for cells secreting the antigen. (II) is
CC useful as a model to investigate the role of corneodesmosin in normal
CC skin function. AAS43492-AAS43749 represent corneodesmosin coding
CC sequences, single nucleotide polymorphisms (SNPs) and PCR primers of the
CC invention.
XX
SQ Sequence 21 BP; 5 A; 5 C; 5 G; 6 T; 0 U; 0 Other;

Query Match      6.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 42;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      18 CAGATCCCTCATGAATG 35
Db      4 CAGATCTTCATGAATG 21

RESULT 90
AAS43680
ID AAS43680 standard; DNA; 21 BP.
XX
AC AAS43680;

```

KX		18-DEC-2001	(first entry)
DT		Corneodesmosin PCR primer #150.	
DE		Human; single nucleotide polymorphism; SNP; PCR primer; anti-inflammatory;	
XX		antipsoriatic; corneodesmosin; inflammatory disease; psoriasis; ss.	
KW		Homo sapiens.	
OS		WO200162788-A2.	
PN		30-AUG-2001.	
XX		23-FEB-2001; 2001WO-GB000795.	
PJ		23-FEB-2000; 2000GB-0004312.	
PR		(OXAG-) OXAGEN LTD.	
PA		Olavason M, Lench N, Allen M, Tazi-Alhini R;	
F1		WPI; 2001-570627/64.	
DR			
XX			
PT		Corneodesmosin protein and polynucleotide encoding it, having one or more	
PF		polycephalisms useful in treating, diagnosing or determining	
PP		susceptibility to corneodesmosin-mediated diseases, for e.g. inflammatory	
PS		diseases.	
XX			
D1		Disclosure; Page 38; 6opp; English.	
CC		The invention relates to corneodesmosin protein (I) and nucleic acid (II)	
CC		encoding the corneodesmosin gene, where the gene comprises a base	
CC		substitution, deletion or insertion at one or more positions. (I) and	
CC		((ii)) are useful for screening for agents for use in prognosis, diagnosis	
CC		and treatment of individuals having or being susceptible to	
CC		corneodesmosin-mediated disease, by monitoring the reaction between the	
CC		molecules and the agents. The nucleotide and amino acid polymorphisms are	
CC		useful for diagnosing or determining susceptibility to corneodesmosin-	
CC		mediated disease, which facilitates subsequent treatment of the disease	
CC		for e.g. inflammatory diseases, in particular psoriasis. Fragments of (I)	
CC		are useful in diagnostic, prognostic or therapeutic methods and as	
CC		research tools for e.g. in drug screening. ((ii)) is useful as probes or	
CC		primers for detecting an allele of the polymorphism or in the regulation	
CC		of corneodesmosin genes. Antibodies which binds to (I) are useful for	
CC		screening DNA clone libraries for cells secreting the antigen. ((ii)) is	
CC		useful as a model to investigate the role of corneodesmosin in normal	
CC		skin function. AAS43492-AA53749 represent corneodesmosin coding	
CC		sequences, single nucleotide polymorphisms (SNPs) and PCR primers of the	
CC		invention	
SQ		Sequence 21 BP; S A; 5 C; 5 G; 6 T; 0 U; 0 Other;	
Query Match	6.3%	Score 14.8; DB 1; Length 21;	
Best Local Similarity	88.9%;	Pred. No. 42;	
Matches	16; Conservative	0; Mismatches 2; Indels 0; Gaps 0;	
Gy	18	CAGATCCTTCATGAATTGG 35	
Db	4	CAGATGTTTCAATGAATTGG 21	
ID	AAS43678	standard; DNA; 21 BP.	
AC	AAS43678;		
DT	18-DEC-2001	(first entry)	
DE	Corneodesmosin PCR primer #148.		
KM	Human; single nucleotide polymorphism; SNP; PCR primer; anti-inflammatory;		

XX	antipsoriatic; corneodesmosin; inflammatory disease; psoriasis; ss.
XX	
XX	Homo sapiens.
XX	
XX	WO200162788-A2.
XX	
XX	30-AUG-2001.
XX	
XX	23-FEB-2001; 2001WO-GB000795.
XX	
XX	23-FEB-2000; 2000GB-00004312.
XX	
XX	(OXAG-) OXAGEN LTD.
XX	
XX	Olaveson M, Lench N, Allen M, Tazi-Ahmini R;
XX	WPI; 2001-570627/64.
XX	
XX	Corneodesmosin protein and polynucleotide encoding it, having one or more
XX	polymorphisms useful in treating, diagnosing or determining
XX	susceptibility to corneodesmosin-mediated diseases, for e.g. inflammatory
XX	diseases.
XX	
XX	Disclosure; Page 38; 60pp; English.
XX	
XX	The invention relates to corneodesmosin protein (I) and nucleic acid (II)
XX	encoding the corneodesmosin gene, where the gene comprises a base
XX	substitution, deletion or insertion at one or more positions. (I) and
XX	(II) are useful for screening for agents for use in prognosis, diagnosis
XX	and treatment of individuals having or being susceptible to
XX	corneodesmosin-mediated disease, by monitoring the reaction between the
XX	molecules and the agents. The nucleotide and amino acid polymorphisms are
XX	useful for diagnosing or determining susceptibility to corneodesmosin-
XX	mediated disease, which facilitates subsequent treatment of the disease
XX	for e.g. inflammatory diseases, in particular psoriasis. Fragments of (I)
XX	are useful in diagnostic, prognostic or therapeutic methods and as
XX	research tools for e.g. in drug screening. (II) is useful as probes or
XX	primers for detecting an allele of the polymorphism or in the regulation
XX	of corneodesmosin gene. Antibodies which binds to (I) are useful for
XX	screening DNA clone libraries for cells secreting the antigen. (II) is
XX	useful as a model to investigate the role of corneodesmosin in normal
XX	skin function. AAS43492-AAS43749 represent corneodesmosin coding
XX	sequences, single nucleotide polymorphisms (SNPs) and PCR primers of the
XX	invention
XX	
XX	Sequence 21 BP; 5 A; 5 C; 5 G; 6 T; 0 U; 0 Other;
XX	
XX	Query Match 6.3%; Score 14.8; DB 1; Length 21;
XX	Best Local Similarity 88.9%; Pred. No. 42;
XX	Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0
XX	
XX	18 CAGATCCCTCATGAATGG 35
XX	
XX	4 CAGATGCTTCATGAATGG 21
XX	
XX	RESULT 92
XX	AAS43672
XX	AAS43672 standard; DNA; 21 BP.
XX	
XX	AAS43672;
XX	
XX	18-DEC-2001 (first entry)
XX	
XX	Corneodesmosin PCR primer #142.
XX	
XX	Human; single nucleotide polymorphism; SNP; PCR primer; antiinflammatory;
XX	antipsoriatic; corneodesmosin; inflammatory disease; psoriasis; ss.
XX	
XX	Homo sapiens.
XX	
XX	WO200162788-A2.
XX	

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PD 30-AUG-2001.
XX
XX 23-FEB-2001; 2001WO-GB000795.
XX
XX 23-FEB-2000; 2000GB-00004312.
XX
XX (OXAG-) OXAGEN LTD.
XX
XX Olaveson M, Lench N, Allen M, Tazi-Ahmini R;
XX WPI; 2001-570627/64.
XX
XX Corneodesmosin protein and polynucleotide encoding it, having one or more
XX polymorphisms useful in treating, diagnosing or determining
XX susceptibility to corneodesmosin-mediated diseases, for e.g. inflammatory
XX diseases.
XX
XX Disclosure; Page 38; 60pp; English.
XX
XX The invention relates to corneodesmosin protein (I) and nucleic acid (II)
XX encoding the corneodesmosin gene, where the gene comprises a base
XX substitution, deletion or insertion at one or more positions. (I) and
XX (II) are useful for screening for agents for use in prognosis, diagnosis
XX and treatment of individuals having or being susceptible to
XX corneodesmosin-mediated disease, by monitoring the reaction between the
XX molecules and the agents. The nucleotide and amino acid polymorphisms are
XX useful for diagnosing or determining susceptibility to corneodesmosin-
XX mediated disease, which facilitates subsequent treatment of the disease
XX for e.g. inflammatory diseases, in particular psoriasis. Fragments of (I)
XX are useful in diagnostic, prognostic or therapeutic methods and as
XX research tools for e.g. in drug screening. (II) is useful as probes or
XX primers for detecting an allele of the polymorphism or in the regulation
XX of corneodesmosin gene. Antibodies which bind to (I) are useful for
XX screening DNA clone libraries for cells secreting the antigen. (II) is
XX useful as a model to investigate the role of corneodesmosin in normal
XX skin function. AAS43492-AAS43749 represent corneodesmosin coding
XX sequences, single nucleotide polymorphisms (SNPs) and PCR primers of the
XX invention
XX
SQ Sequence 21 BP; 5 A; 5 C; 5 G; 6 T; 0 U; 0 Other;
Query Match 6.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 42;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 18 CAGATCCCTCATGATGG 35
DB 4 CAGATGCTTCATGATGG 21
RESULT 93
AAS43676
ID AAS43676 standard; DNA; 21 BP.
XX
XX AAS43676;
XX
XX 18-DEC-2001 (first entry)
XX
XX Corneodesmosin PCR primer #146.
XX
XX Human; single nucleotide polymorphism; SNP; PCR primer; antiinflammatory;
XX antipsoriatic; corneodesmosin; inflammatory disease; psoriasis; ss.
XX
XX Homo sapiens.
XX
XX WO200162788-A2.
XX
XX 30-AUG-2001.
XX
XX 23-FEB-2001; 2001WO-GB000795.
XX
XX 23-FEB-2000; 2000GB-00004312.
XX

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PA (OXAG-) OXAGEN LTD.
XX
XX Olaveson M, Lench N, Allen M, Tazi-Ahmini R;
XX WPI; 2001-570627/64.
XX
XX Corneodesmosin protein and polynucleotide encoding it, having one or more
XX polymorphisms useful in treating, diagnosing or determining
XX susceptibility to corneodesmosin-mediated diseases, for e.g. inflammatory
XX diseases.
XX
XX Disclosure; Page 38; 60pp; English.
XX
XX The invention relates to corneodesmosin protein (I) and nucleic acid (II)
XX encoding the corneodesmosin gene, where the gene comprises a base
XX substitution, deletion or insertion at one or more positions. (I) and
XX (II) are useful for screening for agents for use in prognosis, diagnosis
XX and treatment of individuals having or being susceptible to
XX corneodesmosin-mediated disease, by monitoring the reaction between the
XX molecules and the agents. The nucleotide and amino acid polymorphisms are
XX useful for diagnosing or determining susceptibility to corneodesmosin-
XX mediated disease, which facilitates subsequent treatment of the disease
XX for e.g. inflammatory diseases, in particular psoriasis. Fragments of (I)
XX are useful in diagnostic, prognostic or therapeutic methods and as
XX research tools for e.g. in drug screening. (II) is useful as probes or
XX primers for detecting an allele of the polymorphism or in the regulation
XX of corneodesmosin gene. Antibodies which bind to (I) are useful for
XX screening DNA clone libraries for cells secreting the antigen. (II) is
XX useful as a model to investigate the role of corneodesmosin in normal
XX skin function. AAS43492-AAS43749 represent corneodesmosin coding
XX sequences, single nucleotide polymorphisms (SNPs) and PCR primers of the
XX invention
XX
SQ Sequence 21 BP; 5 A; 5 C; 5 G; 6 T; 0 U; 0 Other;
Query Match 6.3%; Score 14.8; DB 1; Length 21;
Best Local Similarity 88.9%; Pred. No. 42;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 18 CAGATCCCTCATGATGG 35
DB 4 CAGATGCTTCATGATGG 21
RESULT 94
AAS43674
ID AAS43674 standard; DNA; 21 BP.
XX
XX AAS43674;
XX
XX 18-DEC-2001 (first entry)
XX
XX Corneodesmosin PCR primer #144.
XX
XX Human; single nucleotide polymorphism; SNP; PCR primer; antiinflammatory;
XX antipsoriatic; corneodesmosin; inflammatory disease; psoriasis; ss.
XX
XX Homo sapiens.
XX
XX WO200162788-A2.
XX
XX 30-AUG-2001.
XX
XX 23-FEB-2001; 2001WO-GB000795.
XX
XX 23-FEB-2000; 2000GB-00004312.
XX
XX (OXAG-) OXAGEN LTD.
XX
XX Olaveson M, Lench N, Allen M, Tazi-Ahmini R;
XX WPI; 2001-570627/64.
XX

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Best Local Similarity 88.9%; Pred. No. 42;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 149 CTTCTCCTTCGCATCA 166
Db 18 CTTCTCCTTCGCATCA 1

RESULT 97

ADM85397/C
ID ADM85397 standard; DNA; 21 BP.

XX ADM85397;

XX 07-APR-2005 (first entry)

XX MAP3K9 marker amplification forward primer #1336.

XX mixed lineage kinase; MLK; asthma; at-risk haplotype; MAP3K9;

KW antiasthmatic; respiratory-gen.; antiinflammatory; antineumatic;

KW antiarthritic; antipsoriatic; neuroprotective; gastrointestinal-gen.;

KW respiratory disease; chronic obstructive pulmonary disease;

XX chronic bronchitis; inflammation; ss; primer; PCR.

XX Unidentified.

XX WO2005007144-A2.

XX 27-JAN-2005.

XX 14-JUL-2004; 2004WO-US022446.

XX 14-JUL-2003; 2003US-0487072P.

XX 05-APR-2004; 2004US-0559611P.

XX (DECO-) DECODE GENETICS EHF.

XX Hakonarson H, Gurney ME, Halapi E;

XX WPI: 2005-122681/13.

XX Use of mixed lineage kinase family kinase inhibitor in the manufacture of

XX a medicament for treatment of asthma associated at-risk haplotype for

XX asthma, at-risk haplotype in MAP3K9 gene or increased MLK1 protein

XX expression or activity.

XX Disclosure: Fig 12; 640pp; English.

XX The invention relates to the novel use of a mixed lineage kinase (MLK)

XX family kinase inhibitor for treating asthma. Where the asthma is

XX associated with a risk factor selected from an at-risk haplotype for

XX asthma, at-risk haplotype in MAP3K9 gene, polymorphism in MAP3K9 nucleic

XX acid, dysregulation of MAP3K9 mRNA expression, dysregulation of a MAP3K9

XX mRNA isoform, and/or increased MLK1 protein expression. The invention

XX further comprises: a method for the diagnosis or identification of

XX susceptibility to asthma; a method for the use of a first nucleic acid

XX molecule for diagnosing asthma or susceptibility to asthma in a sample; a

XX method for assaying the presence of a first nucleic acid molecule in a

XX sample; a method for assessing the response to treatment with an MLK

XX family kinase nucleic acid inhibitor in a target population or in an

XX individual with an at-risk haplotype for asthma, at-risk haplotype in the

XX MAP3K9 gene, polymorphism in the MAP3K9 nucleic acid, dysregulation of

XX MAP3K9 mRNA expression, dysregulation of MAP3K9 mRNA isoform, increased

XX MLK1 protein expression, increased MLK1 biochemical activity or increased

XX MLK1 protein isoform expression; a method for assessing the response to

XX treatment with an MLK1 inhibitor in a target population including an

XX individual with an at-risk haplotype for asthma, as above; a kit for

XX assaying a sample for the presence or absence of at least one haplotype

XX comprising 2 or more alleles associated with asthma comprising: at least

XX one nucleic acid capable of detecting the presence or absence of at least

XX one specific allele; a reagent kit for assaying the presence of at least

XX one haplotype comprising 2 or more alleles comprising: at least one

XX labeled nucleic acid capable of detecting at least one specific allele of

CC the haplotype, and reagents for detection of the label; and a reagent kit

CC for assaying a sample for the presence of at least one haplotype

CC comprising 2 or more alleles comprising: at least one nucleic acid

CC comprising at least one nucleotide sequence that is at least partially

CC complementary to a part of nucleotide sequence of MAP3K9, capable of

CC acting as a primer for a primer extension reaction and capable of

CC detecting 2 or more specific alleles of the haplotype. The MLK family

CC kinase inhibitor has the following activities: antiasthmatic, respiratory

CC -gen., antiinflammatory, antineumatic, antiarthritic, antipsoriatic,

CC neuroprotective, and gastrointestinal-gen. The MLK family kinase

CC inhibitor is useful for the treatment of asthma associated with a risk

CC factor selected from at-risk haplotype for asthma, at-risk haplotype in

CC MAP3K9 gene, polymorphism in MAP3K9 nucleic acid, dysregulation of MAP3K9

CC mRNA expression, dysregulation of MAP3K9 mRNA isoform, increased MLK1

CC protein expression, increased MLK1 biochemical activity and/or increased

CC MLK1 protein isoform expression; and in diagnosis or identification of

CC susceptibility to asthma. The inhibitor is also useful for the treatment

CC of other respiratory diseases associated with MAP3K9 or other members of

CC the JNK pathway such as chronic obstructive pulmonary disease, chronic

CC bronchitis and other inflammatory diseases such as rheumatoid arthritis,

CC psoriasis, multiple sclerosis and inflammatory bowel disease. This

CC polynucleotide sequence represents a forward primer which is used in

CC amplifying a marker of the MAP3K9 kinase, where MAP3K9 is a part of

CC Mitogen-Activated Protein Kinase (MAPK) signal transduction pathways, of

CC the invention.

XX Sequence 21 BP; 8 A; 6 C; 3 G; 4 T; 0 U; 0 Other;

XX Query Match 6.3%; Score 14.8; DB 1; Length 21;

XX Best Local Similarity 88.9%; Pred. No. 42;

XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 49 CCTTGGATGATGAGT 66

Db 21 CCTTGGATGATGAGT 4

RESULT 98

AEBC02566

ID AEBC02566 standard; DNA; 21 BP.

XX AEBC02566;

XX 03-NOV-2005 (first entry)

XX Human IGE short interfering nucleic acid SEQ ID NO 169.

XX antiallergic; antiinflammatory; antiasthmatic; dermatological;

XX immunosuppressive; expression; RNA interference; allergy;

XX atopic dermatitis; urticaria; dermatological disease;

XX immediate type hypersensitivity; immunosuppressive; asthma;

XX antiasthmatic; allergic rhinitis; antiallergic; antiinflammatory;

XX ear, nose, throat disease; inflammation; respiratory disease;

XX immune disorder; IGE; short interfering nucleic acid; siRNA;

XX gene silencing; ss.

XX Homo sapiens.

XX WO2005080410-A1.

XX 01-SEP-2005.

XX 21-FEB-2005; 2005WO-NZ000021.

XX 20-FEB-2004; 2004US-0546434P.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX Watson JD, Murison GJ, Grigor MR, Havukkala IU, Munro G;

XX Abernethy N, Webster G;

XX WPI: 2005-591970/60.

PT New composition comprises small interfering nucleic acid molecule (sina)
PT capable of reducing expression of a target gene that is active in a IgE-
PT mediated disorder, useful for treating, e.g. allergic rhinitis or atopic
PT dermatitis.

PS Disclosure; SEQ ID NO 169; 178bp; English.

The invention describes a composition comprising a small interfering nucleic acid molecule (siNA) capable of reducing expression of a target gene that is active in a IGE-mediated disorder, a genetic construct that expresses the siNA, and a binding agent that specifically binds to a target antigen expressed on the surface of the cell. Also described are: a method for the treatment of an IGE-mediated disorder in a patient; prevention of IGE-mediated disorder in a patient; reduction of eosinophilia in a patient; modulating an IGE-mediated immune response to a specific antigen in a patient; and preventing or reducing the severity of an immune response to a specific antigen in a patient. The composition is useful in the preparation of a medicament useful for the treatment of an IGE-mediated disorder, e.g. allergic rhinitis, asthma, anaphylaxis, urticaria, atopic dermatitis, food allergies, diseases that benefit from the reduction of eosinophilia in the tissues of the respiratory system, or disorders having hypersensitivity immune reaction. This sequence represents a siNA for suppression of human IGE expression.

SQ Sequence 21 BP; 4 A; 2 C; 9 G; 6 T; 0 U; 0 Other;

Query Match 6.38; Score 14.8; DB 1; Length 21;

Best Local Similarity 88.9%; Pred. No. 42;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGTCTGGGTCATGGGGC 18

Db 4 TGTTTGGGTCATGGAGGC 21

Search completed: October 2, 2006, 15:45:39
Job time : 0.001 secs

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: October 2, 2006, 15:43:17 ; Search time 0.001 seconds
(without alignments)
1797.376 Million cell updates/sec

Title: US-10-642-945-6_3002-3237

Perfect score: 236
Sequence: 1 tgcctggcctacggggcagc.....ctgtctcgtcgcacaaactg 236

Scoring table: IDENTITY_NUC
Gapop 10.0', Gapext 0.5

Searched: 167 seqs, 3808 residues

Total number of hits satisfying chosen parameters: 334

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 167 summaries

Database : pubmain2.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23.2	9.8	33	1	US-10-891-260-437 Sequence 437, App
2	22.2	9.6	28	1	US-10-310-914A-1140145 Sequence 1140145, A
3	21.8	9.2	25	1	US-11-060-756-81484 Sequence 81484, A
4	21.8	9.2	25	1	US-11-060-756-81500 Sequence 81500, A
5	21.8	9.2	25	1	US-11-060-756-81511 Sequence 81511, A
6	21.4	9.1	23	1	US-10-310-914A-1072814 Sequence 1072814, A
7	20.8	8.8	25	1	US-11-060-756-81487 Sequence 81487, A
8	20.8	8.8	25	1	US-11-060-756-81498 Sequence 81498, A
9	20.8	8.8	25	1	US-11-060-756-81501 Sequence 81501, A
10	20.4	8.6	24	1	US-10-310-914A-596177 Sequence 596177, A
11	20.4	8.6	25	1	US-10-310-914A-116013 Sequence 116013, A
12	20.2	8.6	25	1	US-11-060-756-81488 Sequence 81488, A
13	20.2	8.6	25	1	US-11-060-756-81497 Sequence 81497, A
14	20.2	8.6	25	1	US-11-060-756-81505 Sequence 81505, A
15	20.2	8.6	25	1	US-11-121-849-628945 Sequence 628945, A
16	20.2	8.6	25	1	US-11-121-849-628945 Sequence 628945, A
17	19.8	8.4	23	1	US-10-310-914A-661150 Sequence 661150, A
18	19.8	8.4	25	1	US-10-310-914A-1073215 Sequence 1073215, A
19	19.8	8.4	25	1	US-11-121-849-602992 Sequence 602992, A
20	19.8	8.4	25	1	US-11-121-849-602992 Sequence 602992, A
21	19.2	8.1	25	1	US-11-060-756-81510 Sequence 81510, A
22	19.2	8.1	25	1	US-11-121-849-149128 Sequence 149128, A
23	19.2	8.1	25	1	US-11-121-849-585763 Sequence 585763, A
24	19.2	8.1	25	1	US-11-121-849-585764 Sequence 585764, A
25	19.2	8.1	25	1	US-11-121-849-668361 Sequence 668361, A
26	19.2	8.1	25	1	US-11-121-849-668361 Sequence 668361, A
27	18.8	8.0	22	1	US-10-310-914A-661230 Sequence 661230, A
28	18.8	8.0	23	1	US-10-310-914A-663659 Sequence 663659, A
29	18.8	8.0	23	1	US-10-310-914A-99059 Sequence 99059, A
30	18.8	8.0	24	1	US-10-310-914A-1158304 Sequence 1158304, A
31	18.8	8.0	25	1	US-10-719-900-570264 Sequence 570264, A
32	18.8	8.0	25	1	US-10-956-157-161277 Sequence 161277, A
33	18.8	8.0	25	1	US-10-310-914A-845546 Sequence 845546, A

34	18.6	7.9	25	1	US-10-681-773-20812 Sequence 20812, A
35	18.6	7.9	25	1	US-10-681-773-24075 Sequence 24075, A
36	18.6	7.9	25	1	US-10-681-773-41906 Sequence 41906, A
37	18.6	7.9	25	1	US-10-681-773-42861 Sequence 42861, A
38	18.6	7.9	25	1	US-10-681-773-70955 Sequence 70955, A
39	18.6	7.9	25	1	US-10-681-773-77134 Sequence 77134, A
40	18.6	7.9	25	1	US-10-681-773-77826 Sequence 77826, A
41	18.6	7.9	25	1	US-10-956-157-155282 Sequence 155282, A
42	18.6	7.9	25	1	US-10-956-157-131003 Sequence 131003, A
43	18.6	7.9	25	1	US-10-956-157-199403 Sequence 199403, A
44	18.6	7.9	25	1	US-11-060-756-81506 Sequence 81506, A
45	18.6	7.9	25	1	US-11-121-849-584812 Sequence 584812, A
46	18.6	7.9	25	1	US-11-121-849-597792 Sequence 597792, A
47	18.6	7.9	25	1	US-11-121-849-637715 Sequence 637715, A
48	18.6	7.9	25	1	US-11-121-849-638121 Sequence 638121, A
49	18.6	7.9	25	1	US-11-121-849-663681 Sequence 663681, A
50	18.4	7.8	24	1	US-10-310-914A-131336 Sequence 131336, A
51	18.4	7.8	24	1	US-10-310-914A-131336 Sequence 131336, A
52	18.4	7.8	25	1	US-10-956-157-180126 Sequence 180126, A
53	18.2	7.7	23	1	US-10-310-914A-116036 Sequence 116036, A
54	18.2	7.7	24	1	US-10-310-914A-453805 Sequence 453805, A
55	18.2	7.7	25	1	US-10-681-773-106005 Sequence 106005, A
56	18.2	7.7	25	1	US-10-719-900-221757 Sequence 221757, A
57	18.2	7.7	25	1	US-10-956-157-170117 Sequence 170117, A
58	18.2	7.7	25	1	US-10-310-914A-715048 Sequence 715048, A
59	18.2	7.7	25	1	US-11-121-849-297414 Sequence 297414, A
60	18.2	7.6	18	1	US-10-310-914A-1140091 Sequence 1140091, A
61	17.8	7.5	21	1	US-10-847-918-1939 Sequence 1939, Ap
62	17.8	7.5	21	1	US-10-847-918-1941 Sequence 1941, Ap
63	17.8	7.5	21	1	US-10-847-918-2094 Sequence 2094, Ap
64	17.8	7.5	21	1	US-10-310-914A-116023 Sequence 116023, A
65	17.8	7.5	21	1	US-10-310-914A-845545 Sequence 845545, A
66	17.8	7.5	21	1	US-10-310-914A-967563 Sequence 967563, A
67	17.8	7.5	21	1	US-10-310-914A-1073142 Sequence 1073142, A
68	17.8	7.5	21	1	US-10-310-914A-1073155 Sequence 1073155, A
69	17.8	7.5	21	1	US-10-310-914A-1295208 Sequence 1295208, A
70	17.8	7.5	21	1	US-11-063-391-290 Sequence 290, App
71	17.8	7.5	22	1	US-10-310-914A-628574 Sequence 628574, A
72	17.8	7.5	22	1	US-10-310-914A-1180683 Sequence 1180683, A
73	17.8	7.5	25	1	US-10-956-157-281991 Sequence 281991, A
74	17.8	7.5	25	1	US-10-310-914A-399112 Sequence 399112, A
75	17.8	7.5	25	1	US-11-121-849-152798 Sequence 152798, A
76	17.6	7.5	24	1	US-10-310-914A-1073186 Sequence 1073186, A
77	17.6	7.5	24	1	US-10-310-914A-1295216 Sequence 1295216, A
78	17.6	7.5	25	1	US-10-681-773-33765 Sequence 33765, A
79	17.6	7.5	25	1	US-10-681-773-38235 Sequence 38235, A
80	17.6	7.5	25	1	US-10-719-900-320328 Sequence 320328, A
81	17.6	7.5	25	1	US-10-956-157-55283 Sequence 55283, A
82	17.6	7.5	25	1	US-10-956-157-55284 Sequence 55284, A
83	17.6	7.5	25	1	US-10-956-157-123288 Sequence 123288, A
84	17.6	7.5	25	1	US-10-956-157-199404 Sequence 199404, A
85	17.6	7.5	25	1	US-10-843-527-11826 Sequence 11826, A
86	17.6	7.5	25	1	US-10-843-527-22487 Sequence 22487, A
87	17.6	7.5	25	1	US-10-932-182A-168000 Sequence 168000, A
88	17.6	7.5	25	1	US-11-036-317-739119 Sequence 739119, A
89	17.6	7.5	25	1	US-11-036-317-739660 Sequence 739660, A
90	17.6	7.5	25	1	US-11-036-317-860630 Sequence 860630, A
91	17.6	7.5	25	1	US-11-121-849-58191 Sequence 58191, A
92	17.6	7.5	25	1	US-11-121-849-668370 Sequence 668370, A
93	17.6	7.5	25	1	US-11-121-849-668370 Sequence 668370, A
94	17.6	7.5	25	1	US-11-121-849-668370 Sequence 668370, A
95	17.4	7.4	19	1	US-11-083-784-292730 Sequence 292730, A
96	17.4	7.4	19	1	US-11-083-784-292730 Sequence 292730, A
97	17.4	7.4	19	1	US-11-101-244-1546724 Sequence 1546724, A
98	17.4	7.4	19	1	US-11-101-244-1546724 Sequence 1546724, A
99	17.4	7.4	20	1	US-10-310-914A-1158279 Sequence 1158279, A
100	17.2	7.3	22	1	US-10-310-914A-115819 Sequence 115819, A
101	17.2	7.3	22	1	US-10-310-914A-969089 Sequence 969089, A
102	17.2	7.3	22	1	US-10-310-914A-1036172 Sequence 1036172, A
103	17.2	7.3	22	1	US-10-310-914A-1087700 Sequence 1087700, A
104	17.2	7.3	23	1	US-10-310-914A-27857 Sequence 27857, A
105	17.2	7.3	23	1	US-10-310-914A-1158289 Sequence 1158289, A
106	17.2	7.3	24	1	US-10-310-914A-32934 Sequence 32934, A

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107 17.2 7.3 24 1 US-10-310-914A-66335 Sequence 66335, A
108 16.8 7.1 20 1 US-10-298-953-44 Sequence 44, Appl
109 16.8 7.1 20 1 US-10-310-914A-661149 Sequence 661149,
110 16.8 7.1 20 1 US-10-310-914A-845542 Sequence 845542,
111 16.8 7.1 20 1 US-10-310-914A-1073095 Sequence 1073095,
112 16.8 7.1 20 1 US-10-310-914A-1242020 Sequence 1242020,
113 16.8 7.1 21 1 US-10-847-918-1184 Sequence 1184, Ap
114 16.8 7.1 21 1 US-10-847-918-1853 Sequence 1853, Ap
115 16.8 7.1 21 1 US-10-847-918-1942 Sequence 1942, Ap
116 16.8 7.1 21 1 US-10-847-918-1944 Sequence 1944, Ap
117 16.8 7.1 21 1 US-10-847-918-2092 Sequence 2092, Ap
118 16.8 7.1 21 1 US-10-310-914A-828967 Sequence 828967,
119 16.8 7.1 21 1 US-10-310-914A-1009274 Sequence 1009274,
120 16.8 7.1 21 1 US-10-310-914A-1371246 Sequence 1371246,
121 16.8 7.1 23 1 US-10-310-914A-74338 Sequence 74338, A
122 16.8 7.1 24 1 US-10-416-122-2 Sequence 2, Appli
123 16.8 7.0 23 1 US-10-708-204-3803 Sequence 3803, Ap
124 16.6 7.0 23 1 US-10-310-914A-287417 Sequence 287417,
125 16.6 7.0 23 1 US-10-310-914A-360372 Sequence 360372,
126 16.6 7.0 23 1 US-10-310-914A-651766 Sequence 651766,
127 16.6 7.0 23 1 US-10-310-914A-819312 Sequence 819312,
128 16.6 7.0 23 1 US-10-310-914A-967480 Sequence 967480,
129 16.6 7.0 23 1 US-10-310-914A-1186008 Sequence 1186008,
130 16.4 6.9 18 1 US-10-310-914A-115988 Sequence 115988,
131 16.4 6.9 18 1 US-10-310-914A-1053329 Sequence 1053329,
132 16.4 6.9 19 1 US-10-727-780A-425 Sequence 425, App
133 16.4 6.9 19 1 US-10-310-914A-1053330 Sequence 1053330,
134 16.4 6.9 19 1 US-11-083-784-134328 Sequence 143328,
135 16.4 6.9 19 1 US-11-083-784-134365 Sequence 143365,
136 16.4 6.9 19 1 US-11-083-784-863172 Sequence 863172,
137 16.4 6.9 19 1 US-11-083-784-914575 Sequence 914575,
138 16.4 6.9 19 1 US-11-083-784-1250582 Sequence 1250582,
139 16.4 6.9 19 1 US-11-101-244-134365 Sequence 134365,
140 16.4 6.9 19 1 US-11-101-244-134365 Sequence 134365,
141 16.4 6.9 19 1 US-11-101-244-863172 Sequence 863172,
142 16.4 6.9 19 1 US-11-101-244-914575 Sequence 914575,
143 16.4 6.9 19 1 US-11-101-244-1250582 Sequence 1250582,
144 16.4 6.9 21 1 US-10-310-914A-31831 Sequence 31831,
145 16.2 6.9 21 1 US-10-708-204-3346 Sequence 3346, Ap
146 16.2 6.9 21 1 US-10-310-914A-59888 Sequence 59888, A
147 16.2 6.9 21 1 US-10-310-914A-95531 Sequence 95531, A
148 16.2 6.9 21 1 US-10-310-914A-174457 Sequence 174457,
149 16.2 6.9 21 1 US-10-310-914A-612161 Sequence 612161,
150 16.2 6.9 21 1 US-10-310-914A-628516 Sequence 628516,
151 16.2 6.9 21 1 US-10-310-914A-969044 Sequence 969044,
152 16.2 6.9 21 1 US-10-310-914A-1111794 Sequence 1111794,
153 16.2 6.9 21 1 US-10-310-914A-1227944 Sequence 1227944,
154 16.2 6.9 22 1 US-10-310-914A-97305 Sequence 97305, A
155 16.2 6.9 22 1 US-10-310-914A-360369 Sequence 360369,
156 16.2 6.9 22 1 US-10-310-914A-875345 Sequence 875345,
157 16.2 6.9 22 1 US-10-310-914A-910065 Sequence 910065,
158 16.2 6.9 23 1 US-10-082-800A-521 Sequence 521, App
159 16.2 6.9 23 1 US-10-310-914A-596179 Sequence 596179,
160 16.2 6.9 23 1 US-10-310-914A-1171021 Sequence 1171021,
161 16 6.8 18 1 US-10-310-914A-1037134 Sequence 1037134,
162 16 6.8 19 1 US-11-083-784-508230 Sequence 508230,
163 16 6.8 19 1 US-11-101-244-508230 Sequence 508230,
164 16 6.8 20 1 US-09-791-942-85 Sequence 85, Appl
165 16 6.8 20 1 US-10-415-463-85 Sequence 85, Appl
166 16 6.8 20 1 US-10-476-264-285 Sequence 285, App
167 16 6.8 22 1 US-10-310-914A-1037133 Sequence 1037133,

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ALIGNMENTS

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RESULT 1
; Sequence 437, Application US/10891260
; Publication No. US20050227244A1
; GENERAL INFORMATION:
; APPLICANT: Affymetrix, Inc.
; APPLICANT: Matsuzaki, Hajime

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; APPLICANT: Mei, Rui
; TITLE OF INVENTION: Methods of Analysis of Human Polymorphisms
; FILE REFERENCE: 3522.3
; CURRENT APPLICATION NUMBER: US/10/891,260
; PRIOR FILING DATE: 2004-07-13
; PRIOR APPLICATION NUMBER: 10/681,773
; PRIOR FILING DATE: 2003-10-07
; NUMBER OF SEQ ID NOS: 10244
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 437
; LENGTH: 33
; TYPE: DNA
; ORGANISM: homo sapien
; US-10-891-260-437

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Query Match 9.8%; Score 23.2; DB 1; Length 33;
Best Local Similarity 83.3%; Pred. No. 15;
Matches 25; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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Qy 14 GGGGAGATCCCTCATGATGTTAGTGC 43
Db 1 GGGGAGATCCCTTACRATGGCTTGTC 30

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RESULT 2
; Sequence 1140145, Application US/10310914A
; Publication No. US2006003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Bentwich, Isaac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1140145
; LENGTH: 28
; TYPE: RNA
; ORGANISM: Human
; US-10-310-914A-1140145

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Query Match 9.4%; Score 22.2; DB 1; Length 28;
Best Local Similarity 88.3%; Pred. No. 18;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy 13 GGGGAGATCCCTCATGATGTTTA 39
Db 27 GAGGAGATCCCTTATGATGTTCA 1

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RESULT 3
; Sequence 81484, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81484
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
; US-11-060-756-81484

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Query Match 9.2%; Score 21.8; DB 1; Length 25;
 Best Local Similarity 92.0%; Pred. No. 19;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 149 CTTCTCTCTGCGCATGATTTTAA 173
 |||||
 Db 25 CTTCACTCTCTGCGCATGATTTGAA 1

RESULT 4
 US-11-060-756-81500/c
 ; Sequence 81500, Application US/11060756
 ; Publication No. US20050221354A1
 ; GENERAL INFORMATION:

; APPLICANT: Wyeth
 ; APPLICANT: Mounts, William Martin
 ; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
 ; FILE REFERENCE: AM101083 (031896-042000)
 ; CURRENT APPLICATION NUMBER: US/11/060,756
 ; CURRENT FILING DATE: 2005-02-18
 ; NUMBER OF SEQ ID NOS: 303284
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 81500
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: probe
 US-11-060-756-81500

Query Match 9.2%; Score 21.8; DB 1; Length 25;
 Best Local Similarity 92.0%; Pred. No. 19;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 148 CTTCTCTCTGCGCATGATTTTAA 172
 |||||
 Db 25 CTTCACTCTCTGCGCATGATTTGAA 1

RESULT 5
 US-11-060-756-81511/c
 ; Sequence 81511, Application US/11060756
 ; Publication No. US20050221354A1
 ; GENERAL INFORMATION:

; APPLICANT: Wyeth
 ; APPLICANT: Mounts, William Martin
 ; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
 ; FILE REFERENCE: AM101083 (031896-042000)
 ; CURRENT APPLICATION NUMBER: US/11/060,756
 ; CURRENT FILING DATE: 2005-02-18
 ; NUMBER OF SEQ ID NOS: 303284
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 81511
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: probe
 US-11-060-756-81511

Query Match 9.2%; Score 21.8; DB 1; Length 25;
 Best Local Similarity 92.0%; Pred. No. 19;
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 154 CTTCTCTGCGCATGATTTTAA 178
 |||||
 Db 25 CTTCTCTGCGCATGATTTTAA 1

RESULT 6
 US-10-310-914A-1072814/c
 ; Sequence 1072814, Application US/10310914A
 ; Publication No. US20060003322A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Benitich, Isaac

; APPLICANT: Shiller, Kruzat
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 ; TITLE OF INVENTION: uses thereof
 ; FILE REFERENCE: 06087.0200.CPUS01
 ; CURRENT APPLICATION NUMBER: US/10/310,914A
 ; CURRENT FILING DATE: 2002-12-06
 ; NUMBER OF SEQ ID NOS: 1388402
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 1072814
 ; LENGTH: 23
 ; TYPE: RNA
 ; ORGANISM: Human
 US-10-310-914A-1072814

Query Match 9.1%; Score 21.4; DB 1; Length 23;
 Best Local Similarity 95.7%; Pred. No. 20;
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 44 CATCCCTTGATGATGATGAT 66
 |||||
 Db 23 CATCTCTTGATGATGATGAT 1

RESULT 7
 US-11-060-756-81487/c
 ; Sequence 81487, Application US/11060756
 ; Publication No. US20050221354A1
 ; GENERAL INFORMATION:

; APPLICANT: Wyeth
 ; APPLICANT: Mounts, William Martin
 ; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
 ; FILE REFERENCE: AM101083 (031896-042000)
 ; CURRENT APPLICATION NUMBER: US/11/060,756
 ; CURRENT FILING DATE: 2005-02-18
 ; NUMBER OF SEQ ID NOS: 303284
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 81487
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: probe
 US-11-060-756-81487

Query Match 8.8%; Score 20.8; DB 1; Length 25;
 Best Local Similarity 91.7%; Pred. No. 24;
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 150 TTCTCTCTGCGCATGATTTTAA 173
 |||||
 Db 25 TTCACTCTCTGCGCATGATTTTAA 2

RESULT 8
 US-11-060-756-81498/c
 ; Sequence 81498, Application US/11060756
 ; Publication No. US20050221354A1
 ; GENERAL INFORMATION:

; APPLICANT: Wyeth
 ; APPLICANT: Mounts, William Martin
 ; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
 ; FILE REFERENCE: AM101083 (031896-042000)
 ; CURRENT APPLICATION NUMBER: US/11/060,756
 ; CURRENT FILING DATE: 2005-02-18
 ; NUMBER OF SEQ ID NOS: 303284
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 81498
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: probe
 US-11-060-756-81498

Query Match 8.8%; Score 20.8; DB 1; Length 25;

Best Local Similarity 91.7%; Pred. No. 24;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 155 CTTCTGCCATGATTTAAGATTCC 178
Db 25 CTTCTGCCATGATTTAAGATTCC 2

RESULT 9
US-11-060-756-81501/c
; Sequence 81501, Application US/11060756
; Publication No. US200502135441
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81501
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-81501

Query Match 8.6%; Score 20.8; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 24;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 154 CTTCTGCCATGATTTAAGATTTC 177
Db 24 CTTCTGCCATGATTTAAGATTTC 1

RESULT 10
US-10-310-914A-596177
; Sequence 596177, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 596177
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-596177

Query Match 8.6%; Score 20.4; DB 1; Length 24;
Best Local Similarity 63.6%; Pred. No. 26;
Matches 14; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 139 CTTCTGCCATGATTTAAGATTTC 160
Db 3 CTTCTGCCATGATTTAAGATTTC 24

RESULT 11
US-10-310-914A-116013/c
; Sequence 116013, Application US/10310914A
; Publication No. US2006000322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kuzat

; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 116013
; LENGTH: 25
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-116013

Query Match 8.6%; Score 20.4; DB 1; Length 25;
Best Local Similarity 95.5%; Pred. No. 26;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 78 CTTCTGCCATGATTTAAGATTTC 99
Db 25 CTTCTGCCATGATTTAAGATTTC 4

RESULT 12
US-11-060-756-81488/c
; Sequence 81488, Application US/11060756
; Publication No. US2005021354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81488
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-81488

Query Match 8.6%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 28;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 151 TTTCTGCCATGATTTAAGATTTC 175
Db 25 TTTCTGCCATGATTTAAGATTTC 1

RESULT 13
US-11-060-756-81497/c
; Sequence 81497, Application US/11060756
; Publication No. US2005021354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81497
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-81497

Query Match 8.6%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 28;

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Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 156 TTCGCCATGATTTAAGATTCCAG 180
Db 25 TTCGCCATGATTTAAGATTCCAG 1

RESULT 14
US-11-060-756-81505/C
; Sequence 81505, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM1083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81505
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe
US-11-060-756-81505

Query Match 8.6%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 28;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 152 CTCCTTCGCCATGATTTAAGATT 176
Db 25 CACCTTCGCCATGATTTAAGATT 1

RESULT 15
US-11-121-849-628945
; Sequence 628945, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 628945
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-628945

Query Match 8.6%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 28;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 195 GCAATGCTAACGCCATGCTCTTG 219
Db 1 GCAATGCTAACGCCATGCTCTTG 25

RESULT 16
US-11-121-849-630324
; Sequence 630324, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
```

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; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 630324
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-630324

Query Match 8.6%; Score 20.2; DB 1; Length 25;
Best Local Similarity 88.0%; Pred. No. 28;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 195 GCAATGCTAACGCCATGCTCTTG 219
Db 1 GCAATGCTAACGCCATGCTCTTG 25

RESULT 17
US-10-310-914A-661150/C
; Sequence 661150, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 661150
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-661150

Query Match 8.4%; Score 19.8; DB 1; Length 23;
Best Local Similarity 91.3%; Pred. No. 30;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 65 GTTACGAGAGAGCTGTTGTTT 87
Db 23 GTTCTCGAGAGATCTGTTGTTT 1

RESULT 18
US-10-310-914A-1073215/C
; Sequence 1073215, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1073215
; LENGTH: 25
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1073215

Query Match 8.4%; Score 19.8; DB 1; Length 25;
```


Best Local Similarity 91.3%; Pred. No. 31;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 18 CAGATCCCTCATGATGTTAG 40
Db 25 CAGATCCCTCATGATGTTAG 3

RESULT 19

US-11-121-849-597791/C
; Sequence 597791, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:

; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 597791
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-597791

Query Match
Best Local Similarity 91.3%; Pred. No. 31;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 48 CCCTTGCGATGAGTGTAC 70
Db 25 CCCTTGCGATGAGTGTAC 3

RESULT 20

US-11-121-849-602992
; Sequence 602992, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:

; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 602992
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-602992

Query Match
Best Local Similarity 91.3%; Pred. No. 31;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 18 CAGATCCCTCATGATGTTAG 40
Db 1 CAGATCCCTCATGATGTTAG 23

RESULT 21

US-11-060-756-81510/C
; Sequence 81510, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:

; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug

; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81510
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-81510

Query Match
Best Local Similarity 87.5%; Pred. No. 35;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 157 TCTGCCATGATTTAGATCCAG 180
Db 25 TCTGCCATGATTTAGATTTCTTG 2

RESULT 22

US-11-121-849-149128
; Sequence 149128, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:

; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 149128
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-149128

Query Match
Best Local Similarity 87.5%; Pred. No. 35;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 40 GTGCCATCCCTTGATGAGTG 63
Db 2 GTGCCATCCCTCATGATGAGTG 25

RESULT 23

US-11-121-849-595763/C
; Sequence 595763, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:

; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 595763
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien

US-11-121-849-595763

Query Match	8.1%	Score 19.2;	DB 1;	Length 25;
Best Local Similarity	87.5%;	Pred. No. 35;		
Matches	21; Conservative	0; Mismatches	3; Indels	0; Gaps

Oy 64 AGTTCACGTGAGAGCTGGTGT 87
 |||||
 Db 25 AGTCTCTGTGAGAGCTGGCTTT 2

RESULT 24

```

US-11-121-849-595764/c
Sequence 595764, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 595764
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-595764

```

Query Match	8.1%	Score 19.2;	DB 1;	Length 25;
Best Local Similarity	87.5%;	Pred. No. 35;		
Matches 21; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0

QY	60	AGTGAGTTCACGTGAGAGCTGTT	83
Db	24	AGTGAGTCTTGTGAGAGCTGGCT	1

RESULT 25
US-11-121-849-668361/c

```

Sequence 668361, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
TITLE OF INVENTION: Microarrays
PILS REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 668361
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-668361

```

Query Match	8.1%;	Score 19.2;	DB 1;	Length 25;
Best Local Similarity	87.5%;	Pred. No. 35;		
Matches 21; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

[illegible]

RESULT 26
US-11-121-849-673887

; Sequence 673887, Application US/11121849
; Publication No. US20050272080A1
; Publication No. 20050272080A1

```

: GENERAL INFORMATION:
: APPLICANT: John Palma
: TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
: TITLE OF INVENTION: Microarrays
: FILE REFERENCE: 3684.1
: CURRENT APPLICATION NUMBER: US/11/121,849
: CURRENT FILING DATE: 2005-05-03
: PRIOR APPLICATION NUMBER: 60/567,949
: PRIOR FILING DATE: 2004-05-03
: NUMBER OF SEQ ID NOS: 673904
: SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
: SEQ ID NO 673887

```

Query Match	8.1%	Score 19.2;	DB 1;	Length 25;
Best Local Similarity	87.5%	Pred. No. 35;		
Matches 21; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

```
Oy      64 AGTTCACGTGAGAGCTGGTTGTTT    87  
         |||||  
Db      1 AGTTCTCCTGAGAGCTAGTGTTT   24
```

RESULT 27
ME-10-210

```

US-10-310-914A-661230
: Sequence 661230, Application US/1031091A4
: Publication No. US20060003322A1
: GENERAL INFORMATION:
: APPLICANT: Bentwich, Isaac
: APPLICANT: Shlier, Kiyaz
: TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
: TITLE OF INVENTION: uses thereof
: FILE REFERENCE: 06087.0200.CPUS01
: CURRENT APPLICATION NUMBER: US/10/310,914A
: CURRENT FILING DATE: 2002-12-06
: NUMBER OF SEQ ID NOS: 1388402
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 661230
: LENGTH: 22
: TYPE: RNA
: ORGANISM: Human
US-10-310-914A-661230

```

Query Match	8.0%	Score 18.8;	DB 1;	Length 22;
Best Local Similarity	90.9%;	Pred. No. 37;		
Matches 20; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

```

QY      71 GTGAGAGCTGGTTGTTGAAG 92
          |||||
Db      22 GTGAGATCTGGTTGTTAAAG 1

```

RESULT 28
US-10-310

Sequence 66369, Applicant US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shlier, Yvuzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 66369
LENGTH: 23

```
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-66369

Query Match      8.0%; Score 18.8; DB 1; Length 23;
Best Local Similarity 63.6%; Pred. No. 38;
Matches 14; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY      137 CACCTGCTCCCTTCCTTCCTTC 158
Db      1 CGCCUGCCGCCUCCUCCGCUUC 22

RESULT 29
US-10-310-914A-99099
; Sequence 99099, Application US/10310914A
; Publication No. US2006003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 99099
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-99099

Query Match      8.0%; Score 18.8; DB 1; Length 23;
Best Local Similarity 59.1%; Pred. No. 38;
Matches 13; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY      140 CTGCTCCCTTCCTTCCTTCCTTC 161
Db      1 CUGCUCGCCGCCUCCUCCUCC 22

RESULT 30
US-10-310-914A-1158304
; Sequence 1158304, Application US/10310914A
; Publication No. US2006003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1158304
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1158304

Query Match      8.0%; Score 18.8; DB 1; Length 24;
Best Local Similarity 59.1%; Pred. No. 38;
Matches 13; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY      139 CCTGCTCCCTTCCTTCCTTCCTTC 160
Db      3 CCUGCUCGCCGCCUCCUCCUCC 24

RESULT 31
US-10-719-900-570264
```

```
; Sequence 570264, Application US/107199900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 570264
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-570264

Query Match      8.0%; Score 18.8; DB 1; Length 25;
Best Local Similarity 90.9%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      115 CTGCTCCCACTCTTGCAATGAGA 136
Db      2 CTGCACCCCACTCTTGCAAGAGA 23

RESULT 32
US-10-956-157-161277/C
; Sequence 161277, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wveth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 161277
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-161277

Query Match      8.0%; Score 18.8; DB 1; Length 25;
Best Local Similarity 90.9%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      17 GCAGATCCCTCATGATGCTT 38
Db      22 GCAGATCCTTCATGATGCTT 1

RESULT 33
US-10-310-914A-845546/C
; Sequence 845546, Application US/10310914A
; Publication No. US2006003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 845546
; LENGTH: 25
; TYPE: RNA
```

ORGANISM: Human
US-10-914A-845546

Query Match 8.0%; Score 18.8; DB 1; Length 25;
Best Local Similarity 90.9%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 139 CCTGCTCCCTCTCTCTCTG 160
DB 22 CCGCTTCCCTCTCTCTCTG 1

RESULT 34
US-10-681-773-20812

Sequence 20812, Application US/10681773
Publication No. US20040146890A1

GENERAL INFORMATION:

APPLICANT: Matsuizaki, Hajime

APPLICANT: Mei, Rui

APPLICANT: Shen, Mei-Mei

APPLICANT: Kennedy, Giulia

TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans

FILE REFERENCE: 3522.2

CURRENT APPLICATION NUMBER: US/10/681,773

CURRENT FILING DATE: 2003-10-07

PRIOR APPLICATION NUMBER: 60/470,475

PRIOR FILING DATE: 2002-05-14

PRIOR APPLICATION NUMBER: 60/417,190

PRIOR FILING DATE: 2002-10-08

NUMBER OF SEQ ID NOS: 124031

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 20812

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapien

US-10-681-773-20812

Query Match 7.9%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 41;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 19 AGATCCCTCATGATGTTTAGTG 43
DB 1 AGATCCCTTACGATGCTTGTC 25

RESULT 35
US-10-681-773-24075/c

Sequence 24075, Application US/10681773
Publication No. US20040146890A1

GENERAL INFORMATION:

APPLICANT: Matsuizaki, Hajime

APPLICANT: Mei, Rui

APPLICANT: Shen, Mei-Mei

APPLICANT: Kennedy, Giulia

TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans

FILE REFERENCE: 3522.2

CURRENT APPLICATION NUMBER: US/10/681,773

CURRENT FILING DATE: 2003-10-07

PRIOR APPLICATION NUMBER: 60/470,475

PRIOR FILING DATE: 2002-05-14

PRIOR APPLICATION NUMBER: 60/417,190

PRIOR FILING DATE: 2002-10-08

NUMBER OF SEQ ID NOS: 124031

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 24075

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapien

US-10-681-773-24075

Query Match 7.9%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 41;

Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 73 GAGAGCTGTTGTTGAAGACCT 97
DB 25 GAGACTAGTTGTTGAAAAGACCT 1

RESULT 36
US-10-681-773-41906

Sequence 41906, Application US/10681773
Publication No. US20040146890A1

GENERAL INFORMATION:

APPLICANT: Matsuizaki, Hajime

APPLICANT: Mei, Rui

APPLICANT: Shen, Mei-Mei

APPLICANT: Kennedy, Giulia

TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans

FILE REFERENCE: 3522.2

CURRENT APPLICATION NUMBER: US/10/681,773

CURRENT FILING DATE: 2003-10-07

PRIOR APPLICATION NUMBER: 60/470,475

PRIOR FILING DATE: 2002-05-14

PRIOR APPLICATION NUMBER: 60/417,190

PRIOR FILING DATE: 2002-10-08

NUMBER OF SEQ ID NOS: 124031

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 41906

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapien

US-10-681-773-41906

Query Match 7.9%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 41;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 18 CAGATCCCTCATGATGTTTAGTG 42
DB 1 CAGATCCCTTACGATGCTTGTC 25

RESULT 37
US-10-681-773-42861/c

Sequence 42861, Application US/10681773
Publication No. US20040146890A1

GENERAL INFORMATION:

APPLICANT: Matsuizaki, Hajime

APPLICANT: Mei, Rui

APPLICANT: Shen, Mei-Mei

APPLICANT: Kennedy, Giulia

TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans

FILE REFERENCE: 3522.2

CURRENT APPLICATION NUMBER: US/10/681,773

CURRENT FILING DATE: 2003-10-07

PRIOR APPLICATION NUMBER: 60/470,475

PRIOR FILING DATE: 2002-05-14

PRIOR APPLICATION NUMBER: 60/417,190

PRIOR FILING DATE: 2002-10-08

NUMBER OF SEQ ID NOS: 124031

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 42861

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapien

US-10-681-773-42861

Query Match 7.9%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 41;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 74 AGAGCTGTTGTTGAAGACCTG 98
DB 25 AGACTAGTTGTTGAAAAGACCTG 1

```
RESULT 38
US-10-681-773-70955
; Sequence 70955, Application US/10681773
; Publication No. US20040146890A1
; GENERAL INFORMATION:
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: Mei, Rui
; APPLICANT: Shen, Mei-Mei
; APPLICANT: Kennedy, Giulia
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522.2
; CURRENT APPLICATION NUMBER: US/10/681,773
; PRIOR FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: 60/470,475
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/417,190
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 124031
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 70955
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-681-773-70955
```

```
Query Match          7.9%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 41;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Oy      17 GCAGATCCCTCATGATGCTTTAGT 41
Db      1 GCAGATCCCTTACGATGCGCTTGT 25
```

```
RESULT 39
US-10-681-773-77134
; Sequence 77134, Application US/10681773
; Publication No. US20040146890A1
; GENERAL INFORMATION:
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: Mei, Rui
; APPLICANT: Shen, Mei-Mei
; APPLICANT: Kennedy, Giulia
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522.2
; CURRENT APPLICATION NUMBER: US/10/681,773
; PRIOR FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: 60/470,475
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/417,190
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 124031
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 77134
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-681-773-77134
```

```
Query Match          7.9%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 41;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Oy      16 GGCAGATCCCTCATGATGCTTTAG 40
Db      1 GGCAGATCCCTTACGATGCGCTTGT 25
```

```
RESULT 40
US-10-681-773-77826/c
; Sequence 77826, Application US/10681773
```

```
; Publication No. US20040146890A1
; GENERAL INFORMATION:
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: Mei, Rui
; APPLICANT: Shen, Mei-Mei
; APPLICANT: Kennedy, Giulia
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522.2
; CURRENT APPLICATION NUMBER: US/10/681,773
; PRIOR FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: 60/470,475
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/417,190
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 124031
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 77826
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-681-773-77826
```

```
Query Match          7.9%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 41;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Oy      72 TGAGAGCTGCTGTTTGAAGAGCC 96
Db      25 TGAGAACTAGTGTGTGAAGAGCC 1
```

```
RESULT 41
US-10-956-157-55282/c
; Sequence 55282, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55282
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-55282
```

```
Query Match          7.9%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 41;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Oy      149 CTTCTCCTTCTGCCATGATTTTAAG 173
Db      25 CTTCACTTCCACCATGATTTCTAAG 1
```

```
RESULT 42
US-10-956-157-131003
; Sequence 131003, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
```

```
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 131003
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-131003
```

```
Query Match          7.9%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 41;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY      210 ATGCTTCTGTTGTTGCTGCAAAAC 234
      ||||| ||||| ||||| ||||| |||||
Db      1 ATGCTTCTGTACAGCTGCAAAAC 25
```

```
RESULT 43
US-10-956-157-199403
; Sequence 199403, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Wyeth
; APPLICANT: Mounte, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319605
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 199403
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-199403
```

```
Query Match          7.9%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 41;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY      154 CTTCTGCGCATGATTTAAGATTC 178
      ||||| ||||| ||||| ||||| |||||
Db      1 CTTCTGCGCATGATGTCAGTTCC 25
```

```
RESULT 44
US-11-060-756-81506/C
; Sequence 81506, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Wyeth
; APPLICANT: Mounte, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 81506
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe
US-11-060-756-81506
```

```
Query Match          7.9%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 41;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY      158 CTGCGCATGATTTAAGATTCAGGG 182
      ||||| ||||| ||||| ||||| |||||
Db      25 CTGCGATGATTGTAAGTTCTGAG 1
```

```
RESULT 45
US-11-121-849-584812/C
; Sequence 584812, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
```

```
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 584812
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-584812
```

```
Query Match          7.9%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 41;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY      67 TCACGTGAGACTGCTGTTGAAA 91
      ||||| ||||| ||||| ||||| |||||
Db      25 TCACCTGAGACTGATTGCTTAAAA 1
```

```
RESULT 46
US-11-121-849-597792/C
; Sequence 597792, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
```

```
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 597792
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-597792
```

```
Query Match          7.9%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 41;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY      24 CCTCATGATGCTTTAGTCCATCC 48
      ||||| ||||| ||||| ||||| |||||
Db      25 CCTCATGATGATTAAGTGCACCC 1
```

```
RESULT 47
US-11-121-849-637715
; Sequence 637715, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
```

```
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
```

PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 637715
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-637715

Query Match 7.9%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 41;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

24 CCTCATGATGTTAGTGCATCC 48
1 CTTCATGATGTTAGTGCATCC 25

RESULT 48
US-11-121-849-638121
Sequence 638121, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 638121
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-638121

Query Match 7.9%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 41;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

24 CCTCATGATGTTAGTGCATCC 48
1 CTTCATGATGTTAGTGCATCC 25

RESULT 49
US-11-121-849-663681/C
Sequence 663681, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 663681
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-663681

Query Match 7.9%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 41;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

24 CCTCATGATGTTAGTGCATCC 48
1 CTTCATGATGTTAGTGCATCC 25

RESULT 49
US-11-121-849-663681/C
Sequence 663681, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 663681
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-663681

Query Match 7.9%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 41;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

24 CCTCATGATGTTAGTGCATCC 48
1 CTTCATGATGTTAGTGCATCC 25

RESULT 50
US-10-310-914A-131336
Sequence 131336, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiller, Kvuazac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 131336
LENGTH: 24
TYPE: RNA
ORGANISM: Human
US-10-310-914A-131336

Query Match 7.8%; Score 18.4; DB 1; Length 24;
Best Local Similarity 65.0%; Pred. No. 42;
Matches 13; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

105 TCTCATCTCTCTCTCTCCAC 124
2 UCUCANUCUCUCUCUCAC 21

RESULT 52
US-10-956-157-180126
Sequence 180126, Application US/10956157
Publication No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Muehle, William
APPLICANT: Muehle, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
FILE REFERENCE: 031896-043000 (AM 101081)

Query Match 7.9%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 41;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

79 TGGTGTGTAAGAGCTGCCCC 103
25 TGGCTCTTGAAGAGCTGCGAC 1

RESULT 50
US-10-310-914A-131336
Sequence 131336, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiller, Kvuazac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 131336
LENGTH: 21
TYPE: RNA
ORGANISM: Human
US-10-310-914A-131336

Query Match 7.8%; Score 18.4; DB 1; Length 21;
Best Local Similarity 65.0%; Pred. No. 40;
Matches 13; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

105 TCTCATCTCTCTCTCTCCAC 124
1 UCUCANUCUCUCUCUCAC 20

RESULT 51
US-10-310-914A-131349
Sequence 131349, Application US/10310914A
Publication No. US20060003322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shiller, Kvuazac
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: Patentin version 3.3
SEQ ID NO 131349
LENGTH: 24
TYPE: RNA
ORGANISM: Human
US-10-310-914A-131349

Query Match 7.8%; Score 18.4; DB 1; Length 24;
Best Local Similarity 65.0%; Pred. No. 42;
Matches 13; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

105 TCTCATCTCTCTCTCTCCAC 124
2 UCUCANUCUCUCUCUCAC 21

RESULT 52
US-10-956-157-180126
Sequence 180126, Application US/10956157
Publication No. US20050118625A1
GENERAL INFORMATION:
APPLICANT: Muehle, William
APPLICANT: Muehle, William
TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
FILE REFERENCE: 031896-043000 (AM 101081)

Query Match 7.9%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 41;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

24 CCTCATGATGTTAGTGCATCC 48
1 CTTCATGATGTTAGTGCATCC 25

RESULT 49
US-11-121-849-663681/C
Sequence 663681, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 663681
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-663681

Query Match 7.9%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 41;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

24 CCTCATGATGTTAGTGCATCC 48
1 CTTCATGATGTTAGTGCATCC 25

RESULT 49
US-11-121-849-663681/C
Sequence 663681, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 663681
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-663681

Query Match 7.9%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 41;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

24 CCTCATGATGTTAGTGCATCC 48
1 CTTCATGATGTTAGTGCATCC 25

RESULT 49
US-11-121-849-663681/C
Sequence 663681, Application US/11121849
Publication No. US20050272080A1
GENERAL INFORMATION:
APPLICANT: John Palma
TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
FILE REFERENCE: 3684.1
CURRENT APPLICATION NUMBER: US/11/121,849
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: 60/567,949
PRIOR FILING DATE: 2004-05-03
NUMBER OF SEQ ID NOS: 673904
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 663681
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-11-121-849-663681

Query Match 7.9%; Score 18.6; DB 1; Length 25;
Best Local Similarity 84.0%; Pred. No. 41;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

24 CCTCATGATGTTAGTGCATCC 48
1 CTTCATGATGTTAGTGCATCC 25

; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 180126
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-180126

Query Match 7.8%; Score 18.4; DB 1; Length 25;
Best Local Similarity 95.0%; Pred. No. 43;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 216 CTTGTTCTGCTGCAAACT 235
Db 1 CTTGTTCTGCTGCAAACT 20

RESULT 53
US-10-310-914A-116036/c
; Sequence 116036, Application US/10310914A
; Publication No. US20060003222A1
; GENERAL INFORMATION:
; APPLICANT: Benetwich, Isaac
; APPLICANT: Shiler, Kynzar
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 116036
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-116036

Query Match 7.7%; Score 18.2; DB 1; Length 23;
Best Local Similarity 87.0%; Pred. No. 44;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 42 GCCATCCCTTGCTGATGAGTGA 64
Db 23 GCCATCCCTGATGATGAGTGA 1

RESULT 54
US-10-310-914A-453805
; Sequence 453805, Application US/10310914A
; Publication No. US20060003222A1
; GENERAL INFORMATION:
; APPLICANT: Benetwich, Isaac
; APPLICANT: Shiler, Kynzar
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 453805
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-453805

Query Match 7.7%; Score 18.2; DB 1; Length 24;
Best Local Similarity 65.2%; Pred. No. 44;
Matches 15; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 134 AGACACCTGCTCCCTTCTCTCT 156

Db 2 AGCCUCCAGCUCUCCUUCUCUCU 24

RESULT 55
US-10-681-773-106005/c
; Sequence 106005, Application US/10681773
; Publication No. US20040146890A1
; GENERAL INFORMATION:
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: Mei, Rui
; APPLICANT: Shen, Mei-Mei
; APPLICANT: Kennedy, Giulia
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522.2
; CURRENT APPLICATION NUMBER: US/10/681,773
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: 60/470,475
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/417,190
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 124031
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 106005
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-681-773-106005

Query Match 7.7%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 45;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 78 CTGTTGTTGAAAGACCTGCG 100
Db 24 CTAGTTGTTGAAAGACCTGCG 2

RESULT 56
US-10-719-900-221757
; Sequence 221757, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 221757
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-221757

Query Match 7.7%; Score 18.2; DB 1; Length 25;
Best Local Similarity 87.0%; Pred. No. 45;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 64 AGTTCACGTGAGACCTGCTGT 86
Db 1 AGTTCACGTGAGACCTGCTGT 23

RESULT 57
US-10-956-157-170117/c
; Sequence 170117, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth


```

; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 31805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 170117
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-170117
```

```

Query Match
Best Local Similarity 87.0%; Score 18.2; DB 1; Length 25;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 62 TGAGTTCACGTGAGAGCTGGTTG 84
Db 23 TGAGTTCACGCAGATCTGGTTG 1
```

```

RESULT 58
US-10-310-914A-715048/c
; Sequence 715048, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kiyazac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 715048
; LENGTH: 25
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-715048
```

```

Query Match
Best Local Similarity 87.0%; Score 18.2; DB 1; Length 25;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 70 CGTGAGAGCTGGTTGTTGAAG 92
Db 23 CGTGAGAGCTGGTTGTTGCAAG 1
```

```

RESULT 59
US-11-121-849-297414/c
; Sequence 297414, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 297414
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-297414
```

```

Query Match
Best Local Similarity 87.0%; Score 18.2; DB 1; Length 25;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 5 TGGGTCAATGGGGCAGATCCCTC 27
Db 23 TAGGTCAATAGGGCAGATCCCTC 1
```

```

RESULT 60
US-10-310-914A-1140091/c
; Sequence 114091, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kiyazac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 114091
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1140091
```

```

Query Match
Best Local Similarity 100.0%; Score 18; DB 1; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 45 ATCCCTTGTTGGTGTAGT 62
Db 18 ATCCCTTGTTGGTGTAGT 1
```

```

RESULT 61
US-10-847-918-1939/c
; Sequence 1939, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeck
; APPLICANT: Liu, Xiaoping
; APPLICANT: Li, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1939
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-847-918-1939
```

```

Query Match
Best Local Similarity 90.5%; Score 17.8; DB 1; Length 21;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 149 CTTCTCCTTCGCGCATGATT 169
Db 21 CTTCTCCTTCGCGCATGATT 1
```

```

RESULT 62
US-10-847-918-1941
```

```

; Sequence 1941, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1941
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAI-antisense strand
US-10-847-918-1941

Query Match
Best Local Similarity 7.5%; Score 17.8; DB 1; Length 21;
Matches 9; Conservative 10; Mismatches 2; Indels 0; Gaps 0;

Qy 149 CTTCTCCTTCCTGCCATGATT 169
Db 1 CUUCUGUCUGCCAGAUUUU 21

RESULT 63
US-10-847-918-2094
; Sequence 2094, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2094
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAI-antisense strand
US-10-847-918-2094

Query Match
Best Local Similarity 7.5%; Score 17.8; DB 1; Length 21;
Matches 8; Conservative 11; Mismatches 2; Indels 0; Gaps 0;

Qy 150 TTCCTCTTCGCGCATGATT 170
Db 1 UUCUGUCUGCCAGAUUUU 21

RESULT 64
US-10-310-914A-116023/c
; Sequence 116023, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kiyazac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
```

```

; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 116023
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-116023

Query Match
Best Local Similarity 7.5%; Score 17.8; DB 1; Length 21;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 GTCATGGGGCGAGATCCTCA 28
Db 21 GTCATGGGGCGAGATCCTTA 1

RESULT 65
US-10-310-914A-845545/c
; Sequence 845545, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kiyazac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 845545
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-845545

Query Match
Best Local Similarity 7.5%; Score 17.8; DB 1; Length 21;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 140 CTGCTCCCCCTTCCTCTCTG 160
Db 21 CTGCTCCCCCTTCGCTCTG 1

RESULT 66
US-10-310-914A-967563/c
; Sequence 967563, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kiyazac
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 967563
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-967563

Query Match
Best Local Similarity 7.5%; Score 17.8; DB 1; Length 21;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 72 TGAGAGCTGTTGTTGAAAG 92
Db 21 TGAGATCTGCTTTTGAAG 1

RESULT 67

US-10-310-914A-1073142/c
; Sequence 1073142, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kvuzae
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1073142
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1073142

Query Match 7.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 47;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 140 CTGCTCCCCCTTCCTCTG 160
Db 21 CTGCTCCCCCTTCCTCTG 1

RESULT 68
US-10-310-914A-1073155/c
; Sequence 1073155, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kvuzae
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1073155
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1073155

Query Match 7.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 47;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 20 GATCCCTCATGATGCTTAG 40
Db 21 GATCCCTCATGATGCTTAG 1

RESULT 69
US-10-310-914A-1295208/c
; Sequence 1295208, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kvuzae
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01

; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1295208
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1295208

Query Match 7.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 47;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 140 CTGCTCCCCCTTCCTCTG 160
Db 21 CTGCTCCCCCTTCCTCTG 1

RESULT 70
US-11-063-391-290
; Sequence 290, Application US/11063391
; Publication No. US20050202077A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D
; APPLICANT: Murison, J Greg
; APPLICANT: Grigor, Murray R
; APPLICANT: Hayukala, Ilkka J
; APPLICANT: Munro, Grant
; APPLICANT: Aderethy, Nevin
; APPLICANT: Webster, Gill
; TITLE OF INVENTION: Targeted delivery of RNA interference
; FILE REFERENCE: 11000.1100U
; CURRENT APPLICATION NUMBER: US/11/063.391
; CURRENT FILING DATE: 2005-02-22
; NUMBER OF SEQ ID NOS: 980
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 290
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Human
US-11-063-391-290

Query Match 7.5%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 47;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 60 AGTGAGTTCACTGAGAGCTG 80
Db 1 AATGAGTTCACTGAGAGCTG 21

RESULT 71
US-10-310-914A-628574
; Sequence 628574, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kvuzae
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 628574
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-628574

Query Match 7.5% Score 17.8; DB 1; Length 22;
 Best Local Similarity 57.1%; Pred. No. 47;
 Matches 12; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

OY 113 TCCTGCTCCCACTCTTGATG 133
 :||:|||||:|||||:
 Db 1 UCCUGCUCACCACUUVUUGCUG 21

RESULT 72
 US-10-310-914A-1180683/c
 ; Sequence 1180683, Application US/10310914A
 ; Publication No. US2006003322A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bentwich, Isaac
 ; APPLICANT: Shlier, Kuzat
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 ; FILE REFERENCE: 06087.0200.CPUS01
 ; CURRENT APPLICATION NUMBER: US/10/310.914A
 ; CURRENT FILING DATE: 2002-12-06
 ; NUMBER OF SEQ ID NOS: 1388402
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 1180683
 ; LENGTH: 22
 ; TYPE: RNA
 ; ORGANISM: Human
 ; US-10-310-914A-1180683

Query Match 7.5% Score 17.8; DB 1; Length 22;
 Best Local Similarity 90.5%; Pred. No. 47;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 153 TCCTTCTGCCATGATTTTAA 173
 :|||:|||||:|||||:
 Db 22 TCCTTCTGCCATGATTTGAG 2

RESULT 73
 US-10-956-157-281991
 ; Sequence 281991, Application US/10956157
 ; Publication No. US20050118625A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Weeth
 ; APPLICANT: Mounts, William
 ; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
 ; FILE REFERENCE: 031896-043000 (AM 101081)
 ; CURRENT APPLICATION NUMBER: US/10/956.157
 ; CURRENT FILING DATE: 2004-10-04
 ; NUMBER OF SEQ ID NOS: 319805
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 281991
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Probe Sequence
 ; US-10-956-157-281991

Query Match 7.5% Score 17.8; DB 1; Length 25;
 Best Local Similarity 90.5%; Pred. No. 49;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 72 TGAGAGCTGGTTGTTGAAG 92
 :|||:|||||:|||||:
 Db 1 TGAGAGTGTGTTGTTTAAAG 21

RESULT 74
 US-10-310-914A-399112
 ; Sequence 399112, Application US/10310914A
 ; Publication No. US2006000322A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bentwich, Isaac

; APPLICANT: Shlier, Kuzat
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 ; FILE REFERENCE: 06087.0200.CPUS01
 ; CURRENT APPLICATION NUMBER: US/10/310.914A
 ; CURRENT FILING DATE: 2002-12-06
 ; NUMBER OF SEQ ID NOS: 1388402
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 399112
 ; LENGTH: 25
 ; TYPE: RNA
 ; ORGANISM: Human
 ; US-10-310-914A-399112

Query Match 7.5% Score 17.8; DB 1; Length 25;
 Best Local Similarity 81.0%; Pred. No. 49;
 Matches 17; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 178 CAGGACTTCACAGAGCA 198
 :|||:|||||:|||||:
 Db 4 CAGGCTTCCACAGAGCA 24

RESULT 75
 US-11-121-849-152798/c
 ; Sequence 152798, Application US/11121849
 ; Publication No. US20050272080A1
 ; GENERAL INFORMATION:
 ; APPLICANT: John Palma
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
 ; FILE REFERENCE: 3684.1
 ; CURRENT APPLICATION NUMBER: US/11/121.849
 ; CURRENT FILING DATE: 2005-05-03
 ; PRIOR APPLICATION NUMBER: 60/567,949
 ; PRIOR FILING DATE: 2004-05-03
 ; NUMBER OF SEQ ID NOS: 673904
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 152798
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 ; US-11-121-849-152798

Query Match 7.5% Score 17.8; DB 1; Length 25;
 Best Local Similarity 90.5%; Pred. No. 49;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 178 CAGGACTTCACAGAGCA 198
 :|||:|||||:|||||:
 Db 25 CAGGCTTCCACAGAGCA 5

RESULT 76
 US-10-310-914A-1073186/c
 ; Sequence 1073186, Application US/10310914A
 ; Publication No. US2006003322A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bentwich, Isaac
 ; APPLICANT: Shlier, Kuzat
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 ; FILE REFERENCE: 06087.0200.CPUS01
 ; CURRENT APPLICATION NUMBER: US/10/310.914A
 ; CURRENT FILING DATE: 2002-12-06
 ; NUMBER OF SEQ ID NOS: 1388402
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 1073186
 ; LENGTH: 24
 ; TYPE: RNA
 ; ORGANISM: Human
 ; US-10-310-914A-1073186

Query Match 7.5%; Score 17.6; DB 1; Length 24;
 Best Local Similarity 83.3%; Pred. No. 51;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 42 GCCATCCCTTGGTGAAGTGC 65
 Db 24 GCCATCCCTTGGTGAAGTGC 1

RESULT 77

US-10-310-914A-1295216/C
 ; Sequence 1295216, Application US/10310914A
 ; Publication No. US2006003322A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bentwich, Isaac
 ; APPLICANT: Shlier, Kuzat
 ; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
 ; FILE REFERENCE: 06087.0200.CPUS01
 ; CURRENT FILING DATE: 2002-12-06
 ; NUMBER OF SEQ ID NOS: 1388402
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 1295216
 ; LENGTH: 24
 ; TYPE: RNA
 ; ORGANISM: Human
 US-10-310-914A-1295216

Query Match 7.5%; Score 17.6; DB 1; Length 24;
 Best Local Similarity 83.3%; Pred. No. 51;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 7 GGTGATGGGGGAGATCCCTCATG 30
 Db 24 GGTGATGGGGGAGATCCCTCATG 1

RESULT 78

US-10-681-773-23765/C
 ; Sequence 23765, Application US/10681773
 ; Publication No. US20040146890A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Matsuzaki, Hajime
 ; APPLICANT: Mei, Rui
 ; APPLICANT: Shen, Mei-Mei
 ; APPLICANT: Kennedy, Giulia
 ; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
 ; FILE REFERENCE: 3522.2
 ; CURRENT APPLICATION NUMBER: US/10/681,773
 ; CURRENT FILING DATE: 2003-10-07
 ; PRIOR APPLICATION NUMBER: 60/470,475
 ; PRIOR FILING DATE: 2002-05-14
 ; PRIOR APPLICATION NUMBER: 60/417,190
 ; PRIOR FILING DATE: 2002-10-08
 ; NUMBER OF SEQ ID NOS: 124031
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 23765
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-10-681-773-23765

Query Match 7.5%; Score 17.6; DB 1; Length 25;
 Best Local Similarity 83.3%; Pred. No. 52;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 155 CTCTGGCATGATTTTAAATGCC 178
 Db 25 CTCTGGCATGATTTTAAATGCC 2

RESULT 79

US-10-681-773-38235/C
 ; Sequence 38235, Application US/10681773
 ; Publication No. US20040146890A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Matsuzaki, Hajime
 ; APPLICANT: Mei, Rui
 ; APPLICANT: Shen, Mei-Mei
 ; APPLICANT: Kennedy, Giulia
 ; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
 ; FILE REFERENCE: 3522.2
 ; CURRENT APPLICATION NUMBER: US/10/681,773
 ; CURRENT FILING DATE: 2003-10-07
 ; PRIOR APPLICATION NUMBER: 60/470,475
 ; PRIOR FILING DATE: 2002-05-14
 ; PRIOR APPLICATION NUMBER: 60/417,190
 ; PRIOR FILING DATE: 2002-10-08
 ; NUMBER OF SEQ ID NOS: 124031
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 38235
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-10-681-773-38235

Query Match 7.5%; Score 17.6; DB 1; Length 25;
 Best Local Similarity 83.3%; Pred. No. 52;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 152 CTCTGGCATGATTTTAAATGCC 175
 Db 25 CACCTTGGCATGATTTTAAATGCC 2

RESULT 80

US-10-719-900-320328
 ; Sequence 320328, Application US/10719900
 ; Publication No. US2005026164A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 ; FILE REFERENCE: 3528.1
 ; CURRENT APPLICATION NUMBER: US/10/719,900
 ; CURRENT FILING DATE: 2003-11-20
 ; PRIOR APPLICATION NUMBER: 60/427,808
 ; PRIOR FILING DATE: 2002-11-20
 ; NUMBER OF SEQ ID NOS: 982914
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 320328
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-10-719-900-320328

Query Match 7.5%; Score 17.6; DB 1; Length 25;
 Best Local Similarity 83.3%; Pred. No. 52;
 Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 178 CAGGGAATTGCAAGAAGCAATG 201
 Db 1 CAGGGAATTGCAAGAAGCAATG 24

RESULT 81

US-10-956-157-55283/C
 ; Sequence 55283, Application US/10956157
 ; Publication No. US20050118625A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wyeth
 ; APPLICANT: Mounse, William
 ; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
 ; FILE REFERENCE: 031896-043000 (AM 101081)
 ; CURRENT APPLICATION NUMBER: US/10/956,157

;; CURRENT FILING DATE: 2004-10-04
;; NUMBER OF SEQ ID NOS: 319805
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 55283
;; LENGTH: 25
;; TYPE: DNA
;; ORGANISM: Probe Sequence
US-10-956-157-55283

Query Match 7.5%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 52;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 149 CTTCCTTCCTGCGCATGATTTAA 172
Db 24 CTTCCTTCCTGCGCATGATTTAA 1

RESULT 82
US-10-956-157-55284/C
; Sequence 55284, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55284
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-55284

Query Match 7.5%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 52;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 150 TTCTCCTTCCTGCGCATGATTTAA 173
Db 25 TTCTCCTTCCTGCGCATGATTTAA 2

RESULT 83
US-10-956-157-123288
; Sequence 123288, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 123288
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-123288

Query Match 7.5%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 52;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 21 ATCCCTCATGATGTTAGTCC 44
Db 21 ATCCCTCATGATGTTAGTCC 44

Db 1 ATTCCTCATGATGATTAATGCC 24

RESULT 84
US-10-956-157-199404
; Sequence 199404, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 199404
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-199404

Query Match 7.5%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 52;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 154 CTTCTGCGCATGATTTAAGATTC 177
Db 1 CTTCTGCGCATGATTTAAGATTC 24

RESULT 85
US-10-843-527-11826
; Sequence 11826, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: Eric Schell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT FILING DATE: 2004-05-10
; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 11826
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-11826

Query Match 7.5%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 52;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 137 CACCTGCTCCCCCTTCCTCTG 160
Db 2 CACCTGCTCCCCCTTCCTCTG 25

RESULT 86
US-10-843-527-224887/C
; Sequence 224887, Application US/10843527
; Publication No. US20050136395A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: Eric Schell
; TITLE OF INVENTION: Methods of Genetic Analysis of SARS Virus
; FILE REFERENCE: 3602.1
; CURRENT FILING DATE: 2004-05-10

```

; PRIOR APPLICATION NUMBER: 60/469,545
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 238196
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 224887
; LENGTH: 25
; TYPE: DNA
; ORGANISM: SARS Virus
US-10-843-527-224887

```

```

Query Match
Best Local Similarity 7.5%; Score 17.6; DB 1; Length 25;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

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Cy 137 CACCTGCTCCCTTCCTCTCTG 160
Db 24 CAACTCTTCTCTCTCTCTCTG 1

```

```

RESULT 87
US-10-932-182A-168000/c
; Sequence 168000, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 168000
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-168000

```

```

Query Match
Best Local Similarity 7.5%; Score 17.6; DB 1; Length 25;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

Cy 174 ATCCAGGAGCTTCACAAAGAGCA 197
Db 25 ATACCAGGAGCTGCACAAAGAGCA 2

```

```

RESULT 88
US-11-036-317-439119/c
; Sequence 439119, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 439119
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-439119

```

```

Query Match
Best Local Similarity 7.5%; Score 17.6; DB 1; Length 25;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Cy 83 TGTGTGAAGAGCCTGGCCCCCTC 106
Db 24 TATTGTAAGAGACTAGCCCTTC 1

```

```

RESULT 89
US-11-036-317-706660
; Sequence 706660, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 706660
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-706660

```

```

Query Match
Best Local Similarity 7.5%; Score 17.6; DB 1; Length 25;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

Cy 16 GGCAGATCCTCATGAGATGTTTA 39
Db 1 GGCAGATCTCTGAGATGTTTA 24

```

```

RESULT 90
US-11-036-317-986030/c
; Sequence 986030, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 986030
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-986030

```

```

Query Match
Best Local Similarity 7.5%; Score 17.6; DB 1; Length 25;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

Cy 37 TTAGTGCATCCCTTGATGATGA 60
Db 25 TGAATGTCGTCCTTGAGGATGA 2

```

```

RESULT 91
US-11-121-849-370/c
; Sequence 370, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma

```

```

; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 2004-05-03
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 370
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-370

Query Match          7.5%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 52;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy      12 TGGGGGCGATCCCTCATGATG 35
Db      25 TGGAGCGGATTCCTCATGATG 2

RESULT 92
US-11-121-849-588191
; Sequence 588191, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 588191
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-588191

Query Match          7.5%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 52;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy      141 TGCTCCCGCTCTCTTGGCAT 164
Db      2 TGCTTCCCTTCGTTCTGCCAT 25

RESULT 93
US-11-121-849-668370/c
; Sequence 668370, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 668370
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien

US-11-121-849-668370

Query Match          7.5%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 52;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy      12 TGGGGGCGATCCCTCATGATG 35
Db      25 TGGAGCGGATTCCTCATGATG 2

RESULT 94
US-11-121-849-668624/c
; Sequence 668624, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 668624
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-668624

Query Match          7.5%; Score 17.6; DB 1; Length 25;
Best Local Similarity 83.3%; Pred. No. 52;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy      12 TGGGGGCGATCCCTCATGATG 35
Db      25 TGGAGCGGATTCCTCATGATG 2

RESULT 95
US-11-083-784-292730/c
; Sequence 292730, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 292730
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-292730

Query Match          7.4%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 49;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```


Oy 110 TTCTCCTGCTCCACTCTT 128
Db 19 TTCTCCTGACCCACTCTT 1

RESULT 96

US-11-083-784-1546724/c
; Sequence 1546724, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1546724
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1546724

Query Match 7.4%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 49;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 150 TTCTCCTTTCGCCATGATT 168
Db 19 TTCACCTTTCGCCATGATT 1

RESULT 97

US-11-101-244-292730/c
; Sequence 292730, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 292730
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-292730

Query Match 7.4%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 49;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 110 TTCTCCTGCTCCACTCTT 128
Db 19 TTCTCCTGACCCACTCTT 1

RESULT 98

US-11-101-244-1546724/c
; Sequence 1546724, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1546724
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1546724

Query Match 7.4%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 49;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 150 TTCTCCTTTCGCCATGATT 168
Db 19 TTCACCTTTCGCCATGATT 1

RESULT 99

US-10-310-914A-1158279
; Sequence 1158279, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kiyazut
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1158279
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1158279

Query Match 7.4%; Score 17.4; DB 1; Length 20;
Best Local Similarity 57.9%; Pred. No. 50;
Matches 11; Conservative 7; Mismatches 1; Indels 0; Gaps 0;
Oy 22 TCCCTCATGATGTTAG 40
Db 1 UCCUUCAGAUUGUUAG 19

RESULT 100

```

US-10-310-914A-115919/c
; Sequence 115919, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 115919
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-115919

Query Match      7.3% Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 54;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 TGTCTGGGTCAATGGGCGCAGAT 22
Db      22 TATTGGGTCAATGGGCGCGAT 1

RESULT 101
US-10-310-914A-969089/c
; Sequence 969089, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 969089
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-969089

Query Match      7.3% Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 54;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      71 GTGAGAGCTGTTGTTGAAG 92
Db      22 GTGAGATCTGTTAGTTAAAG 1

RESULT 102
US-10-310-914A-1036172
; Sequence 1036172, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1036172
; LENGTH: 22

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```

; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1036172

Query Match      7.3% Score 17.2; DB 1; Length 22;
Best Local Similarity 59.1%; Pred. No. 54;
Matches 13; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY      103 CCTCTCATTCCTCCGCCAC 124
Db      1 CCUCUCUCUCUCGCCAAC 22

RESULT 103
US-10-310-914A-1087700/c
; Sequence 1087700, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1087700
; LENGTH: 22
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1087700

Query Match      7.3% Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 54;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      24 CCTCATGAATGTTAGTCCCA 45
Db      22 CCTCAGATGATTAATGCCA 1

RESULT 104
US-10-310-914A-273857/c
; Sequence 273857, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 273857
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-273857

Query Match      7.3% Score 17.2; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 55;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      137 CACCGCTCCCTTCCTTC 158
Db      23 CACTCTTCCCTTCCTTC 2

RESULT 105
US-10-310-914A-1158269

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; Sequence 1158289, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kvuazt
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1158289
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1158289

Query Match
Best Local Similarity 7.3%; Score 17.2; DB 1; Length 23;
Matches 12; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 157 TCTGCCATGATTTTAAAGATTC 178
DB 1 UCUGCCAUAGAUUGUAAAGUACC 22

RESULT 106
US-10-310-914A-32934/c
; Sequence 32934, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kvuazt
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32934
; LENGTH: 24
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-32934

Query Match
Best Local Similarity 7.3%; Score 17.2; DB 1; Length 24;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 71 GTGAGAGCTGCTGTTGAAG 92
DB 22 GTGGAGATCTGCTTTAAAG 1

RESULT 107
US-10-310-914A-66335
; Sequence 66335, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kvuazt
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 66335
; LENGTH: 24
; TYPE: RNA

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```

; ORGANISM: Human
US-10-310-914A-66335

Query Match
Best Local Similarity 7.3%; Score 17.2; DB 1; Length 24;
Matches 13; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 73 GAGAGCTGCTGTTTGAAGAG 94
DB 3 GAGATUCGUGUUGUAAAAGUC 24

RESULT 108
US-10-298-953-44
; Sequence 44, Application US/10298953
; Publication No. US20040097444A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF SERINE/THREONINE KINASE 16 EXPRESSION
; FILE REFERENCE: HTS-0109
; CURRENT APPLICATION NUMBER: US/10/298,953
; CURRENT FILING DATE: 2002-11-16
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 44
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-298-953-44

Query Match
Best Local Similarity 7.1%; Score 16.8; DB 1; Length 20;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 106 CTCATTCTCCTGCTCCACT 125
DB 1 CACATTCCTCCTGCTCCACT 20

RESULT 109
US-10-310-914A-661149/c
; Sequence 661149, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kvuazt
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 661149
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-661149

Query Match
Best Local Similarity 7.1%; Score 16.8; DB 1; Length 20;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 68 CACGTGAGAGCTGCTGTTT 87
DB 20 CTCGTGAGATCTGCTGTTT 1

RESULT 110
US-10-310-914A-845542/c
; Sequence 845542, Application US/10310914A
; Publication No. US20060003322A1

```

```

; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kyzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 845542
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-845542

Query Match      7.1%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      146 CCCCTTCCTTCCTTCGCGATG 165
Db      20 CCCCTTCGCTTCCTTCGCGCTG 1

RESULT 111
US-10-310-914A-1073095/c
; Sequence 1073095, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kyzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1073095
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1073095

Query Match      7.1%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      140 CTGCTCCCTTCCTTCCTTCT 159
Db      20 CTGCTCCCTTCCTTCCTTCT 1

RESULT 112
US-10-310-914A-1242020/c
; Sequence 1242020, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kyzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1242020
; LENGTH: 20
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1242020

Query Match      7.1%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      140 CTGCTCCCTTCCTTCCTTCT 159
Db      20 CTGCTCCCTTCCTTCCTTCT 1

RESULT 113
US-10-847-918-1184/c
; Sequence 1184, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847.918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1184
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi-sense strand
US-10-847-918-1184

Query Match      7.1%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 59;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      171 AAGATTCAGGAGCTTCACA 190
Db      20 AAGATTCAGGAGCTTCACA 1

RESULT 114
US-10-847-918-1853/c
; Sequence 1853, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847.918
; CURRENT FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; PRIOR FILING DATE: 2003-05-20
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1853
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi-sense strand
US-10-847-918-1853

Query Match      7.1%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 59;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      171 AAGATTCAGGAGCTTCACA 190
Db      20 AAGATTCAGGAGCTTCACA 190

US-10-310-914A-1242020
```

```
Db          20 AAGATTCAGGCGCTTCACA 1

RESULT 115
US-10-847-918-1942/c
; Sequence 1942, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; PRIOR FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1942
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-847-918-1942

Query Match          7.1%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 59;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy          149 CTTCCTCTGCGCATGATT 168
Db          20 CTCTGTCTGCGCATGATT 1

RESULT 116
US-10-847-918-1944
; Sequence 1944, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
; APPLICANT: Wyeeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; PRIOR FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1944
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAI-antisense strand
US-10-847-918-1944

Query Match          7.1%; Score 16.8; DB 1; Length 21;
Best Local Similarity 45.0%; Pred. No. 59;
Matches 9; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

Cy          149 CTTCCTCTGCGCATGATT 168
Db          2 CUCUCUCUCGCGCAUGAUU 21

RESULT 117
US-10-847-918-2092/c
; Sequence 2092, Application US/10847918
; Publication No. US20050119210A1

; GENERAL INFORMATION:
; APPLICANT: Wyeeth
; APPLICANT: Be, Xiaobing
; APPLICANT: Liu, Wei
; APPLICANT: Slonim, Donna
; APPLICANT: Howes, Steve
; TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
; FILE REFERENCE: 031896-026000 (AM101264)
; CURRENT APPLICATION NUMBER: US/10/847,918
; PRIOR FILING DATE: 2004-05-19
; PRIOR APPLICATION NUMBER: US 60/471,729
; NUMBER OF SEQ ID NOS: 14937
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2092
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-847-918-2092

Query Match          7.1%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 59;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy          150 TTCTCCTCTGCGCATGATT 169
Db          21 TTCTGTCTGCGCATGATT 2

RESULT 118
US-10-310-914A-828967/c
; Sequence 828967, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzaat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 828967
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-828967

Query Match          7.1%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 59;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Cy          139 CCGCTCCCTCTCTCTCTTC 158
Db          20 CCGCTCCCTCTCTCTCTTC 1

RESULT 119
US-10-310-914A-1009274/c
; Sequence 1009274, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiler, Kvuzaat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1009274
```

LENGTH: 21
TYPE: RNA
ORGANISM: Human
US-10-914A-1009274

Query Match 7.1% Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 59;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 179 AGGACTTCACAGAGCA 198
Db 20 AGGACTTCACAGAGCA 1

RESULT 120
US-10-310-914A-1371246/c
Sequence 1371246, Application US/10310914A
Publication No. US2006000322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shlier, Kyzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1371246
LENGTH: 21
TYPE: RNA
ORGANISM: Human
US-10-310-914A-1371246

Query Match 7.1% Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 59;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 137 CACCTGCTCCCTCTCTCT 156
Db 20 CTCCTGATCCCCCTCTCT 1

RESULT 121
US-10-310-914A-74338/c
Sequence 74338, Application US/10310914A
Publication No. US2006000322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shlier, Kyzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A
CURRENT FILING DATE: 2002-12-06
NUMBER OF SEQ ID NOS: 1388402
SOFTWARE: PatentIn version 3.3
SEQ ID NO 74338
LENGTH: 23
TYPE: RNA
ORGANISM: Human
US-10-310-914A-74338

Query Match 7.1% Score 16.8; DB 1; Length 23;
Best Local Similarity 90.0%; Pred. No. 61;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 208 CCAGCTCTGTTCTGCT 227
Db 22 CCAGCTCTGTTCTGCT 3

RESULT 122

US-10-416-122-2
Sequence 2, Application US/10416122
Publication No. US20040072199A1
GENERAL INFORMATION:
APPLICANT: Brem, Gottfried
TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF
FILE REFERENCE: KLAUS1.001APC
CURRENT APPLICATION NUMBER: US/10/416,122
CURRENT FILING DATE: 2003-10-24
PRIOR APPLICATION NUMBER: PCT/EP01/12880
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: DE 100 55 368.0
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic oligonucleotide
US-10-416-122-2

Query Match 7.1% Score 16.8; DB 1; Length 24;
Best Local Similarity 90.0%; Pred. No. 61;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 140 CTGCTCCCTCTCTCTCTCT 159
Db 5 CTGCTCCCTCTCTCTCTCT 24

RESULT 123
US-10-708-204-3803
Sequence 3803, Application US/10708204
Publication No. US2005022399A1
GENERAL INFORMATION:
APPLICANT: ROSETTA GENOMICS LTD
TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
FILE REFERENCE: 55033
CURRENT APPLICATION NUMBER: US/10/708,204
CURRENT FILING DATE: 2004-02-16
NUMBER OF SEQ ID NOS: 7351
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3803
LENGTH: 23
TYPE: RNA
ORGANISM: Homo Sapiens
US-10-708-204-3803

Query Match 7.0% Score 16.6; DB 1; Length 23;
Best Local Similarity 65.2%; Pred. No. 64;
Matches 15; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 57 ATGAGTGAGTTCACGTGAGAGCT 79
Db 1 AUCAGUGAGCUCACGAGAGAGCU 23

RESULT 124
US-10-310-914A-287417/c
Sequence 287417, Application US/10310914A
Publication No. US2006000322A1
GENERAL INFORMATION:
APPLICANT: Bentwich, Isaac
APPLICANT: Shlier, Kyzat
TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
FILE REFERENCE: 06087.0200.CPUS01
CURRENT APPLICATION NUMBER: US/10/310,914A

```

; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patentln version 3.3
; SEQ ID NO 287417
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-287417

```

```

Query Match
Best Local Similarity 82.6%; Pred. No. 64; Length 23;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

Qy 100 CCCCCTCTCATCTCTGCTCC 122
Db 23 CCACCCCTCTTCTCCGGCTCCC 1

```

```

RESULT 125
US-10-310-914A-360372/C
; Sequence 360372, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patentln version 3.3
; SEQ ID NO 360372
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-360372

```

```

Query Match
Best Local Similarity 82.6%; Pred. No. 64; Length 23;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

Qy 102 CCCTCTCATCTCTGCTCCAC 124
Db 23 CCCTCTCTTCTCCCTCTCCCCC 1

```

```

RESULT 126
US-10-310-914A-651766/C
; Sequence 651766, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patentln version 3.3
; SEQ ID NO 651766
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-651766

```

```

Query Match
Best Local Similarity 82.6%; Pred. No. 64; Length 23;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 65 GTTCACTGAGAGCTGTTGTTT 87
|||||

```

```

Db 23 GTTCTCATGAGATCTGTTTTTT 1

```

```

RESULT 127
US-10-310-914A-819312/C
; Sequence 819312, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patentln version 3.3
; SEQ ID NO 819312
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-819312

```

```

Query Match
Best Local Similarity 82.6%; Pred. No. 64; Length 23;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

Qy 103 CCTCTCATCTCTGCTCCACT 125
Db 23 CCTCTCATCTCTCCCTCCCAAT 1

```

```

RESULT 128
US-10-310-914A-967480/C
; Sequence 967480, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patentln version 3.3
; SEQ ID NO 967480
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-967480

```

```

Query Match
Best Local Similarity 82.6%; Pred. No. 64; Length 23;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

Qy 65 GTTCACTGAGAGCTGTTGTTT 87
Db 23 GTTCTCATGAGATCTGTTTTTT 1

```

```

RESULT 129
US-10-310-914A-1186008/C
; Sequence 1186008, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kvuza
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06

```

```
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 1186008
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1186008
```

```
Query Match          7.0%; Score 16.6; DB 1; Length 23;
Best Local Similarity 82.6%; Pred. No. 64;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      76 AGCTGCTGTTGAAGAGAGCCG 98
Db      23 AGACGCTGTTTAAAGAGCTCG 1
```

```
RESULT 130
US-10-310-914A-115988/C
; Sequence 115988, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 115988
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-115988
```

```
Query Match          6.9%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 62;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      75 GAGCTGCTGTTGTTGAAG 92
Db      18 GAGCTGCTGTTGTTAAAG 1
```

```
RESULT 131
US-10-310-914A-1053329/C
; Sequence 1053329, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 1053329
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1053329
```

```
Query Match          6.9%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 62;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      146 CCCCTTCTCTCTTGCCA 163
Db      18 CCCCTTCTCTCTTGCCA 1
```

```
RESULT 132
US-10-727-780A-425/C
; Sequence 425, Application US/10727780A
; Publication No. US20050233329A1
; GENERAL INFORMATION:
; APPLICANT: Vaish, Narendra
; APPLICANT: Zimen, Shawn
; APPLICANT: McSwigen, James
; APPLICANT: Sirna Therapeutics, Inc.
; TITLE OF INVENTION: Inhibition of Gene Expression Using Duplex Forming
; FILE REFERENCE: 03-1070 (400.139)
; CURRENT APPLICATION NUMBER: US/10/727.780A
; CURRENT FILING DATE: 2003-12-03
; NUMBER OF SEQ ID NOS: 772
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 425
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence
US-10-727-780A-425
```

```
Query Match          6.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 63;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      148 CCTTCTCTCTTGCCAG 165
Db      19 CCTTCTCTCTTGCCAG 2
```

```
RESULT 133
US-10-310-914A-1053330/C
; Sequence 1053330, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310.914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 1053330
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1053330
```

```
Query Match          6.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 63;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      146 CCCCTTCTCTCTTGCCA 163
Db      18 CCCCTTCTCTCTTGCCA 1
```

```
RESULT 134
US-11-083-784-134328/C
; Sequence 134328, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
```



```
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ PRIOR FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 134328
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-134328
```

```
Query Match      6.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 63;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      107 TCATTCCTGCTGCCAC 124
Db      19 TCATTCCTGCTGCCAC 2
```

```
RESULT 135
US-11-083-784-134365/c
/ Sequence 134365, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ PRIOR FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 134365
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-134365
```

```
Query Match      6.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 63;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      105 TCTCATTCCTGCTCCC 122
Db      18 TCTCATTCCTGCTCCC 1
```

```
RESULT 136
US-11-083-784-863172/c
/ Sequence 863172, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
```

```
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ PRIOR FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 863172
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-863172
```

```
Query Match      6.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 63;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      105 TCTCATTCCTGCTCCC 122
Db      19 TCTCATTCCTGCTCCC 2
```

```
RESULT 137
US-11-083-784-914575/c
/ Sequence 914575, Application US/11083784
/ Publication No. US20050245475A1
/ GENERAL INFORMATION:
/ APPLICANT: Dharmacon, Inc.
/ APPLICANT: Khvorova, Anastasia
/ APPLICANT: Reynolds, Angela
/ APPLICANT: Leake, Devin
/ APPLICANT: Marshall, William
/ APPLICANT: Scaringe, Stephen
/ TITLE OF INVENTION: Functional and Hyperfunctional siRNA
/ FILE REFERENCE: 13499US
/ CURRENT APPLICATION NUMBER: US/11/083,784
/ PRIOR FILING DATE: 2005-03-18
/ PRIOR APPLICATION NUMBER: US/10/714,333
/ PRIOR FILING DATE: 2003-11-14
/ PRIOR APPLICATION NUMBER: 60/502,050
/ PRIOR FILING DATE: 2003-09-10
/ PRIOR APPLICATION NUMBER: 60/426,137
/ PRIOR FILING DATE: 2002-11-14
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 914575
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-914575
```

```
Query Match      6.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 63;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      150 TTCTCCTTCTGCCATGAT 167
Db      19 TTCTCCTTCTGCCATGAT 2
```

```
RESULT 138
US-11-083-784-1250582
/ Sequence 1250582, Application US/11083784
```

```
Publication No. US20050245475A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/083,784
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: US/10/714,333
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 1250582
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-083-784-1250582
```

```
Query Match 6.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 55.6%; Pred. No. 63;
Matches 10; Conservative 7; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy 70 CGTGAGAGCTGGTGT 87
Db 1 CGUGAGUCGUGUUU 18
```

```
RESULT 139
US-11-101-244-134328/c
Sequence 134328, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 134328
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-134328
```

```
Query Match 6.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 63;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy 107 TCATTCCTGCTCCAC 124
Db 19 TCATTCCTGCTCCAC 2
```

```
RESULT 140
US-11-101-244-134365/c
```

```
Sequence 134365, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 134365
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-134365
```

```
Query Match 6.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 63;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy 105 TCTCATTCCTGCTCCC 122
Db 18 TCTCATTCCTGCTCCC 1
```

```
RESULT 141
US-11-101-244-863172/c
Sequence 863172, Application US/11101244
Publication No. US20050246794A1
GENERAL INFORMATION:
APPLICANT: Dharmacon, Inc.
APPLICANT: Khvorova, Anastasia
APPLICANT: Reynolds, Angela
APPLICANT: Leake, Devin
APPLICANT: Marshall, William
APPLICANT: Scaringe, Stephen
TITLE OF INVENTION: Functional and Hyperfunctional siRNA
FILE REFERENCE: 13499US
CURRENT APPLICATION NUMBER: US/11/101,244
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: 60/502,050
PRIOR FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: 60/426,137
PRIOR FILING DATE: 2002-11-14
NUMBER OF SEQ ID NOS: 1591911
SOFTWARE: Proprietary
SEQ ID NO 863172
LENGTH: 19
TYPE: RNA
ORGANISM: Homo sapiens
US-11-101-244-863172
```

```
Query Match 6.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 63;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Oy 105 TCTCATTCCTGCTCCC 122
Db 19 TCTCATTCCTGCTCCC 2
```

```
RESULT 142
US-11-101-244-914575/c
Sequence 914575, Application US/11101244
```

```
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scarsdale, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 914575
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-914575

Query Match          6.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 63;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      150 TTCTCTTCTGCGCATGAT 167
Db      19  TTTCTCTTCTGCGCATGAT 2

RESULT 143
US-11-101-244-1250582
; Sequence 1250582, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scarsdale, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1250582
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1250582

Query Match          6.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 55.6%; Pred. No. 63;
Matches 10; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

OY      70 CGTGAGACCTGCTGTTT 87
Db      1  CGUGAGACUCGUGUGUUU 18

RESULT 144
US-10-310-914A-313831
; Sequence 313831, Application US/10310914A
; Publication No. US20060003322A1

; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyaz
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 313831
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-313831

Query Match          6.9%; Score 16.4; DB 1; Length 21;
Best Local Similarity 61.1%; Pred. No. 65;
Matches 11; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

OY      140 CTGCTCCCTCTCTCCTT 157
Db      3  CUGCUCCTCCCTCUCCTCU 20

RESULT 145
US-10-708-204-3346/C
; Sequence 3346, Application US/10708204
; Publication No. US2005022399A1
; GENERAL INFORMATION:
; APPLICANT: ROSETTA GENOMICS LTD
; TITLE OF INVENTION: BIOINFORMATIALLY DETECTABLE GROUP OF NOVEL REGULATORY
; TITLE OF INVENTION: OLIGONUCLEOTIDES ASSOCIATED WITH ALZHEIMER'S DISEASE AND USES
; FILE REFERENCE: 55033
; CURRENT APPLICATION NUMBER: US/10/708,204
; CURRENT FILING DATE: 2004-02-16
; NUMBER OF SEQ ID NOS: 7351
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 3346
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-10-708-204-3346

Query Match          6.9%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 68;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      135 GACACCTGCTCCCTTCTCC 155
Db      21  GACCCCTGTTCTCCCTTCTCC 1

RESULT 146
US-10-310-914A-59888/C
; Sequence 59888, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kiyaz
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 59888
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-59888
```

```
Query Match      6.9%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 68;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      94 GCCTGCCCCCTCTCATTTCTC 114
DB      21 GCCTGACCCCCCTCTTCTC 1

RESULT 147
US-10-310-914A-95531/c
; Sequence 95531, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 95531
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-95531

Query Match      6.9%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 68;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY      142 GCTCCCTCTCTCTCTGCCC 162
DB      21 GCTCCACTCTCTCTCTGCC 1

RESULT 148
US-10-310-914A-174457
; Sequence 174457, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 174457
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-174457

Query Match      6.9%; Score 16.2; DB 1; Length 21;
Best Local Similarity 57.1%; Pred. No. 68;
Matches 12; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY      79 TGGTTGTTTGAAGAGCCTCG 99
DB      1 UGGGUCUUUGAAGAGCCTCG 21

RESULT 149
US-10-310-914A-612161
; Sequence 612161, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 612161
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-612161

Query Match      6.9%; Score 16.2; DB 1; Length 21;
Best Local Similarity 57.1%; Pred. No. 68;
Matches 12; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY      24 CCTCATGATGTTAGTGGC 44
DB      1 CCUCAGAAUAGCUCUGGCC 21

RESULT 150
US-10-310-914A-628516
; Sequence 628516, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 628516
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-628516

Query Match      6.9%; Score 16.2; DB 1; Length 21;
Best Local Similarity 57.1%; Pred. No. 68;
Matches 12; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY      108 CATTCCTGCTCCACTCTT 128
DB      1 CAGGUCCTGCTCCACTCTT 21

RESULT 151
US-10-310-914A-969044/c
; Sequence 969044, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kyuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 969044
; LENGTH: 21
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-969044
```


FILE REFERENCE: 21402-290C

1 CURRENT FILING DATE: 2002-03-07
 2 PRIOR APPLICATION NUMBER: USSN 60/274,322
 3 PRIOR FILING DATE: 2001-03-08

PRIOR APPLICATION NUMBER: USSN 60/338,092

```

? PRIOR FILING DATE: 2001-12-03
? PRIOR APPLICATION NUMBER: USSN 60/274,281
? PRIOR FILING DATE: 2001-03-08
? PRIOR APPLICATION NUMBER: USSN 60/274,191
? PRIOR FILING DATE: 2001-03-08
? PRIOR APPLICATION NUMBER: USSN 60/325,681
? PRIOR FILING DATE: 2001-09-27
? PRIOR APPLICATION NUMBER: USSN 60/304,354
? PRIOR FILING DATE: 2001-07-10
? PRIOR APPLICATION NUMBER: USSN 60/279,995
? PRIOR FILING DATE: 2001-03-30
? PRIOR APPLICATION NUMBER: USSN 60/294,899
? PRIOR FILING DATE: 2001-05-31
? PRIOR APPLICATION NUMBER: USSN 60/287,424
? PRIOR FILING DATE: 2001-04-30
? Remaining Prior Application data removed - See File Wrapper or PALM.
? NUMBER OF SEQ ID NOS: 768
? SEQ ID NO 521

```

```

: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:

```

US-10-092-900A-521	-	-
Query Match	6.9%	Score 16.2; DB 1; Length 23;

100 CCCCCCTCATTTCTCCGCTC 120

[illegible]

```
US-10-310-914A-1171021/c
; Sequence 1171021, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1171021
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1171021
```

```
Query Match          6.9%; Score 16.2; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 70;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      154 CTTCTGCCATGATTTAAGA 174
          ||||| ||||| |||||
Db       21 CCTTCTACATGACTGTAGA 1
```

```
RESULT 161
US-10-310-914A-1037134/c
; Sequence 1037134, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shlier, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; FILE REFERENCE: 06087.0200.CPUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1037134
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1037134
```

```
Query Match          6.8%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      143 CTCGCCCTTCCTCTTC 158
          ||||| ||||| |||||
Db       18 CTCGCCCTTCCTCTTC 3
```

```
RESULT 162
US-11-083-784-508230/c
; Sequence 508230, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
```

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; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 508230
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-508230
```

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Query Match          6.8%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      105 TCTCATTTCTCTGCTC 120
          ||||| ||||| |||||
Db       19 TCTCATTTCTCTGCTC 4
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```
RESULT 163
US-11-101-244-508230/c
; Sequence 508230, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 508230
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-508230
```

```
Query Match          6.8%; Score 16; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      105 TCTCATTTCTCTGCTC 120
          ||||| ||||| |||||
Db       19 TCTCATTTCTCTGCTC 4
```

```
RESULT 164
US-09-791-942-85
; Sequence 85, Application US/09791942
; Patent No. US2002014716A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Robert Kothlein
; APPLICANT: Takashi Kei Kishimoto
; APPLICANT: Lex M. Cowseart
; TITLE OF INVENTION: ANTISENSE MODULATION OF TALIN EXPRESSION
; FILE REFERENCE: RTS-0099
; CURRENT APPLICATION NUMBER: US/09/791,942
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 85
```

```
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Antisense Oligonucleotide
US-09-791-942-85
```

```
Query Match          6.8%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      105 TCTCATTCCTGCTC 120
          |||||
Db      3 TCTCATTCCTGCTC 18
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```
RESULT 165
US-10-415-463-85
/ Sequence 85, Application US/10415463
/ Publication No. US20040110705A1
/ GENERAL INFORMATION:
/ APPLICANT: Isis Pharmaceuticals, Inc.
/ APPLICANT: C. Frank Bennett
/ TITLE OF INVENTION: ANTISENSE MODULATION OF TALIN EXPRESSION
/ FILE REFERENCE: RSP-0198
/ CURRENT APPLICATION NUMBER: US/10/415,463
/ CURRENT FILING DATE: 2003-11-13
/ PRIOR APPLICATION NUMBER: 09/702,251
/ PRIOR FILING DATE: 2000-10-30
/ NUMBER OF SEQ ID NOS: 89
/ SEQ ID NO 85
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Antisense Oligonucleotide
US-10-415-463-85
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```
Query Match          6.8%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      105 TCTCATTCCTGCTC 120
          |||||
Db      3 TCTCATTCCTGCTC 18
```

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RESULT 166
US-10-476-264-285/C
/ Sequence 285, Application US/10476264
/ Publication No. US20050123910A1
/ GENERAL INFORMATION:
/ APPLICANT: Cookson, William Omond Charles Michael
/ APPLICANT: Moffat, Miriam Fleur
/ APPLICANT: Allen, Maxine
/ APPLICANT: Lench, Nick
/ TITLE OF INVENTION: Enzyme and SNP marker for disease
/ FILE REFERENCE: 16721-002US1
/ CURRENT APPLICATION NUMBER: US/10/476,264
/ CURRENT FILING DATE: 2003-10-24
/ PRIOR APPLICATION NUMBER: PCT/GB02/01887
/ PRIOR FILING DATE: 2002-04-24
/ PRIOR APPLICATION NUMBER: GB0110044.5
/ PRIOR FILING DATE: 2001-04-24
/ PRIOR APPLICATION NUMBER: GB0110046.0
/ PRIOR FILING DATE: 2001-04-24
/ PRIOR APPLICATION NUMBER: GB0124594.3
/ PRIOR FILING DATE: 2001-10-12
/ PRIOR APPLICATION NUMBER: GB0124575.2
/ PRIOR FILING DATE: 2001-10-12
/ NUMBER OF SEQ ID NOS: 421
/ SOFTWARE: PatentIn version 3.1
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/ SEQ ID NO 285
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Primer
US-10-476-264-285
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Query Match          6.8%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      191 AGAGCAATGCTAAC 206
          |||||
Db      18 AGAGCAATGCTAAC 3
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RESULT 167
US-10-310-914A-1037133/C
/ Sequence 1037133, Application US/10310914A
/ Publication No. US20060003322A1
/ GENERAL INFORMATION:
/ APPLICANT: Bentwich, Isaac
/ APPLICANT: Shlier, Kyuzat
/ TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
/ FILE REFERENCE: 06087,0200.CPUS01
/ CURRENT APPLICATION NUMBER: US/10/310,914A
/ CURRENT FILING DATE: 2002-12-06
/ NUMBER OF SEQ ID NOS: 138402
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 1037133
/ LENGTH: 22
/ TYPE: RNA
/ ORGANISM: Human
US-10-310-914A-1037133
```

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Query Match          6.8%; Score 16; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      143 CTCCCCCTTCCTTC 158
          |||||
Db      19 CTCCCCCTTCCTTC 4
```

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Search completed: October 2, 2006, 15:43:17
Job time : 0.001 secs
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